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OM nucleic - nucleic search, using sw model

Run on: February 4, 2006, 15:40:16 ; Search time 2893 Seconds
(without alignments)
18733.937 Million cell updates/sec

Title: US-10-723-552-3
Perfect score: 8132
Sequence: 1 GCGTGGTGACGACTGGGG.....CTGTTGTCATCAAAAAAAA 8132

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4996997 seqs, 3332346308 residues

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N Geneseq 21:*

- 1: geneseqn1980s:*
- 2: geneseqn1990s:*
- 3: geneseqn2000s:*
- 4: geneseqn2001as:*
- 5: geneseqn2001bs:*
- 6: geneseqn2002as:*
- 7: geneseqn2002bs:*
- 8: geneseqn2003as:*
- 9: geneseqn2003bs:*
- 10: geneseqn2003cs:*
- 11: geneseqn2003ds:*
- 12: geneseqn2004as:*
- 13: geneseqn2004bs:*
- 14: geneseqn2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	8132	100.0	8132	4	AAF77727
2	8132	100.0	8132	12	ADK43414
3	8132	100.0	8132	13	ADK43414
4	7860	96.7	7892	2	AA74884
5	6931.2	85.2	8918	6	ABQ76883
6	6832.4	84.0	8918	6	ABQ76885
7	6531.8	80.3	7873	4	AA77725
8	6319	77.7	8763	6	ABQ76884
9	6288.8	77.3	8840	6	ABQ76886
10	6282.4	77.3	8209	2	AAV09700
11	6248.8	76.8	8196	2	AAV09699
12	6174.6	75.9	7362	4	AA77725
13	5460	67.1	8060	2	AA77725
14	5460	67.1	8060	12	ADK43412
15	5460	67.1	8060	13	ADK43412
16	5374	66.1	6076	4	AA77725
17	5374	66.1	6076	4	AA77725
18	5374	66.1	6076	4	AA77725
19	4970.8	61.1	7333	4	AA77726

20	4970.8	61.1	7333	12	ADK43413
21	4970.8	61.1	7333	13	ADK43413
22	4950.2	60.9	7333	2	AA774883
23	4042.4	49.7	4402	4	AA774883
24	3973.2	48.9	4918	4	AA774883
25	2915.2	35.8	3320	2	AAV09698
26	2237	27.5	8655	2	AAV09698
27	2237	27.5	8655	2	AAV09698
28	2176	26.8	8088	3	AAZ45540
29	2167.8	26.7	185548	13	ADK43413
30	2162.8	26.6	8535	2	AA77727
31	2113.2	26.0	215980	6	AA77727
32	2016.4	24.8	3482	2	AAV82749
33	1910.8	23.5	1923	14	ADY28027
34	1910.8	23.5	1923	14	ADY28027
35	1910.8	23.5	1923	14	ADY28027
36	1910.8	23.5	1923	14	ADY28027
37	1772.8	21.8	11384	10	ADH76479
38	1765	21.7	8889	10	ADH76472
39	1765	21.7	11394	10	ADH76473
40	1728.6	21.3	8202	2	AA77727
41	1722	21.2	2034	14	ADY28033
42	1722	21.2	2034	14	ADY28033
43	1692.4	20.8	8278	4	AA77725
44	1676.2	20.6	1959	8	AAV75053
45	1674.6	20.6	1959	8	AAV75054

ALIGNMENTS

RESULT 1

AAF77727
ID AAF77727 standard; DNA; 8132 BP.

XX AAF77727;

XX 23-MAY-2001 (first entry)

XX Nucleotide sequence of a retrovirus found in miniature swine.

XX Retrovirus; graft transplantation; xenotransplantation; miniature swine;
XX ss.

XX Unidentified.

XX US6190861-B1.

XX 20-FEB-2001.

XX 13-DEC-1996; 96US-00766528.

XX 14-DEC-1995; 95US-00572645.

XX (GEHO) GEN HOSPITAL CORP.

XX Fishman JA;

XX WPI; 2001-256211/26.

XX P-ESDB; AAF73285, AAF73286, AAF73287.

XX Assessing risk of endogenous retroviruses in clinical practice and in
XX xenotransplantation, comprises using probe sequences derived from swine
XX or miniature swine retroviral genome.

XX Claim 1; Fig 3; 127pp; English.

XX The present invention relates to a method for screening a cell or tissue
XX for the presence or expression of a retrovirus (RV), comprising
XX contacting a target nucleic acid from the cell or tissue with a second
XX nucleic acid from the present invention (e.g. the present sequence or a
XX fragment thereof). The method is useful for RV detection and to assess
XX graft transplantation risk. Screening of animals allows the elimination

CC of donors with active replication of known viruses. Inactive proviruses
CC can be detected and inactivated, allowing identification and elimination
CC of potential human pathogens derived from swine in a manner not possible
CC in the outbred human organ donor population and is important to the
CC development of human xenotransplantation
XX

SQ Sequence 8132 BP; 2248 A; 1977 C; 2037 G; 1870 T; 0 U; 0 Other;

Query Match		100.0%;	Score 8132;	DB 4;	Length 8132;
Best Local Similarity		100.0%;	Pred. No. 0;		
Matches 8132;		Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	GGGTGGTGACGACTGTGGGCCCCACGCGCTTGGAAATAAATCCTCTTGCTGTTTGCA	60		
DB	1	GGGTGGTGACGACTGTGGGCCCCACGCGCTTGGAAATAAATCCTCTTGCTGTTTGCA	60		
QY	61	TCGAAGCCGCTTCTCGTAGTGATTAAGGGAGTCGCCCTTTCCGAGCCTGGAGGTTCTT	120		
DB	61	TCGAAGCCGCTTCTCGTAGTGATTAAGGGAGTCGCCCTTTCCGAGCCTGGAGGTTCTT	120		
QY	121	TTTGCTGGCTTACATTTGGGGCTCGTCGGGATCTGTGCGGCCACCCCTAAACACCG	180		
DB	121	TTTGCTGGCTTACATTTGGGGCTCGTCGGGATCTGTGCGGCCACCCCTAAACACCG	180		
QY	181	AGAACCGACTTGGAGGTAAAAAGGATCCTCTTTTAAACGTGTATGCATGTACCGGCCGC	240		
DB	181	AGAACCGACTTGGAGGTAAAAAGGATCCTCTTTTAAACGTGTATGCATGTACCGGCCGC	240		
QY	241	GTCTCTGTTCTGAGTGTCTGTTTTCAGTGGTGGCGCTTTCGGTTTGCAGCTGCTCTC	300		
DB	241	GTCTCTGTTCTGAGTGTCTGTTTTCAGTGGTGGCGCTTTCGGTTTGCAGCTGCTCTC	300		
QY	301	AGSCCGTAAAGGCTGGGGACTGTGATCAGCAGCTGTCTAGGAGTACACAGCTGCTG	360		
DB	301	AGSCCGTAAAGGCTGGGGACTGTGATCAGCAGCTGTCTAGGAGTACACAGCTGCTG	360		
QY	361	CCCTGGGGACGCCCCGGGAGGTGAGGAGACGAGGACGCTTGGTCTCCTACTGTC	420		
DB	361	CCCTGGGGACGCCCCGGGAGGTGAGGAGACGAGGACGCTTGGTCTCCTACTGTC	420		
QY	421	GGTCAGAGACCGAAATTCGTTGCTGAAGGAAAGCTTCCCTCCGAGACCGTCCGACT	480		
DB	421	GGTCAGAGACCGAAATTCGTTGCTGAAGGAAAGCTTCCCTCCGAGACCGTCCGACT	480		
QY	481	CTTTTCGCTGCTTGTGGAAGCCTGACGGGTCACTGTGCTGTGGATCTGTTGGTTCTG	540		
DB	481	CTTTTCGCTGCTTGTGGAAGCCTGACGGGTCACTGTGCTGTGGATCTGTTGGTTCTG	540		
QY	541	TTTTGTGTGCTTTGTGTCTTGTCTACAGTTTAAATATGGGACAGACGGTGA	600		
DB	541	TTTTGTGTGCTTTGTGTCTTGTCTACAGTTTAAATATGGGACAGACGGTGA	600		
QY	601	CGACCCCTCTTAGTTGACTCTCGACATTTGGACTGAAGTTAAATCCAGGGCTCATATT	660		
DB	601	CGACCCCTCTTAGTTGACTCTCGACATTTGGACTGAAGTTAAATCCAGGGCTCATATT	660		
QY	661	TGTCAGTTCAGGTTAAGAGGGACCTTGGCAGACTTTCGTGTCTCTGAATGCCGACAT	720		
DB	661	TGTCAGTTCAGGTTAAGAGGGACCTTGGCAGACTTTCGTGTCTCTGAATGCCGACAT	720		
QY	721	TCGATGTTGGATGGCCATCAGAGGGGACCTTTAAATCTCGAGATTATCTCGGCTGTTAAAG	780		
DB	721	TCGATGTTGGATGGCCATCAGAGGGGACCTTTAAATCTCGAGATTATCTCGGCTGTTAAAG	780		
QY	781	CAGTTATTTTTCAGACTGGACCCGGCTCTCATCCCGATCAGGAGCCCTATATCCTTACGT	840		
DB	781	CAGTTATTTTTCAGACTGGACCCGGCTCTCATCCCGATCAGGAGCCCTATATCCTTACGT	840		
QY	841	GGCAGATTGGCAGAGGATCTCCCGCATGGGTTAAACCATGCTGAATTAAGCCAGAA	900		
DB	841	GGCAGATTGGCAGAGGATCTCCCGCATGGGTTAAACCATGCTGAATTAAGCCAGAA	900		
QY	901	AGCCAGGTCCCGAATTCGGCTCTTTGGAGAGAAAAACAAACACTCGGCTGAAAAAGTCA	960		

DB	901	AGCCAGGTCCCGAATTCGGCTCTTGGAGAGAAAAACAAACACTCGGCTGAAAAAGTCA	960		
QY	961	AGCCCTCTCTCATATCTACCCCGAGATTGAGAGCCACCGGCTTGGCCGGAACCCCAAT	1020		
DB	961	AGCCCTCTCTCATATCTACCCCGAGATTGAGAGCCACCGGCTTGGCCGGAACCCCAAT	1020		
QY	1021	CTGTTTCCCCACCCCTTATCTGGCACAGGGTCCCGAGAGGACCTTTGGCCCTCTCTG	1080		
DB	1021	CTGTTTCCCCACCCCTTATCTGGCACAGGGTCCCGAGAGGACCTTTTGCCCTCTCTG	1080		
QY	1081	GAGCTCCGCGGTGGAGGACCTGTGCAGGGACTCGAGCGCGAGGGCGCCACCCCG	1140		
DB	1081	GAGCTCCGCGGTGGAGGACCTGTGCAGGGACTCGAGCGCGAGGGCGCCACCCCG	1140		
QY	1141	AGCGGACAGACGAGATCGGCACATTAACCGCTCGCACGTACCGCCCTCCACACCGGGG	1200		
DB	1141	AGCGGACAGACGAGATCGGCACATTAACCGCTCGCACGTACCGCCCTCCACACCGGGG	1200		
QY	1201	GCCAAATTGACGCCCTTCCAGTATTGGCCCTTTTCTTCTGCAGATCTCTATAATTGAAA	1260		
DB	1201	GCCAAATTGACGCCCTTCCAGTATTGGCCCTTTTCTTCTGCAGATCTCTATAATTGAAA	1260		
QY	1261	CTAACCATCCCTTCTCGGAGGATCCCAAGGCTCACGGGTTGGTGGATCCCTTA	1320		
DB	1261	CTAACCATCCCTTCTCGGAGGATCCCAAGGCTCACGGGTTGGTGGATCCCTTA	1320		
QY	1321	TGTTCTCTCACAGCCTACTTGGGATGATTGTCAACAGCTGTGCAGACACTCTTACAA	1380		
DB	1321	TGTTCTCTCACAGCCTACTTGGGATGATTGTCAACAGCTGTGCAGACACTCTTACAA	1380		
QY	1381	CCGAGGAGCAGAGAGAAATTCATTAGAGCTAGAAAAAATGTTCTCGGGCCGACGGGC	1440		
DB	1381	CCGAGGAGCAGAGAGAAATTCATTAGAGCTAGAAAAAATGTTCTCGGGCCGACGGGC	1440		
QY	1441	GACCCACGCGGTGCAAAATGAGATTGACATGGGATTCCTTAACTCCGCCCGTTGGG	1500		
DB	1441	GACCCACGCGGTGCAAAATGAGATTGACATGGGATTCCTTAACTCCGCCCGTTGGG	1500		
QY	1501	ACTTACAAACGCTGAAGGTAGGAGAGCTTGAAAAATCTATCGCAGGCTCTGGTGGCGG	1560		
DB	1501	ACTTACAAACGCTGAAGGTAGGAGAGCTTGAAAAATCTATCGCAGGCTCTGGTGGCGG	1560		
QY	1561	GTCTCGGGGCGCTCAAGACCGGCCACTAAATTTGGCTAAGGTAAAGAAAGTATGCAGG	1620		
DB	1561	GTCTCGGGGCGCTCAAGACCGGCCACTAAATTTGGCTAAGGTAAAGAAAGTATGCAGG	1620		
QY	1621	GACCGAATGAACCCCTCTGTTTTTCTTGAGAGGCTCTTGGAGGCTTCAGGCGGTACA	1680		
DB	1621	GACCGAATGAACCCCTCTGTTTTTCTTGAGAGGCTCTTGGAGGCTTCAGGCGGTACA	1680		
QY	1681	CCCTTTTTCATCCCACTCAGAGGCCAAAAAGCCCTCAGTGGCTTTGGCCTTTATAGGAC	1740		
DB	1681	CCCTTTTTCATCCCACTCAGAGGCCAAAAAGCCCTCAGTGGCTTTGGCCTTTATAGGAC	1740		
QY	1741	AGTCAGCCTTTGGATATTAGAAAGAAAGCTTCAGAGACTGGAAGGTTTACAGGAGCTGAGT	1800		
DB	1741	AGTCAGCCTTTGGATATTAGAAAGAAAGCTTCAGAGACTGGAAGGTTTACAGGAGCTGAGT	1800		
QY	1801	TAGTGATCTAGTGAAGGCGCAGAAAAGTATTTACAAAAGGGAGACAGAGAAGAAA	1860		
DB	1801	TAGTGATCTAGTGAAGGCGCAGAAAAGTATTTACAAAAGGGAGACAGAGAAGAAA	1860		
QY	1861	GGGAACAAAGAAAGAGAGAGAAAGAGAGAAAGGAGGAGGAAAGAGCTATTAACGCAAG	1920		
DB	1861	GGGAACAAAGAAAGAGAGAGAAAGAGAGAAAGGAGGAGGAAAGAGCTATTAACGCAAG	1920		
QY	1921	AGAAGAAATTTGACTAAGATCTTGGCTGCAGTGGTTGAAAGGAAAAAGCAATACGGAAGAG	1980		
DB	1921	AGAAGAAATTTGACTAAGATCTTGGCTGCAGTGGTTGAAAGGAAAAAGCAATACGGAAGAG	1980		
QY	1981	AGGAGATTTTAGGAAAAATTAGTTCAGGCCCTAGACAGTCAAGGACCTGGGCAATAGGA	2040		

1981 AGAGAGATTTAGGAAAAATTAGTCTAGGCGCTTAGACAGTCAAGGAACTCTGGCAATAGGA 2040 Db
2041 CCCCACTCGACAGGACCAATGTGCATATTGTAAAGAAAGAGACACTGGGCAAGAACT 2100 Qy
2041 CCCCACTCGACAGGACCAATGTGCATATTGTAAAGAAAGAGACACTGGGCAAGAACT 2100 Db
2101 GCCCAAGAGGGAACAAAGGACCAAGGATCTCTAGTCTCTAGAGAGAGATAAAGATTAGG 2160 Qy
2101 GCCCAAGAGGGAACAAAGGACCAAGGATCTCTAGTCTCTAGAGAGAGATAAAGATTAGG 2160 Db
2161 GGAGACGGGGTTCGGACCCCTCCCGAGCCCAAGGTAACCTTTGAAGGTGGAGGGCAAC 2220 Qy
2161 GGAGACGGGGTTCGGACCCCTCCCGAGCCCAAGGTAACCTTTGAAGGTGGAGGGCAAC 2220 Db
2221 CAGTTGAGTTCCTGGTTGATACCGGAGCGGAAACATTCAGTGTCTACTACAGCCATTAGGAA 2280 Qy
2221 CAGTTGAGTTCCTGGTTGATACCGGAGCGGAAACATTCAGTGTCTACTACAGCCATTAGGAA 2280 Db
2281 AACTAAAGATATAAATACTCTGGGTGATGGGTGCTCCAGGCGCAACACAGTATCCATGGA 2340 Qy
2281 AACTAAAGATATAAATACTCTGGGTGATGGGTGCTCCAGGCGCAACACAGTATCCATGGA 2340 Db
2341 CTACCCGGAAGACAGTTGACTTGGGAGTGGGACGGGTAAACCCACTCGTTTCTGGTCAATAC 2400 Qy
2341 CTACCCGGAAGACAGTTGACTTGGGAGTGGGACGGGTAAACCCACTCGTTTCTGGTCAATAC 2400 Db
2401 CTGAGTCCCGACAGCCCTCTTAGGTAGAGACTTATTGACCAAGATGGGAGCAAAATTT 2460 Qy
2401 CTGAGTCCCGACAGCCCTCTTAGGTAGAGACTTATTGACCAAGATGGGAGCAAAATTT 2460 Db
2461 CTTTGAACAAAGGGAACCAAGAGTGTCTGCAATAACAAACCTTATCACTGTGTGACCC 2520 Qy
2461 CTTTGAACAAAGGGAACCAAGAGTGTCTGCAATAACAAACCTTATCACTGTGTGACCC 2520 Db
2521 TCCAAATTAGATGACGAATATCGACTATCTCTCCCTCTAGTAAAGCCCTGATCAAAATATAC 2580 Qy
2521 TCCAAATTAGATGACGAATATCGACTATCTCTCCCTCTAGTAAAGCCCTGATCAAAATATAC 2580 Db
2581 AATTCTGGTTGGAACAGTTTCCCAAGCCTGGGAGAGAAACCGCAGGATGGTTGGCAA 2640 Qy
2581 AATTCTGGTTGGAACAGTTTCCCAAGCCTGGGAGAGAAACCGCAGGATGGTTGGCAA 2640 Db
2641 AGCAAGTTCCTGAGTAAAGAGCTCAAGAGGAAATTCGGCCGCATGTCCAAAGATTAAATCC 2700 Qy
2641 AGCAAGTTCCTGAGTAAAGAGCTCAAGAGGAAATTCGGCCGCATGTCCAAAGATTAAATCC 2700 Db
2701 AGTACCCCTTGAGTAAAGAGCTCAAGAGGAAATTCGGCCGCATGTCCAAAGATTAAATCC 2760 Qy
2701 AGTACCCCTTGAGTAAAGAGCTCAAGAGGAAATTCGGCCGCATGTCCAAAGATTAAATCC 2760 Db
2761 AACAGGGCATCTAGTTCCTGTCCAAATCTCCCTGGAATATCTCCCTGTGTACCGGTTAGAA 2820 Qy
2761 AACAGGGCATCTAGTTCCTGTCCAAATCTCCCTGGAATATCTCCCTGTGTACCGGTTAGAA 2820 Db
2821 AGCCTGGGACTAATGACTATCGACAGTACAGGACTTGGAGAGAGTCAATAAACCGGTGC 2880 Qy
2821 AGCCTGGGACTAATGACTATCGACAGTACAGGACTTGGAGAGAGTCAATAAACCGGTGC 2880 Db
2881 AGGATATACACCCAAACAGTCCCGAACCTTATACCTCTTGTGTCTCTCCACCCCAAC 2940 Qy
2881 AGGATATACACCCAAACAGTCCCGAACCTTATACCTCTTGTGTCTCTCCACCCCAAC 2940 Db
2941 GGAGCTGGTATACAGTATTGACTTAAAGAGTGCCTTCTTCTGCTGTAGATTTACACCCCA 3000 Qy
2941 GGAGCTGGTATACAGTATTGACTTAAAGAGTGCCTTCTTCTGCTGTAGATTTACACCCCA 3000 Db
3001 CTAGCCAAACCACTTTTGGCTTCGATCGAGAGATCCAGGTAACCGGAGAAACCGGGCAGC 3060 Qy
3001 CTAGCCAAACCACTTTTGGCTTCGATCGAGAGATCCAGGTAACCGGAGAAACCGGGCAGC 3060 Db
3061 TCACCTGGACCCGACTCGCCCAAGGGTTCAAGAACTCCCGGACCATCTTTGACGAAGGCC 3120 Qy
3061 TCACCTGGACCCGACTCGCCCAAGGGTTCAAGAACTCCCGGACCATCTTTGACGAAGGCC 3120 Db

3121 TACACAGAGACCTGGCCAACTTTCAGGATCCAAACACCTCTCAGGTGACCTCTCTCCAGTAGC 3180 Qy
3121 TACACAGAGACCTGGCCAACTTTCAGGATCCAAACACCTCTCAGGTGACCTCTCTCCAGTAGC 3180 Db
3181 TGGATGACCTGCTTCTGGCGGGAGCCACCAACAGGACTGCTTTAGAGGCGACCAAGGCAC 3240 Qy
3181 TGGATGACCTGCTTCTGGCGGGAGCCACCAACAGGACTGCTTTAGAGGCGACCAAGGCAC 3240 Db
3241 TACTGCTGCAATTTGCTGACCTAGGCTACAGAGCCTCTGCTAAAGAGGCCAGATTGCA 3300 Qy
3241 TACTGCTGCAATTTGCTGACCTAGGCTACAGAGCCTCTGCTAAAGAGGCCAGATTGCA 3300 Db
3301 GGAGAGAGGTAAACATCTTTGGGGTA CAGTTTGGGGACGGGACGCGATGCGTACGAGG 3360 Qy
3301 GGAGAGAGGTAAACATCTTTGGGGTA CAGTTTGGGGACGGGACGCGATGCGTACGAGG 3360 Db
3361 CACGGAAGAAACTGTAGTCCAGATACCGGCCCCCAACCAACAGCCAAACAAATGAGAGGT 3420 Qy
3361 CACGGAAGAAACTGTAGTCCAGATACCGGCCCCCAACCAACAGCCAAACAAATGAGAGGT 3420 Db
3421 TTTTGGGGACAGCTGGATTGTCAGACTGTGGATCCCGGGTTTGGGACCTTAGCAGCCC 3480 Qy
3421 TTTTGGGGACAGCTGGATTGTCAGACTGTGGATCCCGGGTTTGGGACCTTAGCAGCCC 3480 Db
3481 CACTCTACCCGCTTAAACCAAGAAAGGGGAAATTCCTCTGGGCTCTTGAGACCAAGAGG 3540 Qy
3481 CACTCTACCCGCTTAAACCAAGAAAGGGGAAATTCCTCTGGGCTCTTGAGACCAAGAGG 3540 Db
3541 CATTTGATGCTATCAAAAGGCCCTGCTGAGCCCACTGCTCTGGCCCTCCCTGACGCTAA 3600 Qy
3541 CATTTGATGCTATCAAAAGGCCCTGCTGAGCCCACTGCTCTGGCCCTCCCTGACGCTAA 3600 Db
3601 CTAAACCTTTACCTTTATGTGGATGAGCGTAAAGGAGTAGCCCGGGGAGTTTTAAACC 3660 Qy
3601 CTAAACCTTTACCTTTATGTGGATGAGCGTAAAGGAGTAGCCCGGGGAGTTTTAAACC 3660 Db
3661 AAACCCCTTAGGACCATGGAGAAAGCCTGTCGCTACCTGTCAAAGAGCTCGATCTCTGTAG 3720 Qy
3661 AAACCCCTTAGGACCATGGAGAAAGCCTGTCGCTACCTGTCAAAGAGCTCGATCTCTGTAG 3720 Db
3721 CAGTGTGTGGCCCATATGCTGAAGCTATCGCAGCTGTGGCCATCTGCTCAAGGACG 3780 Qy
3721 CAGTGTGTGGCCCATATGCTGAAGCTATCGCAGCTGTGGCCATCTGCTCAAGGACG 3780 Db
3781 CTGACAAATTTGACTTTTGGGACAGATATATCTGTATAGCCCCCATGCAATTGGAGAACA 3840 Qy
3781 CTGACAAATTTGACTTTTGGGACAGATATATCTGTATAGCCCCCATGCAATTGGAGAACA 3840 Db
3841 TCGTTTCGGCAGCCCCCAGACCGATGGATGACCAACGCCCGCATGACCCACTATCAAAGCC 3900 Qy
3841 TCGTTTCGGCAGCCCCCAGACCGATGGATGACCAACGCCCGCATGACCCACTATCAAAGCC 3900 Db
3901 TGTCTCTCACAGAGAGGTCACGTTGCTTCCACAGCGGCTCTCAACCTTCCACTCTTC 3960 Qy
3901 TGTCTCTCACAGAGAGGTCACGTTGCTTCCACAGCGGCTCTCAACCTTCCACTCTTC 3960 Db
3961 TGCCTGAAGAGACTGATGAACAGTACTCATGATGCTCACTAATTTGATTGAGGAGA 4020 Qy
3961 TGCCTGAAGAGACTGATGAACAGTACTCATGATGCTCACTAATTTGATTGAGGAGA 4020 Db
4021 CTGGGTCGCGCAAGGACCTTACAGACATACCGCTGACTGGAGAGTGTCTAACCCTGTTCA 4080 Qy
4021 CTGGGTCGCGCAAGGACCTTACAGACATACCGCTGACTGGAGAGTGTCTAACCCTGTTCA 4080 Db
4081 CTGACGGAAGCAGCTATGTGGTGAAGAGGATGGCTGGGGCGCGGTGGTGAGC 4140 Qy
4081 CTGACGGAAGCAGCTATGTGGTGAAGAGGATGGCTGGGGCGCGGTGGTGAGC 4140 Db
4141 GGACCCGCAAGCTGCGGCGCAGAGCTCCCGGAGGAACTTACAGCAAAAAGGCTGAGC 4200 Qy
4141 GGACCCGCAAGCTGCGGCGCAGAGCTCCCGGAGGAACTTACAGCAAAAAGGCTGAGC 4200 Db

QY	4201	TCATGGCCCTCAGCGAAGCTTTGGGCTGGCCGACGAGGGAATCCATATAACATTTATACGG	4260
Db	4201	TCATGGCCCTCAGCGAAGCTTTGGGCTGGCCGACGAGGGAATCCATATAACATTTATACGG	4260
QY	4261	ACAGCAGGTAATGCTTTTGGACTGCAACGTATCATGGGCCATCTATAACAAAGGGGT	4320
Db	4261	ACAGCAGGTAATGCTTTTGGACTGCAACGTATCATGGGCCATCTATAACAAAGGGGT	4320
QY	4321	TGCTTACCTCAGCAGGAGGGAATAAAGAAACAAAGAGGAAATTTCTAAGCCTATTAGAAG	4380
Db	4321	TGCTTACCTCAGCAGGAGGGAATAAAGAAACAAAGAGGAAATTTCTAAGCCTATTAGAAG	4380
QY	4381	CGGTACATTTACAAAGAGCTAGCTATTATACATCTGTCTGTGACATCAGAAAGCTAAAG	4440
Db	4381	CGGTACATTTACCAAAAGAGCTAGCTATTATACATCTGTCTGTGACATCAGAAAGCTAAAG	4440
QY	4441	ATCTCATATCCAGAGAAACACAGATGGCTGACCGGGTTCGCAAGCAGGAGCCACGGGTG	4500
Db	4441	ATCTCATATCCAGAGAAACACAGATGGCTGACCGGGTTCGCAAGCAGGAGCCACGGGTG	4500
QY	4501	TTAAACCTTCTGCTATAATAGAAATGCCAAAGCCCCAGAACCCAGACGACAGTACACCC	4560
Db	4501	TTAAACCTTCTGCTATAATAGAAATGCCCAAGCCCCAGAACCCAGACGACAGTACACCC	4560
QY	4561	TAGAAGCTGGCAAGAGATAAAAGATAGACAGATTTCTGTAGACTCCGGAAGGACCT	4620
Db	4561	TAGAAGCTGGCAAGAGATAAAAGATAGACAGATTTCTGTAGACTCCGGAAGGACCT	4620
QY	4621	GCTATACCTCAGATGGGAAGGAATCCTGCCCAACAAAGAGGGTTAGAAATATGTCACAC	4680
Db	4621	GCTATACCTCAGATGGGAAGGAATCCTGCCCAACAAAGAGGGTTAGAAATATGTCACAC	4680
QY	4681	AGATACATCGTTAAACCCACCTAGGAATTAACACACCTGCAGCAGTTGGTCAGAAACATCCC	4740
Db	4681	AGATACATCGTTAAACCCACCTAGGAATTAACACACCTGCAGCAGTTGGTCAGAAACATCCC	4740
QY	4741	CTTATCATGTTCTGAGGCTACCAAGGATGGCTGACTCGGTGTCAAACAATTGTGTCCTT	4800
Db	4741	CTTATCATGTTCTGAGGCTACCAAGGATGGCTGACTCGGTGTCAAACAATTGTGTCCTT	4800
QY	4801	GCCAGCTGTTAATGCTAATCCTTCCAGAAATGCTCCAGAAAGCGCTAAATACGGAACA	4860
Db	4801	GCCAGCTGTTAATGCTAATCCTTCCAGAAATGCTCCAGAAAGCGCTAAATACGGAAGCC	4860
QY	4861	ACCCAGCGCTCACTGGGAAGTGACTTCACTGAGGTAAAGCGGCTAAATACGGAACA	4920
Db	4861	ACCCAGCGCTCACTGGGAAGTGACTTCACTGAGGTAAAGCGGCTAAATACGGAACA	4920
QY	4921	AATACCTATTTGTTTGTAGACACCTTTTCAGGATGGGTAGAGGCTTATCTCTAAGA	4980
Db	4921	AATACCTATTTGTTTGTAGACACCTTTTCAGGATGGGTAGAGGCTTATCTCTAAGA	4980
QY	4981	TAAGAGCTTCAACCGTGGTGGCTTAAATAATCTGGAAGAAATTTTCCAGATTTGGAA	5040
Db	4981	TAAGAGCTTCAACCGTGGTGGCTTAAATAATCTGGAAGAAATTTTCCAGATTTGGAA	5040
QY	5041	TACCTAAGCTAATAGGGTCAGACAAATGGTCCAGCTTTTGTGCCAGGTAAGTCAGGGAC	5100
Db	5041	TACCTAAGCTAATAGGGTCAGACAAATGGTCCAGCTTTTGTGCCAGGTAAGTCAGGGAC	5100
QY	5101	TGGCCAAAGATATTGGGGATTGATTGGAACTGCTATTGTCATACAGACCCCAAGCTCAG	5160
Db	5101	TGGCCAAAGATATTGGGGATTGATTGGAACTGCTATTGTCATACAGACCCCAAGCTCAG	5160
QY	5161	GACAGTAGAGAGATGAATAGAACCATTAAGAGACCTTACTATAATTGACGGGGAGA	5220
Db	5161	GACAGTAGAGAGATGAATAGAACCATTAAGAGACCTTACTATAATTGACGGGGAGA	5220
QY	5221	CTGGCGTTAATGATTGGATAGCTCTCCGCTTTGTGCTTTTAGGGTTAGGAAACACCC	5280
Db	5221	CTGGCGTTAATGATTGGATAGCTCTCCGCTTTGTGCTTTTAGGGTTAGGAAACACCC	5280
QY	5281	CTGGACAGTTTGGGCTGACCCCTTATGAATTACTCTACGCGGGAACCCCTTGGTAG	5340

Db	5281	CTGGACAGTTTGGGCTGACCCCTTATGAATTACTCTACGCGGGAACCCCTTGGTAG	5340
QY	5341	AAATTTGCTTCTGTACATAGTGTGACGTCTGCTTTTCCAGAGCTTTGTTCTCTAGGCTCA	5400
Db	5341	AAATTTGCTTCTGTACATAGTGTGACGTCTGCTTTTCCAGAGCTTTGTTCTCTAGGCTCA	5400
QY	5401	AGGCACTTGAGTGGGTGAGACAAACGAGCGTGGAGGCAACTCCGGAAGGCTACTACGGAG	5460
Db	5401	AGGCACTTGAGTGGGTGAGACAAACGAGCGTGGAGGCAACTCCGGAAGGCTACTACGGAG	5460
QY	5461	GAGGAGACTTGAGATCCACATCGTTTCCAAAGTGGAGATTCAGTCTACGTTAGACGCC	5520
Db	5461	GAGGAGACTTGAGATCCACATCGTTTCCAAAGTGGAGATTCAGTCTACGTTAGACGCC	5520
QY	5521	ACCGTGCAGAAACCTCGAGACTCGGTGGAAGGCCCTTATCTCGTACTTTTGGACACAC	5580
Db	5521	ACCGTGCAGAAACCTCGAGACTCGGTGGAAGGCCCTTATCTCGTACTTTTGGACACAC	5580
QY	5581	CAACCGCTGTGAAGTTCGAAGGAATCTCCACCTGGATCCATGCATCCACGTTAAACCCG	5640
Db	5581	CAACCGCTGTGAAGTTCGAAGGAATCTCCACCTGGATCCATGCATCCACGTTAAACCCG	5640
QY	5641	CGCCACCTCCGATTCGGGTGGAAGCGGAAAGACTGAAATCCCTTTAGCTTCGCC	5700
Db	5641	CGCCACCTCCGATTCGGGTGGAAGCGGAAAGACTGAAATCCCTTTAGCTTCGCC	5700
QY	5701	TCATCGCGTGTCTTACTCTGTCAATAAATCTCTCAGACTAATGGTATGGCATAGGA	5760
Db	5701	TCATCGCGTGTCTTACTCTGTCAATAAATCTCTCAGACTAATGGTATGGCATAGGA	5760
QY	5761	GACAGCTGAACTCCCATAAACCTTATCTCTCAGCTGGTTAATTACTGACTCCGCGACA	5820
Db	5761	GACAGCTGAACTCCCATAAACCTTATCTCTCAGCTGGTTAATTACTGACTCCGCGACA	5820
QY	5821	GATTAATATATCAACAACTCAAGGGAGGCTCTTTTAGGAACTGGTGGCTGATCTA	5880
Db	5821	GATTAATATATCAACAACTCAAGGGAGGCTCTTTTAGGAACTGGTGGCTGATCTA	5880
QY	5881	TAGCTTTGCTCAGATCAGTTATCTAGTCTGACCTCACCCCGAGATATCTCCATGCT	5940
Db	5881	TAGCTTTGCTCAGATCAGTTATCTAGTCTGACCTCACCCCGAGATATCTCCATGCT	5940
QY	5941	CACGGATTTATGTTTGGCCAGGACCAACAAATAATGGAACATTTGCGGAAATCCAGA	6000
Db	5941	CACGGATTTATGTTTGGCCAGGACCAACAAATAATGGAACATTTGCGGAAATCCAGA	6000
QY	6001	GATTTCTTTTGAACAATGGAACCTGTGTAACTCTTAATGATGGATATTGGAATGGCCA	6060
Db	6001	GATTTCTTTTGAACAATGGAACCTGTGTAACTCTTAATGATGGATATTGGAATGGCCA	6060
QY	6061	ACCTCTCAGCAGATAGGTAAGTTTCTTATGTCAACACCTATACACAGCTCTGACACAA	6120
Db	6061	ACCTCTCAGCAGATAGGTAAGTTTCTTATGTCAACACCTATACACAGCTCTGACACAA	6120
QY	6121	TTTAATTAACCTGCACTGGATAGAACTGGAAGCCCAAGTGTCTCTCTCAGACCTAGAT	6180
Db	6121	TTTAATTAACCTGCACTGGATAGAACTGGAAGCCCAAGTGTCTCTCTCAGACCTAGAT	6180
QY	6181	TACCTAAATAATAGTTTCTCAGAGAAAGGAAACAAAGAAATATCTTAAATGGGTAAAT	6240
Db	6181	TACCTAAATAATAGTTTCTCAGAGAAAGGAAACAAAGAAATATCTTAAATGGGTAAAT	6240
QY	6241	GGTATGCTTTGGGAATGGTATATTATGGAGCTCGGTGGAACCAACAGGCTCCATTTCTA	6300
Db	6241	GGTATGCTTTGGGAATGGTATATTATGGAGCTCGGTGGAACCAACAGGCTCCATTTCTA	6300
QY	6301	ACTATTTCGCTCAAAATAAACAGCTGGAGCCTCCAATGGCTATAGGACCAATAACGGTC	6360
Db	6301	ACTATTTCGCTCAAAATAAACAGCTGGAGCCTCCAATGGCTATAGGACCAATAACGGTC	6360
QY	6361	TTGACGGGTCAAAAGACCCCAACCCAGGACGAGACCAATCTCTTAACATACTTCTGGA	6420

Db	6361	TTGACGGGTCAAGAGACCCCAACCCCAAGGACACAGGACCATCTCTTAACATAAATCTTCTGGA	6420
Qy	5421	TCAGACCCCACTGAGTCTAACAGCAGACTAATAATGGGGCAAACTTTTATAGCCTCATC	6480
Db	6421	TCAGACCCCACTGAGTCTAACAGCAGACTAATAATGGGGCAAACTTTTATAGCCTCATC	6480
Qy	6481	CAGGAGCTTTTCAAGCTCTTAACTCCAGACTCCAGAGGCTACCTCTTCTTGTGGCTA	6540
Db	6481	CAGGAGCTTTTCAAGCTCTTAACTCCAGACTCCAGAGGCTACCTCTTCTTGTGGCTA	6540
Qy	6541	TGCTTAGCTCGGGCCCACTTACTATGAAGGAATGGCTAGAAAGAGGAAATTCATATGTG	6600
Db	6541	TGCTTAGCTCGGGCCCACTTACTATGAAGGAATGGCTAGAAAGAGGAAATTCATATGTG	6600
Qy	6601	ACAAAGACATAGAGCAATGCATCGCATGCGGATCCCAAAATAGCTTACCCCTTACTGAG	6660
Db	6601	ACAAAGACATAGAGCAATGCATCGCATGCGGATCCCAAAATAGCTTACCCCTTACTGAG	6660
Qy	6661	GTCTTGGAAAGGCACTGCATAGGAAGGTTCCGCCATCCCAACCAACCTTTGTAAAC	6720
Db	6661	GTCTTGGAAAGGCACTGCATAGGAAGGTTCCGCCATCCCAACCAACCTTTGTAAAC	6720
Qy	6721	CACACTGAAGCCTTTAATCAAACTCTGAGAGTCAATATCTGTATCCTGTTATGACAGG	6780
Db	6721	CACACTGAAGCCTTTAATCAAACTCTGAGAGTCAATATCTGTATCCTGTTATGACAGG	6780
Qy	6781	TGTTGGGCATGTAACTAGATTAACCCCTTGTCTTCCACCTTGGTTTAAACCAAACT	6840
Db	6781	TGTTGGGCATGTAACTAGATTAACCCCTTGTCTTCCACCTTGGTTTAAACCAAACT	6840
Qy	6841	AAAGATTTTGTGCAATATGTGTTCCCGAGTGTATTAATCTCCGCAAAAGCA	6900
Db	6841	AAAGATTTTGTGCAATATGTGTTCCCGAGTGTATTAATCTCCGCAAAAGCA	6900
Qy	6901	ATCCTTGATGAATATGACTACAGAAATCATCGACAAAGAGAGAACCCATATCTCTGACA	6960
Db	6901	ATCCTTGATGAATATGACTACAGAAATCATCGACAAAGAGAGAACCCATATCTCTGACA	6960
Qy	6961	CTTGCTGTGATGTCTCGACTTGGAGTGGCAGCAGGTGTAGGAACAGGACAGTGGCCCTG	7020
Db	6961	CTTGCTGTGATGTCTCGACTTGGAGTGGCAGCAGGTGTAGGAACAGGACAGTGGCCCTG	7020
Qy	7021	GTACGGGACACAGCAGCTAGAAACAGGACTTAGTAACCTTACATCGAAATGTGAACAGAA	7080
Db	7021	GTACGGGACACAGCAGCTAGAAACAGGACTTAGTAACCTTACATCGAAATGTGAACAGAA	7080
Qy	7081	GATCTCCAAGCCCTAGAAAATCTGTACGTAACCTGGAGGAATCCCTTAACCTCTTATCT	7140
Db	7081	GATCTCCAAGCCCTAGAAAATCTGTACGTAACCTGGAGGAATCCCTTAACCTCTTATCT	7140
Qy	7141	GAAGTAGCTCTACAGAAATAGAGGGTTAGATTATTTCTTAAAGAGGAGGATTA	7200
Db	7141	GAAGTAGCTCTACAGAAATAGAGGGTTAGATTATTTCTTAAAGAGGAGGATTA	7200
Qy	7201	TGTTGACCTTGAGGAGGATCTGTTTATGTGGATCACTCAGGGCCCATCAGAGAC	7260
Db	7201	TGTTGACCTTGAGGAGGATCTGTTTATGTGGATCACTCAGGGCCCATCAGAGAC	7260
Qy	7261	TCCATGAACAGCTTTAGAGAAAGTGTGAGAAAGCTGCGAAGGAAAGGAAAGGAACTTCAA	7320
Db	7261	TCCATGAACAGCTTTAGAGAAAGTGTGAGAAAGCTGCGAAGGAAAGGAAAGGAACTTCAA	7320
Qy	7321	GGTGGTTTGAAGGATGTTCAACAGGTCTCTTTGGTTGGGTACCTTCTTCTGCTTTA	7380
Db	7321	GGTGGTTTGAAGGATGTTCAACAGGTCTCTTTGGTTGGGTACCTTCTTCTGCTTTA	7380
Qy	7381	ACAGACCCCTTAAATAGTCTCTCTCTGTTACTACAGTTGGCCCATGTATTTAAACAAG	7440
Db	7381	ACAGACCCCTTAAATAGTCTCTCTCTGTTACTACAGTTGGCCCATGTATTTAAACAAG	7440
Qy	7441	TTAATTGCTCTTATTTAGAGAACGAATAGTGCAGTCCAGATCATGTACTTTAGACAACAG	7500
Db	7441	TTAATTGCTCTTATTTAGAGAACGAATAGTGCAGTCCAGATCATGTACTTTAGACAACAG	7500
Qy	7501	TACCAAAGCCCGTCTAGCAGGGAAGCTGGCCGCTAGCTCTACAGTTCTTAAGATTAGAAC	7560
Db	7501	TACCAAAGCCCGTCTAGCAGGGAAGCTGGCCGCTAGCTCTACAGTTCTTAAGATTAGAAC	7560
Qy	7561	TATTACAGAGAGAGAGTGGGGAATGAAGAGGATGAATAACAACTTAAGCTTAATGAGAA	7620
Db	7561	TATTACAGAGAGAGAGTGGGGAATGAAGAGGATGAATAACAACTTAAGCTTAATGAGAA	7620
Qy	7621	GCCTTAAATTTGTTCTGAATTTCCAGAGTTTGTCTTATAGGTAAAGATTAGGTTTTTGTG	7680
Db	7621	GCCTTAAATTTGTTCTGAATTTCCAGAGTTTGTCTTATAGGTAAAGATTAGGTTTTTGTG	7680
Qy	7681	CTGTTTTTAAATATATCGGAAGTAAATAGGCCCTGAGTACATGTCTTAGGCAATGAAACT	7740
Db	7681	CTGTTTTTAAATATATCGGAAGTAAATAGGCCCTGAGTACATGTCTTAGGCAATGAAACT	7740
Qy	7741	TCTTGAACATTTTGTAGATAACAAGAAAGGGAGTTTCTAACTGCTTGTATTAGCTTCTGT	7800
Db	7741	TCTTGAACATTTTGTAGATAACAAGAAAGGGAGTTTCTAACTGCTTGTATTAGCTTCTGT	7800
Qy	7801	AAAACTGGTTGGCCCATAAAGATGTTGAAATGTTGATACACATATCTTGTGACAACTG	7860
Db	7801	AAAACTGGTTGGCCCATAAAGATGTTGAAATGTTGATACACATATCTTGTGACAACTG	7860
Qy	7861	TCTCCCCCAACCCCGAAACATGCGCAATGTGTAACTCTAAAAACAATTTAAATTTGTT	7920
Db	7861	TCTCCCCCAACCCCGAAACATGCGCAATGTGTAACTCTAAAAACAATTTAAATTTGTT	7920
Qy	7921	CCACGAAGCGGGCTCTCGAAGTTTAAATTTGATGCTGTTTGTGATATTTTGAATGATT	7980
Db	7921	CCACGAAGCGGGCTCTCGAAGTTTAAATTTGATGCTGTTTGTGATATTTTGAATGATT	7980
Qy	7981	GGTTGTAAAGCGCGGCTTTGTTGAAACCCCATAAAGCTGTCCCGACTCCACACTCG	8040
Db	7981	GGTTGTAAAGCGCGGCTTTGTTGAAACCCCATAAAGCTGTCCCGACTCCACACTCG	8040
Qy	8041	GGCGCGCAGTCTCTACCCCTGGTGTACGACTGTGGGCCCCCAGCGGCTTGGGAATA	8100
Db	8041	GGCGCGCAGTCTCTACCCCTGGTGTACGACTGTGGGCCCCCAGCGGCTTGGGAATA	8100
Qy	8101	AAAACTCTTGTCTTGTGTCATCAAAAAAAA 8132	
Db	8101	AAAACTCTTGTCTTGTGTCATCAAAAAAAA 8132	
RESULT 2			
ADK43414			
ID	ADK43414	standard; cDNA; 8132 BP.	
XX	ADK43414;		
AC	ADK43414;		
XX	ADK43414;		
DT	20-MAY-2004	(first entry)	
XX	20-MAY-2004	(first entry)	
DE	Miniature swine retrovirus, cDNA.		
XX	Miniature swine retrovirus, cDNA.		
KW	swine retrovirus; gene; virus; transplanted; miniature swine;		
KW	porcine retroviral infection; porcine retrovirus; Tsukuba-1; ss.		
OS	Porcine endogenous retrovirus; Miniature swine retrovirus.		
XX	Porcine endogenous retrovirus; Miniature swine retrovirus.		
XX	US6699663-B1.		
XX	02-MAR-2004.		
XX	14-SEP-2000; 2000US-00661858.		
XX	14-DEC-1995; 95US-00572645.		
PR	13-DEC-1996; 96US-00766528.		
XX	(GEHO) GEN HOSPITAL CORP.		
PA	(GEHO) GEN HOSPITAL CORP.		
XX	Fishman JA;		
PI	Fishman JA;		

Db 1681 CCCCTTTTGATCCCACTCAGAGCCCAAAAAGCCTCAGTGGCTTTGGCCCTTTATAGGAC 1740
Qy
1741 AGTCAGCCTTTGGATATTAGAAAGAGCTTCAGAGACTGGAAAGGTTACAGAGAGCTGAGT 1800
Db
1741 AGTCAGCCTTTGGATATTAGAAAGAGCTTCAGAGACTGGAAAGGTTACAGAGAGCTGAGT 1800
Qy
1801 TAGCTGATCTAGTGAAGGAGCAGAGAAAGTATATTAACAAAGGGAGACAGAAAGAAA 1860
Db
1801 TAGCTGATCTAGTGAAGGAGCAGAGAAAGTATATTAACAAAGGGAGACAGAAAGAAA 1860
Qy
1861 GGGAAACAAAGAAAGAGAGAGAAAGAGAGAAAGGGAGGAAGACGCTAATAAACGGCAAG 1920
Db
1861 GGGAAACAAAGAAAGAGAGAGAAAGAGAGAAAGGGAGGAAGACGCTAATAAACGGCAAG 1920
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Db
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Qy
1981 AGAGAGATTTTAGGAAAATTAGGTGAGGCCCTAGACAGTCAAGGAACTCTGGCAATAGGA 2040
Db
1981 AGAGAGATTTTAGGAAAATTAGGTGAGGCCCTAGACAGTCAAGGAACTCTGGCAATAGGA 2040
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2041 CCCCACTCGAAGGAAACAAAGGACCAAGGATCTAGAGTCAAGGAACTCTGGCAATAGGA 2100
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2161 GGAGACGGGTTTGGGACCCCTCCCGAGCCAGGGTAACTTTGAAAGTGGAGGGGCAAC 2220
Db
2161 GGAGACGGGTTTGGGACCCCTCCCGAGCCAGGGTAACTTTGAAAGTGGAGGGGCAAC 2220
Qy
2221 CAGTTGAGTTCCTGTTGATACCGGAGCGAAACATTCACTGCTACTACAGCCATTAGGAA 2280
Db
2221 CAGTTGAGTTCCTGTTGATACCGGAGCGAAACATTCACTGCTACTACAGCCATTAGGAA 2280
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2281 AACTAAAGATATAAAATCTCTGGGTGATGGTGCACAGGCAACACAGTATCCATGGA 2340
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2461 CTTTGTGAACAGGGAAACAGAGTGTGCAAAATAACAAACCTTACTGCTGTTGACCC 2520
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Db
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2581 AATTCTGTTGGAACAGTTTCCCAAGCTGGGAGAAACCGCAGGGATGGGTTTGGCAA 2640
Db
2581 AATTCTGTTGGAACAGTTTCCCAAGCTGGGAGAAACCGCAGGGATGGGTTTGGCAA 2640
Qy
2641 AGCAAGTTTCCCAAGCTTATTCACCTGAAGGGCCAGTGCACACCAAGTGTCAAGTACAG 2700
Db
2641 AGCAAGTTTCCCAAGCTTATTCACCTGAAGGGCCAGTGCACACCAAGTGTCAAGTACAG 2700
Qy
2701 AGTACCCCTTGAGTAAAGAGCTCAAGAGGAATTCGGCCGCAATGTCAGAGATTAATCC 2760
Db
2701 AGTACCCCTTGAGTAAAGAGCTCAAGAGGAATTCGGCCGCAATGTCAGAGATTAATCC 2760
Qy
2761 AACAGGGCATCTAGTCTCTGTCCTGGAATCTCCCTGGAATCTCCCTGCTACCGGTTAGAA 2820
Db
2761 AACAGGGCATCTAGTCTCTGTCCTGTCCTGGAATCTCCCTGGAATCTCCCTGCTACCGGTTAGAA 2820

Qy 2821 AGCCTGGGACTAATGACTATCGACCAAGTACAGGACTTTGAGAGAGTCAATAAACGGGTGC 2880
Db
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Db
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Db
2941 GGAAGCTGGTATACAGATTTGAGACTTAAAGATGCTCTTCTGCTCGAGATTAACCCCA 3000
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Db
3661 AAACCCCTAGGACCATGAGAAAGACTGTGCGCTACCTGTCAAGAGAGTCCGATCCTGTAG 3720
Qy 3721 CCAGTGGTGGCCCATATGCTGAGGCTATCGCAGCTGTGGCCATCTGCTCAAGGAGG 3780
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QY 4141 GGACCCGACGATCTGGGCGCAGCAGCTGCGGAAGAACTTCAGCACAAGAGCTGAGC 4200
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DB 4201 TCATGGCCCTCAGCAAGCTTTGCGGCTGCGCGAAGGAAATCCATAAACATTTATACGG 4260
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DB 4261 ACAGCAGGTATGCTTTGCGACTGCAACGTCATGCGGCGCATCTATAAACAAAGGGGT 4320
QY 4321 TGTATTACCTCAGAGAGGGAAATAAGAAACAAAGAGAAATTTAAGCCCTATTAGAAG 4380
DB 4321 TGTATTACCTCAGAGAGGGAAATAAGAAACAAAGAGAAATTTAAGCCCTATTAGAAG 4380
QY 4381 CCGTACATTTACCAAAAGCTAGCTATTATACACTGCTCTGACATCAGAAAGCTTAAAG 4440
DB 4381 CCGTACATTTACCAAAAGCTAGCTATTATACACTGCTCTGACATCAGAAAGCTTAAAG 4440
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QY 4501 TTAACTTCTGCTTAATAATAGAAATGCCAAAGCCCCAGAACCCAGACAGTACACCC 4560
DB 4501 TTAACTTCTGCTTAATAATAGAAATGCCAAAGCCCCAGAACCCAGACAGTACACCC 4560
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DB 4561 TAGAAGACTGGCAAGAGATAAAAAGATAGACAGTTCCTGAGACTCCGGAAGGACCT 4620
QY 4621 GCTATACCTCAGATGGGAAGGAAATCCTGCCCCACAAAGAGGGTTAGAAATATGTCCAAC 4680
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DB 5161 GACAGGTAGAGAGGATGAATAGAACCATTTAAAGAGACCTTACTAAATTTGACCGCGGAGA 5220
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QY 5521 ACCGTGCGAGAAACCTCAGAGACTCGGTGGAAGGGCCCTTATCTCGTACTTTTGACACAC 5580
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Db	6121	TTTTTAAATTTACCTGACCTGGATTAGAACTCGAAGCCCAAGTGCTCTCTTTCAGACCTAGAT	6180
Qy	6181	TACCTAAAATAAAGTTTCACTGAGAAAGGAAACAAAGAAATATCTTAAATGGGTAAAT	6240
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Qy	6301	ACTATTGCGCTCAAAATAAAACAGCTGGAGCTTCCAAATGGCTATAGACCAAAATACGGTC	6360
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Db	6481	CAGGAGCTTTTCAAGTCTTAACTCCAGCTCCAGAGGCTACCTCTTCTTGTGGCTA	6540
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Qy	6661	GTTCCTGGAAGGACCTGCATAGGAAGGTTCCCGCCATCCCAACCAACCTTTGTAAC	6720
Db	6661	GTTCCTGGAAGGACCTGCATAGGAAGGTTCCCGCCATCCCAACCAACCTTTGTAAC	6720
Qy	6721	CACACTGAAGCTTTAATCAAACTCTGAGAGTCAATATCTGGTACCTGTTATGACAGG	6780
Db	6721	CACACTGAAGCTTTAATCAAACTCTGAGAGTCAATATCTGGTACCTGTTATGACAGG	6780
Qy	6781	TGCTGGGCATGTAATCTGGAATTAACCCCTTGTGTTTCCACCTTGGTTTTTAACCAAACT	6840
Db	6781	TGCTGGGCATGTAATCTGGAATTAACCCCTTGTGTTTCCACCTTGGTTTTTAACCAAACT	6840
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Qy	6961	CTTCCTGTGATGCTCGGACTTGGAGTGGCAGAGGTGTAGGAAACAGGACAGCTGCCCTG	7020
Db	6961	CTTCCTGTGATGCTCGGACTTGGAGTGGCAGAGGTGTAGGAAACAGGACAGCTGCCCTG	7020
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Db	7021	GTACCGGACCAAGCAGCTAGAAATCTGTCACTAGTAACTTACCTTACCTTATCT	7080
Qy	7081	GATCTCCAGCCCTAGAAAAATCTGTAGTAACTTGGAGGAATCCCTTAACTCTTATCT	7140
Db	7081	GATCTCCAGCCCTAGAAAAATCTGTAGTAACTTGGAGGAATCCCTTAACTCTTATCT	7140
Qy	7141	GAAGTAGTCTTACAGATAGAGAGGGTTAGATTATTATTCTTAAAGAGGAGGATTA	7200
Db	7141	GAAGTAGTCTTACAGATAGAGAGGGTTAGATTATTATTCTTAAAGAGGAGGATTA	7200

RESULT 3
ADS73369
ID ADS73369 standard; DNA; 8132 BP.
XX
XX ADS73369;
DT 16-DEC-2004 (first entry)

XX Swine retroviral genomic DNA.
DE
XX Swine retroviral protein; immunosuppressive; gene therapy; gene; ds.
KW
XX Porcine endogenous retrovirus.
OS
XX Key Location/Qualifiers
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FT CDS 2307..5744
FT /*tag= b
FT /product= "Swine retroviral pol protein"
FT CDS 5620..7536
FT /*tag= c
FT /product= "Swine retroviral env protein"
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XX
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XX
XX 26-NOV-2003; 2003US-00723552.
XX
XX 14-DEC-1995; 95US-00572645.
PR 13-DEC-1996; 96US-00786528.
PR 14-SEP-2000; 2000US-00661858.
XX
XX (GEO) GEN HOSPITAL CORP.
XX
XX Fishman JA;
PI
XX
XX WPI ; 2004-689179/67.
DR P-PSDB; ADS73446, ADS73447, ADS73448.
XX
XX New porcine retroviral polypeptide encoded by a nucleic acid, useful in
PT evaluating an immunosuppressive treatment for the ability to activate a
PT retrovirus, such as an endogenous porcine retrovirus.
XX
XX Claim 1; SEQ ID NO 3; 83pp; English.
PS
XX The present invention relates to the swine retroviral polypeptides and
CC their encoding nucleic acids. The methods and compositions of the present
CC invention are useful for screening a cell or tissue, e.g. a heart, lung,
CC liver, bone marrow, kidney, brain cells, neural tissue, pancreas and
CC intestinal tissue xenograft, for the presence or expression of a swine or
CC miniature swine retrovirus or retroviral sequence. The invention is also
CC useful in evaluating an immunosuppressive treatment for the ability to
CC activate a retrovirus such as an endogenous porcine retrovirus. The
CC invention is also useful in gene therapy. The present sequence is the
CC swine retroviral genomic DNA.
XX
SQ Sequence 8132 BP; 2248 A; 1977 C; 2037 G; 1870 T; 0 U; 0 Other;

Query Match 100.0%; Score 8132; DB 13; Length 8132;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 8132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTGGGTGACGACTGTGGGCCCCAGCGCTTGGGAATAAAATCCTCTGTGTTGCA 60
DB 1 GGTGGGTGACGACTGTGGGCCCCAGCGCTTGGGAATAAAATCCTCTGTGTTGCA 60

QY 61 TCAAGACCGCTTCTCGTGTGATTAAGGGGAGTCGCCCTTTTCCGAGCTGGAGGTTCTT 120
DB 61 TCAAGACCGCTTCTCGTGTGATTAAGGGGAGTCGCCCTTTTCCGAGCTGGAGGTTCTT 120

QY 121 TTTGTGTGTTACATTTGGGGCTCGTCCGGGATCTGTGGGGCCACCCCTTAAACCCG 180
DB 121 TTTGTGTGTTACATTTGGGGCTCGTCCGGGATCTGTGGGGCCACCCCTTAAACCCG 180

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DB 181 AGAACCGACTGGAGTAAAGGATCCTCTTTTAAACGTGTATGATGACGCGCGG 240

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DB 1021 CTGTTCCTCCACCCCTTATCTGGCAGAGGGTCCGCGAGGGACCCCTTTTGGCCCTCTCTG 1080

QY 1081 GAGCTCCGCGGTGGAGGACCTGTCTGAGGAGACTCGGAGCCGAGGGCGCCACCCCG 1140
DB 1081 GAGCTCCGCGGTGGAGGACCTGTCTGAGGAGACTCGGAGCCGAGGGCGCCACCCCG 1140

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QY 1201 GCCAATTGACGCCCTCCAGTATGGCCCTTTTCTTCGACATCTCTAATTTGAAAA 1260
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QY	3781	CTGACAAATTTGACTTTGGGACAGATATAAATCTGTAATAGCCCCCCTATGCAATGGAGACA	3840	Db	4861	ACCCAGGCGCTACCTGGGAAGTGGACTTCACTAGAGTAAGCCGCTAAATACGGAACA	4920
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QY	3841	TGTTTCGGCAGCCCCCAGACCGATGATGATCAACCAAGCCCGCATGACCCACTATCAAGCC	3900	Db	4921	AATACCTATTGGTTTTTTGTAGACACTTTTTCAGGATGGGTAGAGGCTTATCTCTAAGA	4980
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QY	3901	TGCTTCTCAGAGAGGGTCACTGCTCCACAGCCGCTCTCAACCCCTGCCACTCTTC	3960	Db	4981	AAAGACCTTCAACCCGTGGCTAAAAAATACTGGAAGAAATTTTTCAGATTTGGAA	5040
Db	3901	TGCTTCTCAGAGAGGGTCACTGCTCCACAGCCGCTCTCAACCCCTGCCACTCTTC	3960	QY	5041	TTACCTAAGGTAAAGGGTCAGCAATGGTCCAGCTTTTGTGCCAGGTAAGTCAAGGAC	5100
QY	3961	TGCTGGAAGAGACTGATGAACAGTGAATCATGATTTGCCATCAACTATTTGATGAGGAGA	4020	Db	5041	TTACCTAAGGTAAAGGGTCAGCAATGGTCCAGCTTTTGTGCCAGGTAAGTCAAGGAC	5100
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Db	4081	CTGACGGAAGCAGCTATGTGGTGAAGGTAAAGAGTATGCTGGGGCGCGGTGGGACG	4140	QY	5221	CTGGGGTTAATGATTTGGATAGCTCTCTGCCCCCTTTGTGCTTTTAGGGTTAGGAACACC	5280
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QY	4441	ATCTCATATCCAGAGAAACCATGCTGACCGGTTGCCAGCAGGCGAGCCCGGGTG	4500	Db	5521	ACCGTCAGGAAACCTTCGAGACTCGGTGGAAGGCGCTTATCTCGTACTTTTGAACACAC	5580
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Db 8101 AAAATCCTCTTGCTGTTTGCATCAAAAAAAA 8132

RESULT 4

AAT74884
ID AAT74884 standard; cDNA; 7892 BP.
XX AC AAT74884;
XX
DT 27-AUG-2003 (revised)
DT 09-FEB-1998 (first entry)
XX
DE Miniature swine retrovirus cDNA.
XX
KW Retrovirus; porcine; GAG protein; POL protein; ENV protein;
KW xenotransplantation; infectious; provirus; organ transplant; donor;
KW activated virus; PCR; ss.
XX
OS Pig endogenous retrovirus.

Key Location/Qualifiers

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FT /note= "putative ENV protein"
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XX
PD 19-JUN-1997.
XX
PF 13-DEC-1996; 96WO-US019680.
XX
PR 14-DEC-1995; 95US-00572645.
XX
XX (GENO) GEN HOSPITAL CORP.
XX
XX Fishman JA;
XX
XX WPI; 1997-332804/30.
DR P-PSDB; AAW32096, AAW32097, AAW32098.
XX
PT New nucleic acid from porcine retroviruses - used for detecting viruses
PT in transplant or other tissue and for assessing risk of transmitting
PT infection to graft recipient.
XX
PS Claim 22; Fig 3; 128pp; English.

XX This cDNA sequence represents a porcine retrovirus from miniature swine
CC containing the putative coding regions for viral GAG, POL and ENV
CC proteins. This sequence and PCR fragments generated from it (see AAT74812
CC -T74882) can be used to screen organs for the presence of porcine
CC retroviruses prior to xenotransplantation. Transplantation can increase
CC the likelihood of retroviral activation if intact and infectious
CC proviruses are present. The porcine retroviral sequence can be used to
CC generate probes to determine the level (e.g. copy number) of intact (i.e.
CC potentially replicating) porcine provirus sequences in a strain of
CC xenograft transplantation donors. It can be used to detect mutations,
CC genetic lesions or viral recombinants and also to determine the
CC histological localisation of activated retrovirus. Using Polymerase Chain
CC Reaction DNA Quantitation (PQD) on blood mononuclear cells, infectivity
CC titration and susceptibility testing can be performed. Ultimately animal
CC donors without intact porcine retroviral sequences or a lower copy number
CC of viral elements could be selected. (Updated on 27-AUG-2003 to correct
CC OS field.)
XX
SQ Sequence 7892 BP; 2191 A; 1915 C; 1980 G; 1806 T; 0 U; 0 Other;
Query Match 96.7%; Score 7860; DB 2; Length 7892;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 7860; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 1 GCGTGGTGTAACGACTGTGGGCCCCAGCGCGCTTGGAAATAAATCCTCTGTGTTTGA 60
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Db 61 TCAAGACCGCTTCTCGTGAGTGAATTAAGGGGAGTCGCCCTTTCCGAGCCTGGAGGTTCTT 120
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Db 121 TTTTGTGCTGTTTACATTTTGGGGCTCGTCCGGGAGTCTGTCCGGGACACCCCTAACACCCG 180
QY 181 AGAACCGACTTGGAGGTAAGGATCTCTTTTAACTGATGATGATGATGATGATGATGATGATG 240
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Qy	841	GGCAAGATTTGGCAGAGAGATCTCCGCCATCGGGTTAAACCATGGCTGAATAAGCCAAAGAA	900	Db	1921	AGAAGAAATTTGACTAAGATCTTGGCTGCTAGTGGTTGAAGGGAAAGCAATACCGAAGAG	1980
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Db	1501	ACTACAAACAGGCTGAGGATAGGAGACTTGAAAAATCTATCGCCAGGCTCTGCTGGCGG	1560	Qy	2641	AGCAAGTTCGCCCAAGATTATTAACCTGAAGGCCAGTGCACACCCAGTGTCTAGTCTAGAC	2700
Qy	1561	GTCTCCGGGGCCCTCAAGACGGCCCACTAATTTGGCTTAAGGTAAAGAAAGTATGACAGG	1620	Db	2641	AGCAAGTTCGCCCAAGATTATTAACCTGAAGGCCAGTGCACACCCAGTGTCTAGTCTAGAC	2700
Db	1561	GTCTCCGGGGCCCTCAAGACGGCCCACTAATTTGGCTTAAGGTAAAGAAAGTATGACAGG	1620	Qy	2701	AGTACCCCTTGTAGTAAAGAGCTCAAGAGGAAATTCGGCCGCATGTCCAAAGATTAATCC	2760
Qy	1621	GACCGAATGAACCCCTCTGTGTTTTCTGTAGAGGCTCTTGGAGCCCTTACAGGCGGTACA	1680	Db	2701	AGTACCCCTTGTAGTAAAGAGCTCAAGAGGAAATTCGGCCGCATGTCCAAAGATTAATCC	2760
Db	1621	GACCGAATGAACCCCTCTGTGTTTTCTGTAGAGGCTCTTGGAGCCCTTACAGGCGGTACA	1680	Qy	2761	AACAGGCACTCTAGTTTCTGTCCCAATCTCCCTGGAAATCTCCCTGCTTACCGGTTAGAA	2820
Qy	1681	CCCCCTTTGATCCCACTCAGAGGCCCAAAAGCCCTCAGTGGCTTTGGCCCTTATAGGAC	1740	Db	2761	AACAGGCACTCTAGTTTCTGTCCCAATCTCCCTGGAAATCTCCCTGCTTACCGGTTAGAA	2820
Db	1681	CCCCCTTTGATCCCACTCAGAGGCCCAAAAGCCCTCAGT					

2881 AGGATATACCCAAACAGCTCCCGAACCCCTTATAAACCTTTGTGTCTCTCCACCCCCAAC 2940 Db
2941 GGAGCTGGGTATACAGTATTGGACTTAAAGGATGGCCTTCTTGCCTCGAGATTACACCCCA 3000 Qy
2941 GGAGCTGGGTATACAGTATTGGACTTAAAGGATGGCCTTCTTGCCTCGAGATTACACCCCA 3000 Db
3001 CTAGCCAAACCTTTTGGCTTCGAATGGAGAGATCCAGGTACGGGAAGAACCGGGCAGC 3060 Qy
3001 CTAGCCAAACCTTTTGGCTTCGAATGGAGAGATCCAGGTACGGGAAGAACCGGGCAGC 3060 Db
3061 TCACCTGGACCGACTGCCCCAAGGTTCAAGNACTCCCGACCATCTTTTGGACGAGCC 3120 Qy
3061 TCACCTGGACCGACTGCCCCAAGGTTCAAGNACTCCCGACCATCTTTTGGACGAGCC 3120 Db
3121 TACACAGAGACCTGGCCAACTTCAGGATCCAAACACCTCAGGTGACCTCCCTCCAGTAGC 3180 Qy
3121 TACACAGAGACCTGGCCAACTTCAGGATCCAAACACCTCAGGTGACCTCCCTCCAGTAGC 3180 Db
3181 TGGATGACCTGCTTTGCGGGAGCCACCAACAGAGACTGCTTAGAAGGCCACGAAGGCAC 3240 Qy
3181 TGGATGACCTGCTTTGCGGGAGCCACCAACAGAGACTGCTTAGAAGGCCACGAAGGCAC 3240 Db
3241 TACTGCTGMAATTGCTGACCTTAGGCTACAGAGCTCTGCTAAGAAAGGCCACGATTGCA 3300 Qy
3241 TACTGCTGMAATTGCTGACCTTAGGCTACAGAGCTCTGCTAAGAAAGGCCACGATTGCA 3300 Db
3301 GGAGAGAGTTAAACATACTTGGGGTACAGTTTGGGGACGGGACGATGGCTGACGGAG 3360 Qy
3301 GGAGAGAGTTAAACATACTTGGGGTACAGTTTGGGGACGGGACGATGGCTGACGGAG 3360 Db
3361 CACGGAAGAAAACCTGTAGTCCAGATACCGGCCCCCAACACAGCAGCAAAACAAATGAGAG 3420 Qy
3361 CACGGAAGAAAACCTGTAGTCCAGATACCGGCCCCCAACACAGCAGCAAAACAAATGAGAG 3420 Db
3421 TTTTGGGGACAGCTGGATTGTGAGACTGTGGATCCCGGGTTTGGACCTTAGCAGCCC 3480 Qy
3421 TTTTGGGGACAGCTGGATTGTGAGACTGTGGATCCCGGGTTTGGACCTTAGCAGCCC 3480 Db
3481 CACTCTACCCGCTAAACCAAGAAAAGGGGAATCTCTCGGGCTCTGAGACCAAGAG 3540 Qy
3481 CACTCTACCCGCTAAACCAAGAAAAGGGGAATCTCTCGGGCTCTGAGACCAAGAG 3540 Db
3541 CATTTGATGCTATCAAAAAGGCCCTGTGAGCGCACCTGTCTGGCCCTCCCTGACGTAA 3600 Qy
3541 CATTTGATGCTATCAAAAAGGCCCTGTGAGCGCACCTGTCTGGCCCTCCCTGACGTAA 3600 Db
3601 CTAACCCCTTTACCTTTATGTGGATGAGCGTAAGGGAGTAGCCCGGGAGTTTAAACCC 3660 Qy
3601 CTAACCCCTTTACCTTTATGTGGATGAGCGTAAGGGAGTAGCCCGGGAGTTTAAACCC 3660 Db
3661 AAACCCCTAGGACCATGGAGAAGACCTGTGCTACCTGTCAAAAGAGCTCGATCCTGTAG 3720 Qy
3661 AAACCCCTAGGACCATGGAGAAGACCTGTGCTACCTGTCAAAAGAGCTCGATCCTGTAG 3720 Db
3721 CCAGTGGTGGCCCATATGCTGAAGGCTATCGAGCTGTGGCCATCTGGTCAAGGACG 3780 Qy
3721 CCAGTGGTGGCCCATATGCTGAAGGCTATCGAGCTGTGGCCATCTGGTCAAGGACG 3780 Db
3781 CTGACAAAATTGACTTTGGGACAGAAATATACTGTAATAGCCCCCAGATGCGATTGGAGAAC 3840 Qy
3781 CTGACAAAATTGACTTTGGGACAGAAATATACTGTAATAGCCCCCAGATGCGATTGGAGAAC 3840 Db
3841 TCCTTGGCAGCCCCCAGACCGATGGATGACCAACGCCCGCATGACCACTATCAAGCC 3900 Qy
3841 TCCTTGGCAGCCCCCAGACCGATGGATGACCAACGCCCGCATGACCACTATCAAGCC 3900 Db
3901 TGCTTTCTCACAGAGAGGGTCACTGCTGCTCCACAGCCGCTCTCAACCCCTGCCACTCTTC 3960 Qy
3901 TGCTTTCTCACAGAGAGGGTCACTGCTGCTCCACAGCCGCTCTCAACCCCTGCCACTCTTC 3960 Db
3961 TGCTTGAAGAGACTGATGAACCAAGTGAATGCGATCACTGATGCGCATCACTATTGATTGAGGAGA 4020 Qy
3961 TGCTTGAAGAGACTGATGAACCAAGTGAATGCGATCACTGATGCGCATCACTATTGATTGAGGAGA 4020 Db

4021 CTGGGGTCCGCAAGACCTTTACAGACATACCGCTGACTGGAGAACTGCTTAACCTGTTCA 4080 Qy
4021 CTGGGGTCCGCAAGACCTTTACAGACATACCGCTGACTGGAGAACTGCTTAACCTGTTCA 4080 Db
4081 CTGACGGGAAGCAGCTTATGTTGGTGGAGGTAAAGAGATGGCTGGGGCGGGTGGAGC 4140 Qy
4081 CTGACGGGAAGCAGCTTATGTTGGTGGAGGTAAAGAGATGGCTGGGGCGGGTGGAGC 4140 Db
4141 GGACCCGACGATCTGGGCCAGCAGCTGCCGGAAGAACTTTCAGACAACAAAGAGGCTGAGC 4200 Qy
4141 GGACCCGACGATCTGGGCCAGCAGCTGCCGGAAGAACTTTCAGACAACAAAGAGGCTGAGC 4200 Db
4201 TCATGGCCCTCACGCAAGCTTTGCGGTGGCCGGAAGAAATCCATAAATTTATACGG 4260 Qy
4201 TCATGGCCCTCACGCAAGCTTTGCGGTGGCCGGAAGAAATCCATAAATTTATACGG 4260 Db
4261 ACAGCAGGTATGCTTTGGGACTGACACAGTACATGGGGCCATCTATAACAAAGAGGGGT 4320 Qy
4261 ACAGCAGGTATGCTTTGGGACTGACACAGTACATGGGGCCATCTATAACAAAGAGGGGT 4320 Db
4321 TGCTTACCTCAGCAGGGAGGAAATAAAGAAACAAAGAGGAAATTTCTAAGCCTATTAGAAG 4380 Qy
4321 TGCTTACCTCAGCAGGGAGGAAATAAAGAAACAAAGAGGAAATTTCTAAGCCTATTAGAAG 4380 Db
4381 CCGTACATTTTACCAAAAAGGCTAGCTATTATACATGCTCTGGACATCAGAAAAGCTAAAG 4440 Qy
4381 CCGTACATTTTACCAAAAAGGCTAGCTATTATACATGCTCTGGACATCAGAAAAGCTAAAG 4440 Db
4441 ATCTCATATCCAGAGAAACAGATGGCTGACGGGTTGCCAAGCAGGACGCCAGGGTG 4500 Qy
4441 ATCTCATATCCAGAGAAACAGATGGCTGACGGGTTGCCAAGCAGGACGCCAGGGTG 4500 Db
4501 TTAACTTCTGCTTAATAAGAAATGCCAAAGCCCAAGAACCCAGACGACAGTACACCC 4560 Qy
4501 TTAACTTCTGCTTAATAAGAAATGCCAAAGCCCAAGAACCCAGACGACAGTACACCC 4560 Db
4561 TAGAAGACTGGCAAGAGATAAAAAAGATAGACAGTCTCTGAGACTCCGGAAGGACCT 4620 Qy
4561 TAGAAGACTGGCAAGAGATAAAAAAGATAGACAGTCTCTGAGACTCCGGAAGGACCT 4620 Db
4621 GCTATACCTCAGATGGGAAGAAATCTGCCCAACAAAGAGGTTAGATAATGTCCAAC 4680 Qy
4621 GCTATACCTCAGATGGGAAGAAATCTGCCCAACAAAGAGGTTAGATAATGTCCAAC 4680 Db
4681 AGATACATCGTCTAAACCCACCTAGGAACTAAACACCTGACAGAGTTGGTCAGAAATCCC 4740 Qy
4681 AGATACATCGTCTAAACCCACCTAGGAACTAAACACCTGACAGAGTTGGTCAGAAATCCC 4740 Db
4741 CTTATCATGTTCTGAGGCTACAGGAGTGGCTGACTCGGTGGTCAAAATTTGTGTGCCCT 4800 Qy
4741 CTTATCATGTTCTGAGGCTACAGGAGTGGCTGACTCGGTGGTCAAAATTTGTGTGCCCT 4800 Db
4801 GCCAGCTGGTTAATGCTAATCTTCCAGAACTGCCCTCCAGGGAAGACACTAAGGGGAAGCC 4860 Qy
4801 GCCAGCTGGTTAATGCTAATCTTCCAGAACTGCCCTCCAGGGAAGACACTAAGGGGAAGCC 4860 Db
4861 ACCCAGCGCTCACTGGGAAGTGGACTTCACTGAGGTAAGCGCGGTAAATACGGHAACA 4920 Qy
4861 ACCCAGCGCTCACTGGGAAGTGGACTTCACTGAGGTAAGCGCGGTAAATACGGHAACA 4920 Db
4921 AATACCTATTGGTTTTTGTAGACACTTTTTCAGGATGGGTAGAGGCTTATCTCTAAGA 4980 Qy
4921 AATACCTATTGGTTTTTGTAGACACTTTTTCAGGATGGGTAGAGGCTTATCTCTAAGA 4980 Db
4981 AAGAGACTTCAACCGGTGGCTTAAATAATCTGGAAGAAATTTTCCAAAGATTGGAA 5040 Qy
4981 AAGAGACTTCAACCGGTGGCTTAAATAATCTGGAAGAAATTTTCCAAAGATTGGAA 5040 Db
5041 TACCTAAGGTAAATAGGGTCAGACATGGTCCAGCTTTTGTGCCAGGTAAGTCAGGGAC 5100 Qy
5041 TACCTAAGGTAAATAGGGTCAGACATGGTCCAGCTTTTGTGCCAGGTAAGTCAGGGAC 5100 Db

QY	5101	TGSCCAAGATATTGGGGATTGATTGAAACTGTCATTTGTGCATACAGACCCCAAGCTCAG	5160	Db	6181	TACCTAAAAATAAGTTTCACTGAGAAAGGAAAAACAAGAAAAATATCTTAAATGGGTAAAT	6240
Db	5101	TGGCCAAAGATATTGGGGATTGATTGAAACTGTCATTTGTGCATACAGACCCCAAGCTCAG	5160	QY	6241	GGTATGCTTTGGGGAATGATATATTGAGGCTCGGGTAAACAACAACAGGCTCCATTCTTA	6300
QY	5161	GACAGGTAGAGAGGATGAATAGAACCAITTAAGAGACCTTACTAAATTGAACGCGGAGA	5220	Db	6241	GGTATGCTTTGGGGAATGATATATTGAGGCTCGGGTAAACAACAACAGGCTCCATTCTTA	6300
Db	5161	GACAGGTAGAGAGGATGAATAGAACCAITTAAGAGACCTTACTAAATTGAACGCGGAGA	5220	QY	6301	ACTATTTCGCTCAAAATAAACAGCTGGAGCTTCCAAATGGCTATAGGACCAAAATACGGTC	6360
QY	5221	CTGGCGTTTAATGATTGGATAGCTCTCTGCTGCTTTTCCAGACCTTTAGGGTTAGGAACACCC	5280	Db	6301	ACTATTTCGCTCAAAATAAACAGCTGGAGCTTCCAAATGGCTATAGGACCAAAATACGGTC	6360
Db	5221	CTGGCGTTTAATGATTGGATAGCTCTCTGCTGCTTTTCCAGACCTTTAGGGTTAGGAACACCC	5280	QY	6361	TTGACGGGTTCAAGAGACCCCAACCCAGGACCAAGGACCACTCTTAACTAACTTCTGGA	6420
QY	5281	CTGACAGTTTGGGCTGACCCCTCTATGAATTAATCTACCGGGGACCCCTTCTGTTAG	5340	Db	6361	TTGACGGGTTCAAGAGACCCCAACCCAGGACCAAGGACCACTCTTAACTAACTTCTGGA	6420
Db	5281	CTGACAGTTTGGGCTGACCCCTCTATGAATTAATCTACCGGGGACCCCTTCTGTTAG	5340	QY	6421	TCAGAGCCCACTGAGTCTAAACAGCAGCTTAAATGGGGGCAAAATCTTTTACGCTCATC	6480
QY	5341	AAATTGCTTCTGATACATAGTGTGACGTGCTGCTTTTCCAGACCTTTGTTCTTAGGCTCA	5400	Db	6421	TCAGAGCCCACTGAGTCTAAACAGCAGCTTAAATGGGGGCAAAATCTTTTACGCTCATC	6480
Db	5341	AAATTGCTTCTGATACATAGTGTGACGTGCTGCTTTTCCAGACCTTTGTTCTTAGGCTCA	5400	QY	6481	CAGGAGCTTTTCAAGCTCTTAACTCCAGACTCCAGAGGCTACCTCTTCTTGGGCTA	6540
QY	5401	AGGCACTTGGTGGGTGAGCAACAGGACGCTGGAGGCACTCCGGGAGGCTACTCAGGAG	5460	Db	6481	CAGGAGCTTTTCAAGCTCTTAACTCCAGACTCCAGAGGCTACCTCTTCTTGGGCTA	6540
Db	5401	AGGCACTTGGTGGGTGAGCAACAGGACGCTGGAGGCACTCCGGGAGGCTACTCAGGAG	5460	QY	6541	TGCTTAGCTTCGGGCCCACTTACTATGAAGGAAATGGCTTAGAAGAGGAAATTCATGTG	6600
QY	5461	GAGGAGCTTGCAGATCCCAATCGTTTCCAGTGGGAGATTCAGTCTAGCTTAGACGCC	5520	Db	6541	TGCTTAGCTTCGGGCCCACTTACTATGAAGGAAATGGCTTAGAAGAGGAAATTCATGTG	6600
Db	5461	GAGGAGCTTGCAGATCCCAATCGTTTCCAGTGGGAGATTCAGTCTAGCTTAGACGCC	5520	QY	6601	ACAAAAGACATAGAGACCAATGCATATGGGATCCCAAAATAAGCTTACCTTACTGTAG	6660
QY	5521	ACCGTGCAGGAAACCTCGAGACTCGGTGGAGGGCCCTTATCTCGTACTTTTACACAC	5580	Db	6601	ACAAAAGACATAGAGACCAATGCATATGGGATCCCAAAATAAGCTTACCTTACTGTAG	6660
Db	5521	ACCGTGCAGGAAACCTCGAGACTCGGTGGAGGGCCCTTATCTCGTACTTTTACACAC	5580	QY	6661	GTCTTCTGGAAAAGGCACTGTCATAGGAAAGGTTTCCCCCAATCCCAACCACTTTGTAAAC	6720
QY	5581	CAACGGCTGGAAGTGCAGAGGAAATCTCCACCTGGATCCATGATCCAGGTTAAACCGG	5640	Db	6661	GTCTTCTGGAAAAGGCACTGTCATAGGAAAGGTTTCCCCCAATCCCAACCACTTTGTAAAC	6720
Db	5581	CAACGGCTGGAAGTGCAGAGGAAATCTCCACCTGGATCCATGATCCAGGTTAAACCGG	5640	QY	6721	CACACTGAAAGCTTTTAACTCAAACTCTGAGAGTCAATATCTGGTACCTGTTATGACAGG	6780
QY	5641	GGCCACCTCCGATTCGGGGTGAAGAGCGAAAGACTGAAATCCCTTTAAGCTTCGCC	5700	Db	6721	CACACTGAAAGCTTTTAACTCAAACTCTGAGAGTCAATATCTGGTACCTGTTATGACAGG	6780
Db	5641	GGCCACCTCCGATTCGGGGTGAAGAGCGAAAGACTGAAATCCCTTTAAGCTTCGCC	5700	QY	6781	TGCTGGGCACTGTAATCTGGAATTAACCCCTTGTGTTTCCACCTTGGTTTTTAAACCAACT	6840
QY	5701	TCCATCGCGTGGTTTCTTACTCTGTCATTAACCTCTCAGACTAATGATGCGCATAGGA	5760	Db	6781	TGCTGGGCACTGTAATCTGGAATTAACCCCTTGTGTTTCCACCTTGGTTTTTAAACCAACT	6840
Db	5701	TCCATCGCGTGGTTTCTTACTCTGTCATTAACCTCTCAGACTAATGATGCGCATAGGA	5760	QY	6841	AAAGATTTTTCGCAATTTGCTTCCCAATTTGTTCCCGAGTGTATTAATCTATCCGAAAAAGCA	6900
QY	5761	GACAGCTGAATCCCAATAAACCTTACTCTACCTGGTTAATTAATGATGCGGACACA	5820	Db	6841	AAAGATTTTTCGCAATTTGCTTCCCAATTTGTTCCCGAGTGTATTAATCTATCCGAAAAAGCA	6900
Db	5761	GACAGCTGAATCCCAATAAACCTTACTCTACCTGGTTAATTAATGATGCGGACACA	5820	QY	6901	ATCCTTGTGAATATGACTACAGAAATCATCGAATAAGAGAGAACCCATATCTCTGACA	6960
QY	5821	GGTATTAATATCAACACTCAAGGGGAGGCTCTTTTAGGAACTTGGTGGCCTGATCTA	5880	Db	6901	ATCCTTGTGAATATGACTACAGAAATCATCGAATAAGAGAGAACCCATATCTCTGACA	6960
Db	5821	GGTATTAATATCAACACTCAAGGGGAGGCTCTTTTAGGAACTTGGTGGCCTGATCTA	5880	QY	6961	CTTCTGTGATGCTCGGACCTTGGAGTGGCAGAGGTTAGGAAACAGGACGCTGCCCTG	7020
QY	5881	TAGCTTTGCTCAGATCAGTTATTTCTTAGTCTGACCTCACCCCGAGATATCTTCCATGCT	5940	Db	6961	CTTCTGTGATGCTCGGACCTTGGAGTGGCAGAGGTTAGGAAACAGGACGCTGCCCTG	7020
Db	5881	TAGCTTTGCTCAGATCAGTTATTTCTTAGTCTGACCTCACCCCGAGATATCTTCCATGCT	5940	QY	7021	GTCAAGGACCAACAGAGCTTAGAAAACAGGACTTAGTAACTTACATCGAATGTAACAGAA	7080
QY	5941	CACGATTTTATGTTTCCGAGGACCAACCAATTAATGGAATAATTCGGAATCCGACA	6000	Db	7021	GTCAAGGACCAACAGAGCTTAGAAAACAGGACTTAGTAACTTACATCGAATGTAACAGAA	7080
Db	5941	CACGATTTTATGTTTCCGAGGACCAACCAATTAATGGAATAATTCGGAATCCGACA	6000	QY	7081	GATCTTCAAGCTTGAAGAAATCTGTGAGTAACTTGAGGAAATCCCTTAACTCTTATCT	7140
QY	6001	GATTTCTTTTGAACAATGGAAGTGTAACTCTAATGATGATGATGGAATGGAATGCGCA	6060	Db	7081	GATCTTCAAGCTTGAAGAAATCTGTGAGTAACTTGAGGAAATCCCTTAACTCTTATCT	7140
Db	6001	GATTTCTTTTGAACAATGGAAGTGTAACTCTAATGATGATGATGGAATGGAATGCGCA	6060	QY	7141	GAAGTAGTCTCAGATAGAGGGTGTAGTTTATTTCTTAAAGAGAGGAGGATTA	7200
QY	6061	ACCTCTCAGCAGGATAGGTTAAGTTTCTTATGTCACACCTATACCACTCTGAGCAA	6120	Db	7141	GAAGTAGTCTCAGATAGAGGGTGTAGTTTATTTCTTAAAGAGAGGAGGATTA	7200
Db	6061	ACCTCTCAGCAGGATAGGTTAAGTTTCTTATGTCACACCTATACCACTCTGAGCAA	6120	QY	7201	TGTTAGCTTTGAAGAGGAAATCTGTTTTTATGTTGATCATTCAGGGGCCATCAGAGAC	7260
QY	6121	TTTAAATTAACCTGATAGAACTGGAAGCCCAAGTCTCTCTTACAGACTAGAT	6180	Db	7201	TGTTAGCTTTGAAGAGGAAATCTGTTTTTATGTTGATCATTCAGGGGCCATCAGAGAC	7260
Db	6121	TTTAAATTAACCTGATAGAACTGGAAGCCCAAGTCTCTCTTACAGACTAGAT	6180	QY	7261	TCCATGAACAGCTTAGAGAAAGGTTGGAGAGGCTCGAAGGGGAAAAAGGAAATCTCTCAA	7320
QY	6181	TACCTAAAAATAAGTTTCACTGAGAAAGGAAAAACAAGAAAAATATCTTAAATGGGTAAAT	6240				

D	b		7261	TCCATGACAAAGCTTAGAGAAAAGTTGGAGAAGCGTGAAGGAAAAAGGAAACTACTCAA	732380
Q	y		7321	GGGTGGTTTTGAGGGATGGTTCAACAGAGTCCTCTTTTGTTGGCTACCCCTACTTTCTGCTTTTA	73380
D	b		7321	GGGTGGTTTTGAGGGATGGTTCAACAGAGTCCTCTTTTGTTGGCTACCCCTACTTTCTGCTTTTA	73380
Q	y		7381	ACAGGACCCTTAATAGTGCCTCCTCTCTGTTACTCACAGTTGGGCCCATGTATTATTACAAG	7440
D	b		7381	ACAGGACCCTTAATAGTGCCTCCTCTCTGTTACTCACAGTTGGGCCCATGTATTATTACAAG	7440
Q	y		7441	TTAATTGCCTTCATTAGAGAACCAATAAGTGCAGTCCAGATCATGGTACTTTAGACACAACAG	7500
D	b		7441	TTAATTGCCTTCATTAGAGAACCAATAAGTGCAGTCCAGATCATGGTACTTTAGACACAACAG	7500
Q	y		7501	TACCAAGCCCGCTCTAGCAGGGAAGCTGGCGCGCTAGCTCTACCAAGTCTTAAGATTAGAAC	7560
D	b		7501	TACCAAGCCCGCTCTAGCAGGGAAGCTGGCGCGCTAGCTCTACCAAGTCTTAAGATTAGAAC	7560
Q	y		7561	TATTAAACAGAGAAAGTGGGGAATGAAAGGATGAAAAATCAACCTTAAGCTAATGAGAA	7620
D	b		7561	TATTAAACAGAGAAAGTGGGGAATGAAAGGATGAAAAATCAACCTTAAGCTAATGAGAA	7620
Q	y		7621	GCTTAAAAATGTTCTGNAATTCAGAGTTTGCTTCTTATAGGTAAAGATTAGGTTTTTTTG	7680
D	b		7621	GCTTAAAAATGTTCTGNAATTCAGAGTTTGCTTCTTATAGGTAAAGATTAGGTTTTTTTG	7680
Q	y		7681	CTGTTTTTAAAAATATGCGGAAGTAAAAATAGGCCCTGAGTACATGTCTTAGGCATGAAACT	7740
D	b		7681	CTGTTTTTAAAAATATGCGGAAGTAAAAATAGGCCCTGAGTACATGTCTTAGGCATGAAACT	7740
Q	y		7741	TCTTGAAACTATTTTGAGATAACAAGAAAGGAGTTTCTAACTGCTTTGTTTAGCTTCTGT	7800
D	b		7741	TCTTGAAACTATTTTGAGATAACAAGAAAGGAGTTTCTAACTGCTTTGTTTAGCTTCTGT	7800
Q	y		7801	AAAAC TGTTGGCCATAAAGATGTTGAAATGTTGATACATATCTTGGTGACAACATG	7860
D	b		7801	AAAAC TGTTGGCCATAAAGATGTTGAAATGTTGATACATATCTTGGTGACAACATG	7860
 RESULT 5 ABQ76883 ID ABQ76883 standard; DNA; 8918 BP. XX XX ABQ76883; XX XX XX DT 06-MAR-2003 (first entry) XX XX PERV clone PK15-PERV-A(58) DNA. XX XX PERV; porcine; env; gag; infection; vaccine; virucide; immunization; KW pig breeding; chromosome mapping; protection; ds. XX XX Porcine endogenous retrovirus. XX XX DE10111433-Al. XX XX PN XX PD PD 19-SEP-2002. XX PF 09-MAR-2001; 2001DE-01011433. XX PR 09-MAR-2001; 2001DE-01011433. XX XX (BUND) BUNDESREPUBLIK DEUT PAUL-EHRLICH-INST. XX PA Toenjes RR, Krach U; XX PI WPI; 2002-699548/76. XX XX PT Replication-competent molecular clones of porcine endogenous retrovirus, PT useful as sources of env peptides for vaccination and for viral detection. XX PS Claim 3; Fig 14; 52pp; German.					

XX	CC	This invention describes novel replication-competent molecular clones of
CC	CC	porcine endogenous retrovirus (PERV) isolated from a porcine BAC
CC	CC	(bacterial artificial chromosome) library which are replication competent
CC	CC	after transfer into permissive cells. The invention also discloses (a)
CC	CC	env and gag polypeptides encoded by the molecular clones of the invention
CC	CC	; (b) porcine nucleic acids that represent the 5' and 3' flanking
CC	CC	sequences of the integration site of a replication competent molecular
CC	CC	clone in the porcine genome; (c) oligonucleotides for detecting
CC	CC	integrated PERV; (d) a method for detecting appearance of infectious PERV
CC	CC	particles in a sample; (e) a vaccine for immunization against replication
CC	CC	-competent PERV, comprising an env protein and (f) a method for isolating
CC	CC	the molecular clones of the invention. The products of the invention are
CC	CC	have virucide activity. The clones are from native PERV and make possible
CC	CC	comparisons of proviral sequences of different origins at the molecular,
CC	CC	structural and cellular levels, and mapping of proviral sequences at
CC	CC	chromosomal positions in specific breeds of pigs. Also different breeds
CC	CC	of pigs can be screened for presence of specific infectious PERV, i.e. to
CC	CC	identify PERV-free animals. Also vaccines that contain the env
CC	CC	polypeptides encoded by the clones of the invention are useful for
CC	CC	protection against replication-competent PERV. The products of the
CC	CC	invention are functional, replication-competent, full-length, proviral
CC	CC	clones isolated directly from the pig genome, i.e. they are 'native',
CC	CC	PERV. This sequence represents a PERV clone fragment described in the
CC	CC	disclosure of the invention
XX	CC	
SQ	CC	Sequence 8918 BP; 2435 A; 2174 C; 2253 G; 2056 T; 0 U; 0 Other;
	Query Match	85.2%; Score 6931.2; DB 6; Length 8918;
	Best Local Similarity	91.4%; Pred. No. 0;
	Matches 7574; Conservative	0; Mismatches 548; Indels 164; Gaps 15;
QY	1	GCCTGCTGTACGACTGTGGCCCCCAGCGCGCTTGGAAATAAAATCTCTTGTGTTTGA 60
DB	560	GCCTGGCGTACGACTGTGGCCCCCAGCGCGCTCGGAATAAAATCTCTTGTGTTTGA 619
QY	61	TCAAGACCGCTTCTCGTAGTGATTAAGGGGAGTCGCCCTTTCCCGAGCTCGAGG---- 115
DB	620	TCAAGACCGCTTCTCGTAGTGATT--TGGGGTGTCCCTCTTCCGAGTCAGGACGAGAGG 678
QY	116	----TTCTTTTTCGTGCTTACATTTGGGGCTCGTCGGGATCTGTCGGGCCACCCC 171
DB	679	GATTTTAACTCGACTCGCCCTTTCAGTTTGGTGGTGGCGCGGAAACCCGCGACTACCCC 738
QY	172	TACACCCGAGAACCGACTTGGAGGTAAAAAGGATCCTCTTTTAAACGTGT--ATGCATG 229
DB	739	TACACCCGAGAACCGACTTGGAGGT--AAAGGATCCCTTTGGACGTGTGAGTGTGTG 797
QY	230	TACCGCCGCGGCTCTCTGTTCTGAGTGTCTGTTTTTCACTGTGTCGCGCTTTCGGTTGCA 289
DB	798	TGTCGGCTGGCGTCTCTGTTCTGAGTGTCTGTTTTCGGTGTATCGCGCTTTCGGTTGCA 857
QY	290	GCTGTCTCTCAGGCCGTAAGGCTCGGGGACTGTGATCAGCAGAGCTGTAGAGGATC 349
DB	858	GCTGTCTCTCAGACCGTAAGGACTGGGGACTGTGATCAGCAGAGCTGTAGAGGATC 917
QY	350	ACAGGCTGTGTCCTTGGGGACGCCCCCGGAGGTGAGGAGCAGCGGACGCCTGTGTGT 409
DB	918	ACAGGCTGCACCTCTGGGGACGCCCCCGGAGGTGGGAGAGCAGGACGCCTGTGTGT 977
QY	410	CTCTACTGTGCGTCAGAGSACCGAAATCTGTTTGTGAAACGGAAGCTTCCCGCTCCGCG 469
DB	978	CTCTCTTGTGCGTCAAGGACCGGAGTTCGTGTTTGAAGCGGAAGCTTCCCGCTCCGCG 1037
QY	470	ACGCTCGACTCTTTTGCCTGTGTTGGAAGAGCTGGAACGGGTCACTGTGTCGATCT 529
DB	1038	GCGCTCCGACTCTTTTGCCTGTGTTGGAAGAGCGCGGACGGGTCTGTGATCT 1097
QY	530	GTTGGTTTCTGTTTGTGTGTCCTTGTCTGTGTGTCCTTGTCTACAGTTTTTAATATGGG 589
DB	1098	GTTGGTTTCTGTTTGTGTGTCCTTGTCTGTGTGTCCTTGTCTACAGTTTTTAATATGGG 1157
QY	590	ACAGACGGTGACGACCCCTCTTAGTTTGTACTCTCGACCAATGTGACTGAACTTAATCCAG 649

Db	1158	ACAGCGGTGACGACCCCTCTTAGTTTGAAGTCTCGACCAATGAGCTGAAATCCAG	1217	Db	2238	CAGGCGGTTCAACCCCTTTTGATCCTACCTCGGAGGCTCAGAAAGCCTCAATGGCTCTGGC	2297
Qy	650	GGCTCAATAATTTGTCTAGTTTCAAGTAAAGAGGACCTTGGCAGACTTCTGTCTCTCTGA	709	Qy	1730	CTTTATAGGACAGTCTAGCCCTTGATATTAGAAAGAGCTTCAAGAGACTGGAAGGGTTACA	1789
Db	1218	GGCTCAATAATTTGTCTAGTTTCAAGTAAAGAGGACCTTGGCAGACTTCTGTCTCTCTGA	1277	Db	2298	CTTCAATAGGACAGTCTAGCCCTGATATCAGAAAGAGCTTCAAGAGACTGGAAGGGTTACA	2357
Qy	710	ATGCGGCACATTCGATCTGATGGCCATCAGAGGGGACCTTTAAATTTCTCAGATTAATCCT	769	Qy	1790	GGAGGCTGAGTTACGTGATCTAGTGAAGGAGGAGAGAAAGTATATTACAAAAGGGAGAC	1849
Db	1278	ATGCGGCACATTCGATCTGATGGCCATCAGAGGGGACCTTTAAATTTCTCAGATTAATCCT	1337	Db	2358	GGAGGCTGAGTTACATGATCTAGTGAAGGAGGAGAGAAAGTGTATTATACAAAAGGGAGAC	2417
Qy	770	GGCTGTTTAAAGCAGTTATTTTTCAGACTGACCCGGCTCTCATCCCGATCAGAGGCCCTA	829	Qy	1850	AGAAAGAAAGGAAACAAAGAAAGAGAGAGAAAGAGAGAAAGGAGGAGAAAGACCTGAA	1909
Db	1338	GGCTGTTTAAAGCAGTTATTTTTCAGACTGACCCGGCTCTCATCCCGATCAGAGGCCCTA	1397	Db	2418	AGAAGAAAGAAAGGAAACAAAGAAAGAGAGAGAAAGAGAGAAAGGAGGAGAAAGACCTGAA	2477
Qy	830	TATCTTTACGTGGCAGATTTGGCAGAGGATCTCCCGCATGGTTTAAACCATGGCTGAA	889	Qy	1910	TAAACGGCAAGAGAGAAATTTTGAATCTTTGGCTGCAAGTCTTTGGCTGCAAGTCTTTGAAGGAGAAAGCAA	1969
Db	1398	TATCTTTACGTGGCAGATTTGGCAGAGGATCTCCCGCATGGTTTAAACCATGGCTGAA	1457	Db	2478	TAAACGGCAAGAGAGAAATTTTGAATCTTTGGCTGCAAGTCTTTGGCTGCAAGTCTTTGAAGGAGAAAGCAA	2537
Qy	890	TAAAGCCAAAGCCAGGTCCTCCGAAATTCGGCTCTTTGGAGAGAGAAACAAACACTCGGC	949	Qy	1970	TACGGAAAGAGAGAGAGATTTTATAGGAAATATTAGTCTAGGCCCTTAGACAGTCAAGGAAACCT	2029
Db	1458	TAAAGCCAAAGCCAGGTCCTCCGAAATTCGGCTCTTTGGAGAGAGAAACAAACACTCGGC	1517	Db	2538	TAGGAAAGAGAGAGAGATTTTATAGGAAATATTAGTCTAGGCCCTTAGACAGTCAAGGAAACCT	2597
Qy	950	TGAAAAAGTCAAGCCCTCTCTCATATCTATACCCCGAGATTGAGGAGCCACCGGCTTGGCC	1009	Qy	2030	GGGCAATAGGACCCCACTCGACAAAGGACCAATCTGTCATATTGTAAAGAAAGAGAGACACTG	2089
Db	1518	TGAAAAAGTCAAGCCCTCTCTCATATCTATACCCCGAGATTGAGGAGCCACCGGCTTGGCC	1577	Db	2598	GGGCAATAGGACCCCACTCGACAAAGGACCAATCTGTCATATTGTAAAGAAAGAGAGACACTG	2657
Qy	1010	GGAAACCCCAATCTGTTCCCGACCCCTTATCTGGCAAGGGTCCCGGAGGGAGACCTT	1069	Qy	2090	GGCAAGGAACTGCCCAAGAAAGGAAACAAAGGACCAAGGATCCTAGCTCTTAGAAGAAAGA	2149
Db	1578	GGAAACCCCAATCTGTTCCCGACCCCTTATCTGGCAAGGGTCCCGGAGGGAGACCTT	1637	Db	2658	GGCAAGGAACTGCCCAAGAAAGGAAACAAAGGACCAAGGATCCTAGCTCTTAGAAGAAAGA	2717
Qy	1070	TGCCCCCTCTGGAGCTCGGCGGTGGAGGACCTCTGCGAGGACTCGAGAGCCGAGGGG	1129	Qy	2150	TAAAGATTATGGGAGAGCGGGTTGGACCCCTCCCGAGCCCGAGGCTTCTTTGAAGGT	2209
Db	1638	TGCCCCCTCTGGAGCTCGGCGGTGGAGGACCTCTGCGAGGACTCGAGAGCCGAGGGG	1697	Db	2718	TAAAGATTATGGGAGAGCGGGTTGGACCCCTCCCGAGCCCGAGGCTTCTTTGAAGGT	2777
Qy	1130	GGCACCCCGAGGCGGACAGACGAGATCGGACATTAACCGCTGGCGACACTACCGCCCTCC	1189	Qy	2210	GGAGGGCAACCACTGAGTTGAGTTCTGGTTGATACCGGAGCGGAAACATTCAGTCTACTACA	2269
Db	1698	GGCACCCCGAGGCGGACAGACGAGATCGGACATTAACCGCTGGCGACACTACCGCCCTCC	1757	Db	2778	GGAGGGCAACCACTGAGTTGAGTTCTGGTTGATACCGGAGCGGAAACATTCAGTCTACTACA	2837
Qy	1190	CACACCGGGGGGCAATTTGACGCCCTCTCAGTATTTGGCCCTTTTCTTCTGAGATCTCTA	1249	Qy	2270	GCCATTAGGAAACTTAAAGATAAAAATCTCTGGGTGATGGGTGCCACAGGGGCAACACA	2329
Db	1758	CATACCGGGGGGCAATTTGACGCCCTCTCAGTATTTGGCCCTTTTCTTCTGAGATCTCTA	1817	Db	2838	GCCNTTAGGAAACTTAAAGATAAAAATCTCTGGGTGATGGGTGCCACAGGGGCAACACA	2897
Qy	1250	TAAITGGAAACTAACCATCCCCCTTCTCGAGGATCCCAACGCTCAGCGGGTTGGT	1309	Qy	2330	GTATTCATGGAATAACCGAAGAACAGTTGACTTTGGGAGTGAGCGGGTAAACCCACTCGTT	2389
Db	1818	TAAITGGAAACTAACCATCCCCCTTCTCGAGGATCCCAACGCTCAGCGGGTTGGT	1877	Db	2898	ATATCCATGACTTACCCGAAAGAACAGTTGACTTTGGGAGTGAGCGGGTAAACCCACTCGTT	2957
Qy	1310	GGAGTCCCTTATGTTCTCTCACGACCTTCTTGGATGATTTGTCAACAGCTGCTGCAGAC	1369	Qy	2390	TCGTGTCATACCTGAGTGCCCGACGACCCCTCTTGGTGTAGTGTAGTGTATTTGACCAAGATCGG	2449
Db	1878	GGAGTCCCTTATGTTCTCTCACGACCTTCTTGGATGATTTGTCAACAGCTGCTGCAGAC	1937	Db	2958	TCTGGTCATACCTGAGTGCCCGACGACCCCTCTTAGGTAGAGACTTACTGACCAAGATGGG	3017
Qy	1370	ACTCTTCAACCGAGGAGCGAGAGAAATTTCTATTAGAGCTAGAAAAATGTTCTCTGG	1429	Qy	2450	AGCACAAATTTCTTTTGAACAAAGGAAACCAAGAGTGTCTGCAATTAACAAACCTTATCAC	2509
Db	1938	ACTCTTCAACCGAGGAGCGAAGAGAAATTTCTGTTAGAGCTAGAAAAATGTTCTCTGG	1997	Db	3018	AGCACAAATTTCTTTTGAACAAAGGAAACCAAGAGTGTCTGCAATTAACAAACCTTATCAC	3077
Qy	1430	GGCCGACGGGCGACCCACGGGTTGCAAAATAGAGATTGACATGGATTTCCCTTAACCTCG	1489	Qy	2510	TGCTTGACCCCTCCAAATTTAGATGAGAAATATCGACTATATCTCCCTTAGTAAAGCCCTGA	2569
Db	1998	GGCCGACGGGCGACCCACGGAGTTGCAAAATAGAGATTGACATGGATTTCCCTTGAATCG	2057	Db	3078	TGCTTGACCCCTCCAAATTTAGATGAGAAATATCGACTATATCTCCCTTAGTAAAGCCCTGA	3137
Qy	1490	CCCCGTTGGGACTACACCGGCTGAAGGTAGGAGAGCTTGAATAATCTATCGCGAGGC	1549	Qy	2570	TCAAAAATATACAAATTTCTGGTTGGAAACAGTTTCCCAAGCCCTGGGAGGAAACCGGAGGAT	2629
Db	2058	CCCCGTTGGGACTACACCGGCTGAAGGTAGGAGAGCTTGAATAATCTATCGCGAGGC	2117	Db	3138	TCAAAAATATACAAATTTCTGGTTGGAAACAGTTTCCCAAGCCCTGGGAGGAAACCGGAGGAT	3197
Qy	1550	TCTGTGTGGGCTCTCCCGGGCGCTCAAGAGCGGCCACTAATTTGGCTAAGGTAAGAGA	1609	Qy	2630	GGGTTTGGCAAGCAAGTTCCCGCACAGTTTATCACTGAAGGCGAGTGGCCACACCACT	2689
Db	2118	TCTGTGTGGGCTCTCCCGGGCGCTCAAGAGCGGCCACTAATTTGGCTAAGGTAAGAGA	2177	Db	3198	GGGTTTGGCAAGCAAGTTCCCGCACAGTTTATCACTGAAGGCGAGTGGCCACACCACT	3257
Qy	1610	AGTGTATGAGGAGCCGAATGAACCCCTCTGTGTTTTCTTGAGAGGCTCTTGGAGCCCTT	1669	Qy	2690	GTCACTCAGACAGTACCCCTTTGAGTAAAGAAAGCTCAAGAAAGAAATTCGGCCGACCTGTA	2749
Db	2178	GGTGTATGAGGAGCCGAATGAACCCCTCTGTGTTTTCTTGAGAGGCTCTTGGAGCCCTT	2237	Db	3258	GTCACTCAGACAGTACCCCTTTGAGTAAAGAAAGCTCGAAGAGAAATTCGGCCGACCTGTA	3317
Qy	1670	CAGGCGGTACACCCCTTTGATCCCACTCAGAGGCCCAAAAGCCTCAGTGGCTTTGGC	1729	Qy	2750	AAGATTAAATCCAAAGGCGATCTAGTTCCTGTGCAATCTCCCTGGAAATCTCCCTCTGCT	2809
				Db	3318	AAGATTAAATCCAAAGGCGATCTAGTTCCTGTGCAATCTCCCTGGAAATCTCCCTCTGCT	3377

QY	2810	ACCGGTTAGAAAGCCTGGAGCTAATGACTATCGACCAGTACAGGACTTGAGAGAGTCAA	2869	QY	3890	CTATCAAAGCCTGCTTCTCA	3949
Db	3378	ACCGGTTAGAAAGCCTGGAGCTAATGACTATCGACCAGTACAGGACTTGAGAGAGTCAA	3437	Db	4458	CTATCAAAGCCTGCTTCTCA	4517
QY	2870	TAAACGGGTGCAGGATATACACCAACAGTCCGAAACCTTATACCTCTTGCTCT	2929	QY	3950	TGCCACTCTTCTGCTGAAGAGACTGATGAACAGTACTCATGATTGTCATCAACTATT	4009
Db	3438	TAAACGGGTGCAGGATATACACCAACAGTCCGAAACCTTATACCTCTTGCTCT	3497	Db	4518	TGCCACTCTTCTGCTGAAGAGACTGATGAACAGTACTCATGATTGTCATCAACTATT	4577
QY	2930	CCACCCCAACGAGCTGGTATACAGTATTGGACTTAAAGGATGCCCTTCTTGCTGAG	2989	QY	4010	GATTGAGAGACTGGGGTCCGCAAGGACCTTACAGACATACCGCTGACTGGAGAGTGT	4069
Db	3498	CCACCCCAACGAGCTGGTATACAGTATTGGACTTAAAGGATGCCCTTCTTGCTGAG	3557	Db	4578	GATTGAGAGACTGGGGTCCGCAAGGACCTTACAGACATACCGCTGACTGGAGAAATGTT	4637
QY	2990	ATTACACCCCACTAGCCAACTTTTTCCTTTCGAATGGAGAGATCCAGGTACGGGAAG	3049	QY	4070	AACCTGGTTCACTGACGGAGCAGCTATGTGTGGAAGGTAAAGGATGGCTGGGGCGG	4129
Db	3558	ACTACATCCCACTAGCCAACTTTTTCCTTTCGAATGGAGAGATCCAGGTACGGGAAG	3617	Db	4638	AACCTGGTTCACTGACGGAGCAGCTATGTGTGGAAGGTAAAGGATGGCTGGGGCGG	4697
QY	3050	AACCGGCGAGCTCACCTGGACCGGCTGCCCAAGGGTTCAAGAACTCCCGACCATCTT	3109	QY	4130	GGTGTGGACGGGACCCGCAACGATCTGGGCCAGCAGCTGCCGGAAGAACTTTCAGCAC	4189
Db	3618	AACCGGCGAGCTCACCTGGACCGGCTGCCCAAGGGTTCAAGAACTCCCGACCATCTT	3677	Db	4698	GGTGTGGACGGGACCCGCAACGATCTGGGCCAGCAGCTGCCGGAAGAACTTTCAGCAC	4757
QY	3110	TGACGAAGCCCTACACAGAGACTGGCCAACTTTCAGGATCCAAACCCCTCAGGTGACCT	3169	QY	4190	AAAGGCTGAGCTCATGGCCCTCACCAAGCTTTTGGCGCTGGCCGAAGGAAATCCATAAA	4249
Db	3678	TGACGAAGCCCTACACAGAGACTGGCCAACTTTCAGGATCCAAACCCCTCAGGTGACCT	3737	Db	4758	AAAGGCTGAGCTCATGGCCCTCACCAAGCTTTTGGCGCTGGCCGAAGGAAATCCATAAA	4817
QY	3170	CCTCCAGTACGTGGATGACCTGCTTCTGGCGGAGCCACAAACAGGACTGCTTGAAGG	3229	QY	4250	CATTTATACGGAACAGAGTATGCCCTTTGCGACTGCAACGTTACATGGGGCCATCTATAA	4309
Db	3738	CCTCCAGTACGTGGATGACCTGCTTCTGGCGGAGCCACAAACAGGACTGCTTGAAGG	3797	Db	4818	CATTTATACGGAACAGAGTATGCCCTTTGCGACTGCAACGTTACATGGGGCCATCTATAA	4877
QY	3230	CAGGAAGCACTACTGCTGGAATTTGCTGACCTAGGCTACAGAGCTCTGCTAAGAGGC	3289	QY	4310	ACAAAGGGGTTGCTTACTCTCAGCAGGGAGGGAATAAAGAACAAAGAGGAAATTTCTAAG	4369
Db	3798	TACGAAGGCACTACTGCTGGAATTTGCTGACCTAGGCTACAGAGCTCTGCTAAGAGGC	3857	Db	4878	GCAAAGGGGTTGCTTACTCTCAGCAGGGAGGGAATAAAGAACAAAGAGGAAATTTCTAAG	4937
QY	3290	CCAGATTTTCAGGAGAGGTAAACATCTTGGGGTACAGTTTGGGAGCGGCGAGGATG	3349	QY	4370	CCTATTAGAAGCGGTACATTTACCAAAAGGCTAGCTATTATACACTGCTCTGGACATCA	4429
Db	3858	CCAGATTTTCAGGAGAGGTAAACATCTTGGGGTACAGTTTGGGAGCGGCGAGGATG	3917	Db	4938	CCTATTAGAAGCGGTACATTTGCCAAAGGCTAGCTATTATACACTGCTCTGGACATCA	4997
QY	3350	GCTGACGGAGGACCGAAGAACTGTAGTCCAGATACCGGGCCCAACACAGCCAAACA	3409	QY	4430	GAAGCTAAAGTCTCATATCCAGAGGAAACAGATGGCTGACCGGGTTGCCAAGCAGGC	4489
Db	3918	GCTGACGGAGGACCGAAGAACTGTAGTCCAGATACCGGGCCCAACACAGCCAAACA	3977	Db	4998	GAAGCTAAAGTCTCATATCCAGAGGAAACAGATGGCTGACCGGGTTGCCAAGCAGGC	5057
QY	3410	AATGAGAGATTTTGGGAGCAGCTGGATTTTGCAGACTGTGGATCCCGGGTTTGGGAC	3469	QY	4490	AGCCAGGAGGTAAACCTTCTGCCTATATAGAAATGCCAAGCCCAAGCCCAAGACCCAGAGC	4549
Db	3978	AGTGAGAGATTTTGGGAGCAGCTGGATTTTGCAGACTGTGGATCCCGGGTTTGGGAC	4037	Db	5058	AGCCAGGAGGTAAACCTTCTGCCTATATAGAAACACCAAGCCCAAGACCCGAGC	5117
QY	3470	CTTAGCAGCCCACTCTACCGCTAACCAAGAAAGGGAATTTCTCTGGCTCCTGA	3529	QY	4550	ACAGTACACCCCTAGAAGACTGGCAAGAGATAAAGATAGACCACTCTCTGAGACTCC	4609
Db	4038	CTTAGCAGCCCACTCTACCGCTAACCAAGAAAGGGAATTTCTCTGGCTCCTGA	4097	Db	5118	ACAGTACACCCCTAGAAGACTGGCAAGAAATAAAGATAGACCACTCTCTGAAACTCC	5177
QY	3530	GCACGAAGAGCAATTTGATGCTATCAAAAGGCCCTGTGAGCGCACCTGCTGCGCCT	3589	QY	4610	GGAAAGGACCTGCTATACCTCAGATGGGAGGAAATCTGCCCCCAAAAGAGGGTTAGA	4669
Db	4098	GCACGAAGAGCAATTTGATGCTATCAAAAGGCCCTGTGAGCGCACCTGCTGCGCCT	4157	Db	5178	GGAGGGGACCTGCTATACCTCAGATGGGAGGAAATCTGCCCCCAAAAGAGGGTTAGA	5237
QY	3590	CCCTGACGTAACTAAACCTTTTACCTTTATGTGGATGAGCGTAAGGGAGTAGCCGGGG	3649	QY	4670	ATATGTCCAAACAGATACATCGTCTAACCCACTAGGAACCTAACCTGAGAGTGGT	4729
Db	4158	CCCTGACGTAACTAAACCTTTTACCTTTATGTGGATGAGCGTAAGGGAGTAGCCGGGG	4217	Db	5238	ATATGTCCAAACAGATACATCGTCTAACCCACTAGGAACCTAACCTGAGAGTGGT	5297
QY	3650	AGTTTTAACCCAAACCTTAGGACCATGGAGAGACCTGTGCGCTACTCTCRAAGAGCT	3709	QY	4730	CAGAAACATCCCCTTATCATGTTCTGAGGCTACAGAGGTGGCTGACTCGGTGGTCAACA	4789
Db	4218	AGTTTTAACCCAAACCTTAGGACCATGGAGAGACCTGTGCGCTACTCTCRAAGAGCT	4277	Db	5298	CAGAAACATCCCCTTATCATGTTCTGAGGCTACAGAGGTGGCTGACTCGGTGGTCAACA	5357
QY	3710	CGATCCTGTAGCCAGTGGTGGCCCATATGCCCTGAAGGCTATCGCAGCTGTGGCCATCT	3769	QY	4790	TTGTGTGCCCTGCCAGCTGTTAATGCTTAATCTTCCAGAAATGCCCTCCAGGGAAGAGCT	4849
Db	4278	CGATCCTGTAGCCAGTGGTGGCCCATATGCCCTGAAGGCTATCGCAGCTGTGGCCATCT	4337	Db	5358	TTGTGTGCCCTGCCAGCTGTTAATGCTTAATCTTCCAGAAATGCCCTCCAGGGAAGAGCT	5417
QY	3770	GFTCAAGGACGTGACAAATTTGATTTGGGACAGAAATATACTGTAAATAGCCCCCATGC	3829	QY	4850	RAAGGGAGCCACCCAGGCGCTCACTGGGAAGTGAACCTTCACTGAGGTAAAGCCGCTAA	4909
Db	4338	GGTCAAGGACGTGACAAATTTGACTTTGGGACAGAAATATACTGTAAATAGCCCCCATGC	4397	Db	5418	RAAGGGAGCCACCCAGGCGCTCACTGGGAAGTGAACCTTCACTGAGGTAAAGCCGCTAA	5477
QY	3830	ATTGGAGACATGTTCCGACGCCCCAGACCGATGGATGACCAACCGCCCGATGACCCA	3889	QY	4910	ATACGGAACAAATACCTATTGTTTTGTAGACACCTTTTCAGGATGGGTAGAGCTTA	4969
Db	4398	GTTGGAGACATGTTCCGACGCCCCAGACCGATGGATGACCAACCGCCCGATGACCCA	4457	Db	5478	ATACGGAACAAATATCTATTGTTTTGTAGACACCTTTTCAGGATGGGTAGAGCTTA	5537
				QY	4970	TCCTACTAAGAAAGAGACTTCAACCGGTGGTGGCTAAAAAATACCTGGAAGAAATTTTTTC	5029

QY 7127 TAACCTCCTTATCTGAAGTAGTCTCTTACAGAAATAGAAAGAGGGTTAGATTTATTATTCTTAA 7186
 Db |||||
 QY 7187 AAGAGGAGGATTTATCTGAGCTTCAAGGAGGAATGCTGTTTATGTTGATCATTCAG 7246
 Db |||||
 QY 7815 AAGAAGGAGGGTTATGTGAGCCTTAAAGAGGAATGCTGCTTTTATGTTGATCATTCAG 7874
 Db |||||
 QY 7247 GGGCCATCAGAGACTCCATGAACAAGCTTTAGAAAAGGTTGAGAAAGCGTTCGAAGGAAA 7306
 Db |||||
 QY 7875 GAGCTATCAGGACTCCATGAGCAAGCTCAGAAAAGGTTGAAAACGTCACAAAGAA 7934
 Db |||||
 QY 7307 AGGAAACTACTCAAGGGTGGTTGAGGGATGGTTCAACAGGTCTCTTTGGTTGGCTACCC 7366
 Db |||||
 QY 7935 AAGAGGCTGGCCAAAGATGGTTGAGGGATGGTTCAACAAGTCCCATGGTGACCAACC 7994
 Db |||||
 QY 7367 TACTTTCTGTTTAAACAGGACCTTAAATAGTCTCTCTCTCTTACTACAGTTGGCCAT 7426
 Db |||||
 QY 7995 TGTCTTCTGCTTAAACAGGACCTTAAATAGTCTCTCTCTTACTAGTTGGGCCTT 8054
 Db |||||
 QY 7427 GTATTATTAAACAGTTAAATGCTTCAATTAGAGAACGAATAAGTGCAGTCCAGATCATGG 7486
 Db |||||
 QY 8055 GCTTAATTAATCGGTTTGTGCTTTGTTAGAACAAAGTGAAGTGCAGTTCGATCATGG 8114
 Db |||||
 QY 7487 TACTTAGACAACAGTACCAAGCCGCTCTAGC---AGGGAAGCTGGCCGCTAGCTTACC 7543
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 QY 8115 TACTTAGACAGCAGTACCAAGGCCCTTCCAAGCTTAAGGAGAACTGACCTTTAGCCTTCT 8174
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 QY 7544 AGTTCTAAGATTAGAACTATTAAACAGAGAAGTGGGGAATGAAGGATGAAATACAAATACA 7603
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 QY 8175 AGTTCTAAGATTAGAACTATTAAACAGAGAAGTGGGGAATGAAGGATGAAATGCA 8234
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 QY 7604 ACCT-----AAGCTAATGAGAAGCTTAAATGTTCTGAATTCAG 7644
 Db |||||
 QY 8235 ACCTGACTCCACGAACCCAGGAAGTTAATAGAAAGCTCTAAATGCCCTCGAATTCAG 8294
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 QY 7645 AGTTTGTCTCTATAGTAAAGATTAGGTTTTTGTCTGTTTAAATATGC----- 7696
 Db |||||
 QY 8295 ACCCTGTTCCCTATAGTAAAGATCATCTTTTGTCTGTTTGGGCTTGTCTTCTGCT 8354
 Db |||||
 QY 7697 -----GGAAGTAAATAGGCCCTCAGTACATGCTCTAGGATGA 7736
 Db |||||
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 Db |||||
 QY 7737 AACTCTCTGAAA-----CTATTTGAGATAACA 7763
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 QY 8415 AACTCTTGAAACTGCTCCTAAGTCTGTTGGCTTCTGTAAACCTGCTTGATTAAGAT 8474
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 QY 7764 AGAAAAGGGAGTTTCTAAGTCTGTTTGTAGCTTCTGTAAACCTGTTGGCCATTAAGAT 7823
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 QY 8475 AAAAAGAGGAGAGTCAATTGCCCTAACGGACCCAGTAAGATCGGGCGTGCCACAAAATG 8534
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 QY 7824 GTTGAATGTTGATACACATATCTGGTGACAAACATGCTCTCCCAACCCCGAAACATGG 7883
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 QY 8715 GTTGTGAACCCCAATAAAGCTGTCAGCTCCACACTCGGGGGCGGAGTCTCTACCCCT 8774
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 QY 8062 GCGTGTGTACGACTGTGGGCCCCAGCGGCTTGGAAATAAATCTCTTGTCTGTTTGA 8121
 Db |||||
 QY 8775 GCGTGGGTACGACTGTGGGCCCCAGCGGCTCGGAATAAATCTCTTGTCTGTTTGA 8834
 Db |||||

QY 8122 TCAGAA 8127
 Db 8835 TCAGAA 8840
 RESULT 6
 ABQ76885
 ID ABQ76885 standard; DNA; 8918 BP.
 XX AC ABQ76885;
 XX DT 06-MAR-2003 (first entry)
 XX DE PERV clone PK15-PERV-A(Bac-130A12) DNA.
 XX KW PERV; porcine; env; gag; infection; vaccine; virucide; immunization;
 XX KW pig breeding; chromosome mapping; protection; ds.
 XX OS Porcine endogenous retrovirus.
 XX PN DE10111433-A1.
 XX PD 19-SEP-2002.
 XX PF 09-MAR-2001; 2001DE-01011433.
 XX PR 09-MAR-2001; 2001DE-01011433.
 XX PA (BUND) BUNDESREPUBLIK DEUT PAUL-EHRLICH-INST.
 XX PI Toenjes RR, Krach U;
 XX DR WPI; 2002-699548/76.
 XX PT Replication-competent molecular clones of porcine endogenous retrovirus,
 XX PT useful as sources of env peptides for vaccination and for viral
 XX PT detection.
 XX PS Claim 7; Fig 16; 52pp; German.
 CC This invention describes novel replication-competent molecular clones of
 CC porcine endogenous retrovirus (PERV) isolated from a porcine BAC
 CC (bacterial artificial chromosome) library which are replication competent
 CC after transfer into permissive cells. The invention also discloses (a)
 CC env and gag polypeptides encoded by the molecular clones of the invention
 CC ; (b) porcine nucleic acids that represent the 5' and 3' flanking
 CC sequences of the integration site of a replication competent molecular
 CC clone in the porcine genome; (c) oligonucleotides for detecting
 CC integrated PERV; (d) a method for detecting appearance of infectious PERV
 CC particles in a sample; (e) a vaccine for immunization against replication
 CC -competent PERV, comprising an env protein and (f) a method for isolating
 CC the molecular clones of the invention. The products of the invention are
 CC have virucide activity. The clones are from native PERV and make possible
 CC comparisons of proviral sequences of different origins at the molecular,
 CC structural and cellular levels, and mapping of proviral sequences at
 CC chromosomal positions in specific breeds of pigs. Also different breeds
 CC of pigs can be screened for presence of specific infectious PERV, i.e. to
 CC identify PERV-free animals. Also vaccines that contain the env
 CC polypeptides encoded by the clones of the invention are useful for
 CC protection against replication-competent PERV. The products of the
 CC invention are functional, replication-competent, full-length, proviral
 CC clones isolated directly from the pig genome, i.e. they are 'native'
 CC PERV. This sequence represents a PERV clone fragment described in the
 CC disclosure of the invention
 XX SQ Sequence 8918 BP; 2428 A; 2174 C; 2254 G; 2061 T; 0 U; 1 Other;
 Query Match 84.0%; Score 6832.4; DB 6; Length 8918;
 Best Local Similarity 91.0%; Pred. No. 0;
 Matches 7542; Conservative 1; Mismatches 573; Indels 176; Gaps 19;
 QY 1 GCGTGGTGTACACTGTGGCCCGCCAGCGCTTGGATAAATCTCTGCTGTTTGA 60
 |||||

Db 560 GCCTGGCTACGACTGTGGCCCCCAGCGCGCTCGGAATAAAAAATCCTCTTGTGTTTGCA 619
Qy 61 TCAAGACCGCTTCTCGTACGTGATTAAGGGAGTCGCGCTTTTCGAGCCTCGAGG----- 115
Db 620 TCAAGACCGCTTCTCGTACGTGATTTGGGGTGTGCGCTCTTCGAGTCAGGACGAGAGG 678
Qy 116 -----TTCTTTTGTGCTCTTACATTTGGGGGCTCGTCCGGATCTGTCCGGCCACCCC 171
Db 679 GATTTTAACTCGACTGCGCTTTCAGTTTGGTGGCTTGGCCGGGAAACCCGCGACTACCCC 738
Qy 172 TAACACCCGAGAACCGACTTGGAGTAAAGAGATCCTCTTTTAAAGTCT--ATGCATG 229
Db 739 TCACACCCGAGAACCGACTTGGAGGT-AAAAGGATCCCTTTGGAACGTGTGAGTGTGTG 797
Qy 230 TACCGGCCGCGCTCTGTTCTGAGTCTGTGTTTTCAGTGTGTGCGCGCTTTTCGGTTTGCA 289
Db 798 TGTCCGCTGGCGTCTCTGTTCTGAGTGTCTGTTTTCGGTGTATGCGCGCTTTCGGTTTGCA 857
Qy 290 GCTGTCTCTCAGGCCGTAAAGGCTGGGGGACTGTGATCAGCAGACGTCTAGAGGATC 349
Db 858 GCTGTCTCTAAGACCGTAAGGACTGGGGG-----ATCAGCAGCGTCTAGAGGATC 912
Qy 350 ACAGGCTGTGCTCGCGTGGGGAGCGCCC-----GGAGGTGAGGAGACCCAGGACGCTG 404
Db 913 ACAGGCTGCCACCTGGGGGACGCCCGCTGTGGGAGGTGGGGAGAGCCAGGGACGCTG 972
Qy 405 GTGCTCTCTACTCTGCGTCAGAGGACCGAATCTGTTGCTGGAAGCAAAAGCTTCCCGCT 464
Db 973 GTGCTCTCTCTGCTCGGTCAGAGGACCGAGTCTGTGTTTGAAGCAAAAGCTTCCCGCT 1032
Qy 465 CCGGACCGCTCCGACTCTTTTGCCTGCTTGTGGAAGACGTGGACCGGCTCAGTGTGTCTG 524
Db 1033 CCGGCGCGTCCGACTCTTTTGCCTGCTTGTGGAAGACCGGACCGGCTCGGTGTGTCTG 1092
Qy 525 GATCTGTGTTCTGTGTTGTGTCTTGTCTGTGTGTCTGTGTGTCTGTGTCTGTGTCTGT 584
Db 1093 GATCTGTGTTCTGTGTTGTGTCTTGTCTGTGTGTCTGTGTCTGTGTCTGTGTCTGTGT 1152
Qy 585 ATGGGACAGCGGTGAGACCCCTCTAGTTTGTGACTCTCGACCATTTGAGCTGAAGTTAAA 644
Db 1153 ATGGGACAGCGGTGAGACCCCTCTAGTTTGTGACTCTCGACCATTTGAGCTGAAGTTAAA 1212
Qy 645 TCCAGGGCTCATAAATTTGTCAAGTTCAAGTTAAGAGGACCTTGGCAGACTTCTGTGTCT 704
Db 1213 TCCAGGGCTCATAAATTTGTCAAGTTCAAGTTAAGAGGACCTTGGCAGACTTCTGTGTCT 1272
Qy 705 TCTGAATGGCCGACATTCGATGTTGGATGGCCATCAGAGGGGACCTTTAAATCTGAGATT 764
Db 1273 TCTGAATGGCCGACATTCGATGTTGGATGGCCATCAGAGGGGACCTTTAAATCTGAGATT 1332
Qy 765 ATCTGTGCTGTTAAGCAGTTATTTTTCAGACTGGACCCGCTCTCATCCCGATCAGGAG 824
Db 1333 ATCTGTGCTGTTAAGCAGTTATTTTTCAGACTGGACCCGCTCTCATCCCGATCAGGAG 1392
Qy 825 CCCTATATCTTACGTGCAAGATTGTGCAGAGGATCCTCGCCCATGGGTTAAACCATGG 884
Db 1393 CCCTATATCTTACGTGCAAGATTGTGCAGAGGATCCTCGCCCATGGGTTAAACCTTGG 1452
Qy 885 CTGAATAAGCAAGAAAGCCAGGTCCTCCGAAATTCCTGGCTTTGGAGAGAAAAACAACAC 944
Db 1453 CTGAATAAGCAAGAAAGCCAGGTCCTCCGAAATTCCTGGCTTTGGAGAGAAAAACAACAC 1512
Qy 945 TCGGCTGAATAAGTCAAGCCCTCTCTCATATCTACCCCGAGATTGAGAGGCCACCGCT 1004
Db 1513 TCGGCTGAATAAGTCAAGCCCTCTCTCATATCTACCCCGAGATTGAGAGGCCACCGCT 1572
Qy 1005 TGGCCGGACCCCAATCTGTTCCCGACCCCTTATCTGGCACAGGTCGCGCAGGGGA 1064
Db 1573 TGGCCGGACCCCAATCTGTTCCCGACCCCTTATCTGGCACAGGTCGCGCAGGGGA 1632
Qy 1065 CCCTTTGCGCTCTCTGAGCTCCGGCGGTGGAGGACCTGTGCAAGGACTCGGAGCCGG 1124
Db 1633 CCCTCTGCGCTCTCTGAGCTCCGGCGGTGGAGGACCTGTGTCAGGGACTCGGACCCGG 1692

Qy 1125 AGGGGCGCCACCCCGAGCGGACAGAGAGATCGGACATTACCGCTGCGCAGCTACGGC 1184
Db 1693 AGGGGCGCCACCCCGAGCGGACAGAGAGATCGGACATTACCGCTGCGCAGCTACGGC 1752
Qy 1185 CCTCCACACCGGGGGCCAAATTGACGCCCTCCAGTATTGGCCCTTTTCTTCTGTCAGAT 1244
Db 1753 CTTCCCATATCCGGGGGCCAATTGACGCCCTCCAGTATTGGCCCTTTTCTTCTGTCAGAT 1812
Qy 1245 CTCCTATAATTGGAATACTAAACCATCCCTTTTCTCGAGGATCCCCAACGCTCACGGG 1304
Db 1813 CTCCTATAATTGGAATACTAAACCATCCCTTTTCTCGAGGATCCCCAACGCTCACGGG 1872
Qy 1305 TTGGTGTGAGTCCCTTATGTTCTCTACCGCCTACTTGGGATGATTTGTCACAGCTCCTG 1364
Db 1873 TTGGTGTGAGTCCCTTATGTTCTCTCACCGCCTACTTGGGATGATTTGTCACAGCTCCTG 1932
Qy 1365 CAGACACTCTTCAACACCGAGGACGAGAGAGAAATCTATTAGAGGCTAGAAAAAATGTT 1424
Db 1933 CAGACACTCTTCAACACCGAGGACGAGAGAGAAATCTGTTAGAGGCTAGAAAAAATGTT 1992
Qy 1425 CTTGGGGCCGACGGGGACCCACGCGTTCGAAAAATGAGATTGACATGGGATTTCCCTTA 1484
Db 1993 CTTGGGGCCGACGGGGACCCACGCGATTGCAAAATGAGATTGACATGGGATTTCCCTTG 2052
Qy 1485 ACTCGCCCCCGTTGGGACTACAAACACGCTGAAAGGTAGGAGAGCTTTGAAAAATCTATCG 1544
Db 2053 ACTCGCCCCCGTTGGGACTACAAACACGCTTGAAGGTAGGAGAGCTTTGAAAAATCTATCG 2112
Qy 1545 CAGGCTCTGTGGGGGTCTCCGGGGCGCTCAAGACGGCCCACTAAATTTGGTCAAGGTA 1604
Db 2113 CAGGCTCTGTGGGGGTCTCCGGGGCGCTCAAGACGGCCCACTAAATTTGGTCAAGGTA 2172
Qy 1605 AGAAGTGTATCAGGAGACCGAATGAACCCCTCTGTCTTTTCTTGAGAGGCTCTTGAA 1664
Db 2173 AGAAGTGTATCAGGAGACCGAATGAACCTCCCTCAGTTTCTTGAGAGGCTCATGAA 2232
Qy 1665 GCCTTCAGGCGGTACACCCCTTTTGATCCCACTCAGAGGCCCAAAAGCCCTCAGTGCT 1724
Db 2233 GCCTTCAGGCGGTACACCCCTTTTGATCCCTACCTCGGAGGCTCAGAAAGCCCTCAGTGCT 2292
Qy 1725 TTGGCTTTTATAGGACAGTCAAGCTTGGATATTAGAAGAGCTTTCAGAGACTCGAAGG 1784
Db 2293 CTGGCTTTTATAGGACAGTCAAGCTTGGATATTAGAAGAGCTTTCAGAGACTCGAAGG 2352
Qy 1785 TTAAGGAGGCTGAGTTTACGTGATCTAGTGAAGGAGCAGAGAAAGTATATTACAAAAG 1844
Db 2353 TTAAGGAGGCTGAGTTTACGTGATCTAGTGAAGGAGCAGAGAAAGTATATTACAAAAG 2412
Qy 1845 GAGA CAGAAGAAAGAAAGGAA CAAAGAAAGAGAGAGAAAGAGAGAAAGGAGGAAAGA 1904
Db 2413 GAGA CAGAAGAAAGAAAGGAA CAAAGAAAGAGAGAGAAAGAGAGAAAGGAGGAAAGA 2472
Qy 1905 CGTAAATAA CCGCAAGAGAGAAATTTGACTAAGATCTTGGCTGAGTGGTTGAGGGGAAA 1964
Db 2473 CGTAAATAA CCGCAAGAGAGAAATTTGACTAAGATCTTGGCTGAGTGGTTGAGGGGAAA 2532
Qy 1965 AGCAATACGGAAGAGAGAGAGATTTTAGGAAAAATTAGTTCAGGCCCTTAGACAGTCAGG 2024
Db 2533 AGCAATACGGAAGAGAGAGAGATTTTAGGAAAAATTAGTTCAGGCCCTTAGACAGTCAGG 2592
Qy 2025 AACCTGGCAATAGGACCCCACTCGACAAGGACCAATGTGCATATTGTAAAGAAAGAGGA 2084
Db 2593 AACCTGGCAATAGGACCCCACTCGACAAGGACCAATGTGCATATTGTAAAGAAAGAGGA 2652
Qy 2085 CACTGGGCAAGGAATCGCCCCCAAGAGGAAACAAAGACCAAGGATCCTTACTCTAGAA 2144
Db 2653 CACTGGGCAAGGAATCGCCCCCAAGAGGAAACAAAGGATCCTTACTCTAGAA 2712
Qy 2145 GAAATTAAGATTAGGGGAGACGGGTTTCGACCCCTCCCGAGCCCGCAGGTAATCTTG 2204
Db 2713 GAAATTAAGATTAGGGGAGACGGGTTTCGACCCCTCCCGAGCCCGCAGGTAATCTTG 2772

Db	4933	CTAAGCCTATTAGAAGCCTTACATTTGCCAAAAAGGCTAGCTATTATACACTGTCTTGGA	4992
Qy	4425	CATCAGAAAGCTAAAGATCTCATATCCAGAGGAAACAGATGGCTGACCGGGTTGCCAAG	4484
Db	4993	CATCAGAAAGCCTAAAGATCTCATATCCAGAGGAAACAGATGGCTGACCGGGTTGCCAAG	5052
Qy	4485	CAGCAGCCAGGGTGTAAACCTTCTGCTATATAGAAATGCCCCAAGCCCCCAGAACCC	4544
Db	5053	CAGCAGCCAGGGTGTAAACCTTCTGCTATGATAGAAACACCCAAAGCCCCCAGAACCC	5112
Qy	4545	AGACGACAGTACACCTAGAGACTGCGACAGAGATTAAGAAGTAGACCAAGTCTCTGAG	4604
Db	5113	GGACGACAGTACACCTAGAGACTGCGCAAGAAATNAAGATAGACCAAGTCTCTGAA	5172
Qy	4605	ACTCCGAGAGGACCTGCTATACCTCAGATGGGAAGAAATCTCTGCCCAACAAAGAGGG	4664
Db	5173	ACTCCGAGAGGACCTGCTATACCTCAGATGGGAAGAAATCTCTGCCCAACAAAGAGGG	5232
Qy	4665	TTAGAATATGTCACACAGATACATCGTCTAACCCACCTAGGAACCTAACACCTGCACAG	4724
Db	5233	TTAGAATATGTCACACAGATACATCGTCTAACCCACCTAGGAACCTAACACCTGCACAG	5292
Qy	4725	TTGTCAGAACATCCCTTATCATGTTCTGAGGCTACAGAGTGGCTGACTCGGTGTC	4784
Db	5293	TTGTCAGAACATCCCTTATCATGTTCTGAGGCTACAGAGTGGCTGACTCGGTGTC	5352
Qy	4785	AAACATTTGTGCGCCCTGCCAGCTGTTAAATGCTAAATCTCTCCAGAAATGCCCTCCAGGGAAG	4844
Db	5353	AAACATTTGTGCGCCCTGCCAGCTGTTAAATGCTAAATCTCTCCAGAAATGCCCTCCAGGGAAG	5412
Qy	4845	AGACTAAGGGGAAGCCACCCAGGCGCTCACTGGGAAGTGGACTTCACTAGGTTAAAGCCG	4904
Db	5413	AGACTAAGGGGAAGCCACCCAGGCGCTCACTGGGAAGTGGACTTCACTAGGTTAAAGCCG	5472
Qy	4905	GCTAAATACGGAAACAAATACCTATGTTTGTGTTTGTAGACACCTTTTCAGATGGGTAGAG	4964
Db	5473	GCTAAATACGGAAACAAATACCTATGTTTGTGTTTGTAGACACCTTTTCAGATGGGTAGAG	5532
Qy	4965	GCTTATCTACTAGAAAGAGACTTCAACCGTGGTGGCTAAGAAATACCTAGGAAATTT	5024
Db	5533	GCTTATCTACTAGAAAGAGACTTCAACCGTGGTGGCTAAGAAATACCTAGGAAATTT	5592
Qy	5025	TTTCCAGATTTGGAATACCTTAAGTAAATAGGCTCAGACAAATGGTCCAGCTTTTGTGGCC	5084
Db	5593	TTTCCAGATTTGGAATACCTTAAGTAAATAGGCTCAGACAAATGGTCCAGCTTTGTTGCC	5652
Qy	5085	CAGGTAAGTCAGGAGCTGGCCAGATATTTGGGATGATTTGGAAATGTCATTTGCAATAC	5144
Db	5653	CAGGTAAGTCAGGAGCTGGCCAGATATTTGGGATGATTTGGAAATGTCATTTGCAATAC	5712
Qy	5145	AGACCCCAAGCTCAGGACAGTGAAGAGATGAATAGAACCATTAAGAGACCTTTACT	5204
Db	5713	AGACCCCAAGCTCAGGACAGTGAAGAGATGAATAGAACCATTAAGAGACCTTTACT	5772
Qy	5205	AAATTTGACCGGAGACTGGCGTTAAATGATTTGGATAGCTCTCTCGCCCTTTGCTCTTTT	5264
Db	5773	AAATTTGACCGGAGACTGGCGTTAAATGATTTGGATAGCTCTCTCGCCCTTTGCTCTTTT	5832
Qy	5265	AGGGTTAGGAACACCCCTGGACAGTTTGGGCTGACCCCTCATGAATTACTACGGGGGA	5324
Db	5833	AGGGTTAGGAACACCCCTGGACAGTTTGGGCTGACCCCTCATGAATTACTACGGGGGA	5892
Qy	5325	CCCCCCCCATTTGGTAGAAATTTGCTTGTATCATAGTGTGAGCTGTCTTTTCCAGGCT	5384
Db	5893	CCCCCCCCATTTGGTAGAAATTTGCTTGTATCATAGTGTGAGCTGTCTTTTCCAGGCT	5952
Qy	5385	TTGTTCTTAGCTCAAGGCACTTCACTGGGTGAGACAAACAGCGTGGAGCACTCCGG	5444
Db	5953	TTGTTCTTAGCTCAAGGCACTTCACTGGGTGAGACAAACAGCGTGGAGCACTCCGG	6012
Qy	5445	GAGGCTTACTCAGGAGGAGAGACTTTCAGATCCACATCGTTTCCAGTGGGAGATTCA	5504
Db	6013	GAGGCTTACTC---AGGAGGAGACTTTCAGATCCACATCGTTTCCAGTGGGAGATTCA	6069
Qy	5505	GTCTAAGTTAGACGCCCAACCGTGCAGGAAACCTCGAGACTCGGTGGAGGGCCCTTATCTC	5564
Db	6070	GTCTAAGTTAGACGCCCAACCGTGCAGGAAACCTCGAGACTCGGTGGAGGGCCCTTATCTC	6129
Qy	5565	GTACTTTTGCACACCAACCGCTGTGAAGTGCAGAGGAATCTCCACTCGATCCATGCA	5624
Db	6130	GTACTTTTGCACACCAACCGCTGTGAAGTGCAGAGGAATCTCCACTCGATCCATGCA	6189
Qy	5625	TCCACAGTTAAACCGCGCCACCTCCCGATTCCGGGGTGGAAAGCCGAAAGAGACTGAAAT	5684
Db	6190	TTCACAGTTAAACCGCGCCACCTTCGATTCCGGGGTGGAAAGCCGAAAGAGACTGAAAT	6249
Qy	5685	CCCTTTAAGCTTCGCTCCATCCGCTGTTTCTTATCTCTGCTCAATACCTCTCAGACTAA	5744
Db	6250	CCCTTTAAGCTTCGCTCCATCCGCTGTTTCTTATCTCTGCTCAATACCTCTCAGACTAA	6309
Qy	5745	TGTTATGCGCATAGGAGACAGCTGAACTCCCAATAAACCTTATCTCTCAGCTGGTTAAT	5804
Db	6310	TGTTAAGCTTCGCTGAGACAGCCGAACTCCCAATAAACCTTATCTCTCAGCTGGTTAAT	6369
Qy	5805	TACTGACTCCGCGACACAGGTATTAATATCAACACACCTCAAGGGGAGGCTCCTTTAGGAAC	5864
Db	6370	TACTGACTCCGCGACACAGGTATTAATATCAACACACCTCAAGGGGAGGCTCCTTTAGGAAC	6429
Qy	5865	CTGGTGGCTGATCTATACGTTTGCCTCAGATCAGTTTATTCCTAGTCT-----GAC	5915
Db	6430	CTGGTGGCTGATCTATACGTTTGCCTCAGATCAGTTTATTCCTAGTCT-----GAC	6489
Qy	5916	CTCACCCCAAGATATCTCCATGCTCAGGATTTTATGTTTGGCCAGGACCAACCAATAA	5975
Db	6490	CACACCCCAAGATATCTCCATGCTCAGGATTTTATGTTTGGCCAGGACCAACCAATAA	6549
Qy	5976	TGGAACAATCTGGGAAATCCAGAGATTTCTTTTGTAAACAATGGAACCTGTGTAACCTC	6035
Db	6550	TGGAACAATCTGGGAAATCCAGAGATTTCTTTTGTAAACAATGGAACCTGTGTAACCTC	6609
Qy	6036	TAATGATGGATATTTGGAATGGCCAACTCTCAGCAGGATAGGTAAGTTTCTTATGT	6095
Db	6610	TAATGATGGATATTTGGAATGGCCAACTCTCAGCAGGATAGGTAAGTTTCTTATGT	6669
Qy	6096	CAACACCTATACAGCTCTGGAACAAATTAATTAATTAATTAATTAATTAATTAATTAAT	6155
Db	6670	TAACAATCTCTACAGTTTATAATCAATTTAATTAATTAATTAATTAATTAATTAATTAAT	6729
Qy	6156	CAAG-----TGCTCTCTCTCAGACCTAGA	6179
Db	6730	ACAGCGGTTACAAAAAGATGTAAGAAATAAGCAAAATAAGCTGTCTTCGTTAGACCTAGA	6789
Qy	6180	TTACCTAAAAATAAGTTTCACTGAGAAAGGAAACCAAGAAAAATATCTTAAATGGGTAAA	6239
Db	6790	TTACTTAAAAATAAGTTTCACTGAAAGGAAACCAAGAAAAATATCTTAAATGGGTAAA	6849
Qy	6240	TGTTATGCTCTGGGGAATGGTATTAATGAGGCTCGGGTAAACAAACAGGCTCATTTCT	6299
Db	6850	TGTTATGCTCTGGGGAATGGTATTAATGAGGCTCGGGTAAACAAACAGGCTCATTTCT	6909
Qy	6300	AATATTTGGCTCAAAAT---AAACAGCTGGAGCCCTCAATGGCTATAGGACCAATATC	6356
Db	6910	GACTATTTGGCTCAGAAATAGAAAACCTCAGATGGAACTCCCGGTTGCTATAGGACCAATAA	6969
Qy	6357	GGTCTTGACCGGTTCAAGAGCCCCCAACCCAGGACCAAGGACCATCTCTTAAC-----	6408
Db	6970	GGGTTTGGCCGAACAAGAGACCTCAATCCAAAGAACAGAGGCACTCTCTTAACCCCTCTGA	7029
Qy	6409	-----ATAACTTTCTGGATCAGACCCCACTGAGTCTTAACAGCACGACTTAAATGGGGC	6461
Db	7030	TTACAATTAACAACCTCTGATCAGTCCCACTGAGCCTTAACATCACTATTAAACAGGGGC	7089
Qy	6462	AAAACTTTTGTAGGCTCATCCAGGAGCTTTTCAAGCTCTTAACTCCACGACTCCAGAGGC	6521
Db	7090	GAACCTTTTAAACCTCATCCAGGAGCTTTTCAAGCTCTTAACTCCACGACTCCAGAGGC	7149

QY 6522 TACCTCTTCTGTTGCTATGCTTAGCTTCGGGCCCACTTACTATAGAGGAATGCTAG 6581
| | | | |
Db 7150 TACCTCTTCTGTTGCTTGTAGCTTCGGGCCCACTTACTATAGAGGAATGCTAG 7209
| | | | |
QY 6582 AAGAGGGAATCAATGTCGACAAAAGAACATAGAGACCAATGCACATGGGATCCCAAAA 6641
| | | | |
Db 7210 AGAGGGAATCAATGTCGACAAAAGAACATAGAGACCAATGTACATGGGATCCCAAAA 7269
| | | | |
QY 6642 TAAGCTTACCTTACTGAGGTTTCTGAAAAAGCACCCTGCATAGAGAAAGTTCCCCATC 6701
| | | | |
Db 7270 TAAGCTTACCTTACTGAGGTTTCTGAAAAAGCACCCTGCATAGAGATGTTCCCCATC 7329
| | | | |
QY 6702 CCACCAACCTTTGTAAACACACTGAAGCCTTTAATCAAACTCTGAGAGTCAA-TATC 6760
| | | | |
Db 7330 CCACCAACCTTTGTAAACACACTGAAGCCTTTAATCGAACTCTGAGAGTCAAGTATC 7389
| | | | |
QY 6761 TGGTACCTGTTATGACAGGTGGTGGCATGTAACTACTGGAATTAACCCCTTGTGTTCCA 6820
| | | | |
Db 7390 TGGTACCTGTTATG-CAGGTGGTGGCATGTAACTACTGGAATTAACCCCTTGTGTTCCA 7448
| | | | |
QY 6821 CCTTGGTTTAAACCAAACTAAAGATTTTGTGCAATATGCTCCAAATTTGTCCCGAGTGT 6880
| | | | |
Db 7449 CCTTGGTTTAAACCAAACTAAAGACTTTTGTGTTATGCTCCAAATTTGTCCCGAGTGT 7508
| | | | |
QY 6881 ATTAATATCCGAAAAAGCAATCCTTGTGAATATGACTACAGAAATCATCGACAAAAA 6940
| | | | |
Db 7509 ACTACTATCCGAAAAAGCAGTCTTGTGAATATGACTATAGATATAATTCGCCCAAAA 7568
| | | | |
QY 6941 GAGAACCCATATCTCGACACTTGTGTGATGCTCGGACTTGGAGTGGCAGCAGGTAG 7000
| | | | |
Db 7569 GAGAGCCATATCCCTTGACACTAGCTGTAACTGCTCGGATTTGGAGTGGCTGCAGGCGTG 7628
| | | | |
QY 7001 GAACAGGACAGCTGCCCTGCTCACGGGACCAAGCAGCTAGAAAACAGGACTTAGTAAC 7060
| | | | |
Db 7629 GAACAGGACGCTGCCCTTAATCACAGGACCGCAACAGCTGGAGAAAGACTTAGTAAC 7688
| | | | |
QY 7061 TACATCGAATTTGAACAGAGATCTCCAAAGCCTAGAAAAATCTGTCAGTAACTGGAGG 7120
| | | | |
Db 7689 TACATCGAATTTGAACGGAAGATCTCCAAAGCCTAGAAAAATCTGTCAGTAACTGGAGG 7748
| | | | |
QY 7121 AATCCCTAACCTCTTATCTGAAGTAGTCTCTACAGAATAGAGAGGTTAGATTATAT 7180
| | | | |
Db 7749 AATCCCTAACCTCTTATCTGAAGTGTCTACAGAACAGAGGGGTTAGATCTGTTAT 7808
| | | | |
QY 7181 TTCTAAAGAGGAGGATATGTTAGCTTGAAGGAGGAATGCTGTTTTTATGTCGATC 7240
| | | | |
Db 7809 TTCTAAAGAGGAGGTTATGTTAGCTTGAAGGAGGAATGCTGTTTTTATGTCGATC 7868
| | | | |
QY 7241 ATTCAGGGCCATCAGAGACTCCATGAACAGCTTAGAGAAAGGTTGGAGAACGTCGAA 7300
| | | | |
Db 7869 ATTCAGGAGCTATCAGGAGCTCCATGAGCAAGCTCAGAGAAAGGTTAGAAAAACGTCA 7928
| | | | |
QY 7301 GGGAAAAAGGAACTACTCAAGGTGGTTTGGAGGATGGTTCAACAGTCTCTTTGGTTGG 7360
| | | | |
Db 7929 AAGAAAAAGAGGCTGCGCAGGATGGTTTGGAGGATGGTTCAACAGTCCCCATGGTGA 7988
| | | | |
QY 7361 CTACCTTACTTCTGCTTAAACAGGACCTTAAATAGTCTCTCTCTTACTCACAGTTG 7420
| | | | |
Db 7989 CCACCTTCTCTGCTCTAACAGGACCCCTACTAATAGTCTCTCTTGTCTTACAGTTG 8048
| | | | |
QY 7421 GGCCATGTATTAATAACAGTTAATTGCCTTCAATTAGAGAACGAATAGTGCAGTCCAGA 7480
| | | | |
Db 8049 GGCCCTGCTTAATTAATCGGTTTGTGCTTTCTGTAGAGAAACAGTGAAGTGCAGTTCCGA 8108
| | | | |
QY 7481 TCATGTACTTAGAACAGTACCAAGCCGCTAGC---AGGAGCTGGCCGCTAGC 7537
| | | | |
Db 8109 TCATGTACTTAGAACAGTACCAAGCCGCTTCCAAAGCTAAGGAGAACTGACCTTTAGC 8168
| | | | |
QY 7538 TCTACCAAGTTCTAAGATTAGAACTATTAAACAGAGAGAGTGGGGAATGAAGAGTAA 7597
| | | | |
Db 8169 CTTCTTAGTTTCTAAGATTAGAACTATTAAACAGAGAGAGTGGGGAATGAAGAGTAA 8228
| | | | |
QY 7598 AATACAACT------AAGCTAATGAGAGCTTAAAAATTTGTTCTGAA 7638
| | | | |

Db 8229 AATGCAACTGACTCTCCAGAACCCAGAGTAAATAGAGCTCTAAATGCCCTCGAA 8288
| | | | |
QY 7639 TTCCAGAGTTTGTTCCTTATAGGTAAAAAGATTAGGTTTTTGTGCTGTTTTAAAAATAGC-- 7696
| | | | |
Db 8289 TTCCAGACCTTGTTCCTTATAGGTAAAAAGATCATATTTTGTGCTTTTAGGGCTTGCTT 8348
| | | | |
QY 7697 -----GGAAGTAAATAGGCCCTGAGTACATGTCTCTAG 7730
| | | | |
Db 8349 TCTGCTCTGTACAAAACTTTGTGGAAGGGAAAAACAGGCCCTGAGTATGTCCTCTAT 8408
| | | | |
QY 7731 GCATCAAACTTCTTGAAA-----CTATTTGAG 7757
| | | | |
Db 8409 GCTTGAAACTTCTTGAAACTGCTCTAACTGCTTGTGTTGGCTTCTGTAACCTGCTTGCA 8468
| | | | |
QY 7758 ATAAACAAGAAAGGAGTTTCTAACTGCTTGTGTTAGCTTCTGTAAAACTGGTTGGCCAT 7817
| | | | |
Db 8469 TAAGATAAAAGAGGAGGAAGTCAATTGCTTAACGGACCCAGTAAGATCGGGCGTGCCAC 8528
| | | | |
QY 7818 AAAGATGTTGAATGTTGATACACATATCTTGGTGACAACTGTCTCCCCACCCCGAAA 7877
| | | | |
Db 8529 AAAATGTTGAAAATCTGATAAATATATCTTGGTGACAAATATGTCTCCCCCAACCAGAGA 8588
| | | | |
QY 7878 CATGCGCAATGTGTAACTCTAAACAATTTAAATTTAAATTTGTCACGAAGCGCGGCTC 7937
| | | | |
Db 8589 CAGGCACAAACATGTAACTCCAGAACAACTTAAATTTAAATTTGTCACAAAGCGCGGCTC 8648
| | | | |
QY 7938 TCGAAGTTTTAAATTTGACTGGTTTGTGATATTTT-GAAATGATTTGGTTGT-AAAGCGCG 7995
| | | | |
Db 8649 TCGAAGTTTTGATTTGACTGGTTTGGATATTTTAAATGATTAGTTTGTAAAGCGCG 8708
| | | | |
QY 7996 GGCCTTGTGTGAACCCCAATAAAAGCTGTCCGACTCCACACTCGGGGCGCGAGTCTCT 8055
| | | | |
Db 8709 GGVTTTGTGTGAACCCCAATAAAAGCTGTCCGACTCCACACTCGGGGCGCGAGTCTCT 8768
| | | | |
QY 8056 ACCCTGCTGTGTGTACGACTGTGGGCCCCAGCGCTTGGAAATAAAATCTCTTGTGCTG 8115
| | | | |
Db 8769 ACCCTGCTGTGGCTACGACTGTGGGCCCCAGCGGCTCGGAATAAAATCTCTTGTGCTG 8828
| | | | |
QY 8116 TTTGATCAAAA 8127
| | | | |
Db 8829 TTTGATCAAGA 8840
| | | | |

RESULT 7

AAC67023

ID AAC67023 standard; DNA; 7873 BP.

XX AAC67023;

XX 27-MAR-2001 (first entry)

XX PERV env protein coding sequence SEQ ID NO: 23.

XX Xenotransplantation; infectious agent; vaccine; ds.

XX Porcine endogenous retrovirus.

XX WO200071726-A1.

XX 30-NOV-2000.

XX 24-MAY-2000; 2000WO-US014296.

XX 24-MAY-1999; 99US-0135631P.

XX (MAYO-) MAYO MEDICAL VENTURES.

XX Federspiel MJ;

XX WPI; 2001-032041/04.

XX Inhibiting or preventing infectious agent transmission in mammalian

Db	4081	GACTCCGGAAGGACCTGCTATACCTCAGATGGGAAGGAAATCCTGCCCCACAAAGAGG	4140	QY	5743	AATGGTATGCGCATAGGAGACAGCCCTGAAGACTCCCATAAACCCTTATCTCTCACCTGGTTA	5802
QY	4664	GTTAGAAATGTCACACAGATACATCGTCTAAACCCACCTAGGAACATAAACCACCTGCAGCA	4723	Db	5135	AATGGTAAACGCTTGTCGACAGCCGAACTCCCATAAACCCTTATCTCTCACCTGGTTA	5194
Db	4141	GTTAGAAATGTCACACAGATACATCGTCTAAACCCACCTAGGAACATAAACCACCTGCAGCA	4200	QY	5803	ATTACTGACTCCGGACAGGTATTAATATCAACACACTCAAGGGAGGCTCCTTTAGGA	5862
QY	4724	GTTGGTTCAGAAATCCCTTATCATGTTCTGAGGCTACACAGGAGTGGCTGACTCGGTGGT	4783	Db	5195	CTTACTGACTCCGGTACAGGTATTAATATTAACAGCAGCTCAAGGGAGGCTCCTCTGGGG	5254
Db	4201	GTTGGTTCAGAAATCCCTTATCATGTTCTGAGGCTACACAGGAGTGGCTGATTTCGGTGGT	4260	QY	5863	ACCTGTGGCCTGATCTATACGTTTGCCTCAGATCAGTTATTCTCTAGTCTCT	5913
QY	4784	CAAAATGTTGGTCCCTGCCAGCTGGTTAATGCTTAATCTTCCAGAAATGCTCCAGGAA	4843	Db	5255	ACCTGTGGCCTGAAATTAATATGCTGCTTCGATCAGTAATCCCTGCTCTCAATGACCAG	5314
Db	4261	CAAAATGTTGGTCCCTGCCAGCTG	4285	QY	5914	ACCTCAACCCCGAGATATCCTCATGCTCAGGATTTTATGTTTGGCCAGGACCAACCAAT	5973
QY	4844	GAGACTAAGGGGAAGCCACCCAGGCGCTCACTGGGAAGTGGACTTCACTGAGGTAAAGCC	4903	Db	5315	GCCACACCCCGAGTACTCGGTGCTTACGGGTTTTTACGTTTGGCCAGGACCCCAAT	5374
Db	4286	-----GTTAAGCC	4294	QY	5974	AATGGNAACATTTGGGAATCCAGAGATTTCTTTGTAAACAATGGAACCTGTGTAACC	6033
QY	4904	GGCTAAATACGGAAACAAATACCTATTGTTTTTTGTAGACACCTTTTCAGGATGGGTAGA	4963	Db	5375	AATGAAGAAATATTTGTGGAATCCTCAGGATTTCTTTTGAAGCAATGGAGCTCGTAAC	5434
Db	4295	GGCTAAATACGGAAACAAATATCTATTGTTTTTTGTAGACACCTTTTCAGGATGGGTAGA	4354	QY	6034	TCTAATGATGGATATTGGAAATGGCCAACTCTCAGCAGGATAGGGTAAAGTTTCTTAT	6093
QY	4964	GGCTTATCTTACTAAGAAAGAGACTTCAACCGTGGTGGCTTAAAAAATACCTGAA- GAAA	5022	Db	5435	TCTAATGATGGATTTGGAATGGCCAGTCTCTCAGCAGACAGAGTAAAGTTACTCTTT	5494
Db	4355	GGCTTATCTTACTAAGAAAGAGACTTCAACCGTGGTGGCTTAAAAAATACCTGAGGAGAA	4414	QY	6094	GTCAACACCTTATACCAAGCTCTGGACAAATTTAATTAACCTGACCTGGATTAAGAACTGGAAGC	6153
QY	5023	TTTTTCCAGATTTGGATACCTAAGTAATAGGTCAGCAATGCTCCAGCTTTTGTG	5082	Db	5495	GTTAACAATCCTACCAAGTTAATCAATTAATATATGGCCATGGGAGATGGAAGATTGG	5554
Db	4415	TTTTTCCAGATTTGGATACCTAAGTAATAGGTCAGCAATGCTCCAGCTTTGTTG	4474	QY	6154	CCCAAG-----TGCTCTCCTTCAGACCTA	6177
QY	5083	CCAGGTAACTCAGGAGTGGCCAAAGATATTGGGATTTGATGGAACTGCATTTGTGCAT	5142	Db	5555	CAACAGGGGTACAAAAGATGTACGAAATAGCAAAATAGCTGTCACTGTTAGACCTA	5614
Db	4475	CCAGGTAACTCAGGAGTGGCCAAAGATATTGGGATTTGATGGAACTGCATTTGTGCAT	4534	QY	6178	GATTACTTAAATAATAGTTTCACTGAGAAAGGAAAAACAAGAAATATCTTAAATAGGTA	6237
QY	5143	ACAGACCCCAAGCTCAGGACAGGTAGAGAGGATGAATAGAACATTTAAAGAGACCTTTA	5202	Db	5615	GATTACTTAAATAATAGTTTCACTGAAAGGAAACAAGAAATATTTCAAAGTGGTA	5674
Db	4535	ACAGACCCCAAGCTCAGGACAGGTAGAGAGGATGAATAGAACATTTAAAGAGACCTTTA	4594	QY	6238	AATGGTATGTTGGGGAATGGTATATTATGGAGGCTCGGGTAAACAACACAGGCTCCATT	6297
QY	5203	CTAAATTGACGGGGAGACTGGCGTTAATGATTTGGATAGCTCTCTGCCCTTTGTGCTTT	5262	Db	5675	AATGGTATGTTGGGGAATAGTGTACTATGGAGGCTCTGGGAGAAAGAAAGGATCTGTT	5734
Db	4595	CTAAATTGACGGGGAGACTGGCGTTAATGATTTGGATAGCTCTCTGCCCTTTGTGCTTT	4654	QY	6298	CTAACTATTGCGCTCAAAAT---AAACAGCTGGAGGCTTCAATGGCTATAGACCAAT	6354
QY	5263	TTAGGGTTAGGAACACCCCTGGACAGTTTGGGCTGAGCCCTATGAATTAATCTTACGGGG	5322	Db	5735	CTGACTATTGCGCTCAGAAATAGAACTCAGATGGAACCTCCGGTTGCTATAGGACCAAT	5794
Db	4655	TTAGGGTTAGGAACACCCCTGGACAGTTTGGGCTGAGCCCTATGAATTAATCTTACGGGG	4714	QY	6355	ACGGTCTTGACGGGTCAAGAGACCCCAACCAAGGACAGACCATCTCTAAC-----	6408
QY	5323	GACCCCTCCCAATTGGTAGAAATTTGCTTCTGTACATAGTGTGACGCTGCTCTTCCAGC	5382	Db	5795	AAGGGTTTGGCCGAAACAAGGACCTCCAAATCCAAAGAACAGAGGCCATCTCTTACCCCTCT	5854
Db	4715	GACCCCTCCCAATTGGTAGAAATTTGCTTCCGTACATAGTGTGCTGACGCTGCTTCCAGC	4774	QY	6409	-----ATAACTTCTTGATCAGACCCCACTGAGTCTTAAACAGACGACTTAAATGGGG	6459
QY	5383	CTTTGTTCTTAGGCTCAGGCATTTGAGTGGGTGAGACACGAGCGTGGAGCACTCC	5442	Db	5855	GATTACAATAACAACCTCTGGATCAGTCCCACTGAGCCTAACATCACTATTAAAAACAGGG	5914
Db	4775	CTTTGTTCTTAGGCTCAGGCATTTGAGTGGGTGAGACACGAGCGTGGAGGCACTCC	4834	QY	6460	GCAAACTTTTATAGCTCATCAGGGAGCTTTTCAAGCTCTTAACTCCAGACTCCAGAG	6519
QY	5443	GGGAGGCTTACTCAGGAGGAGGAGACTTGCAGATCCCACTGCTTTTCAAGTGGGAGATT	5502	Db	5915	GCGAACTTTTAACTCATCAGGGAGCTTTTCAAGCTCTTAACTCCAGACTCCAGAG	5974
Db	4835	GGGAGGCTTACTCAGGAGGAGGAGACTTGCAGATCCCACTGCTTTTCAAGTGGGAGATT	4894	QY	6520	GCTACCTCTTCTTGTGGCTATGCTTAGCTTTCGGGCCACCTTACTATGAAGGAATGGCT	6579
QY	5503	CAGTCTACGTTAGACGCGCACCGTGCAGGAAACCTCGAGACTTCGGTGAAGGGCCCTTATC	5562	Db	5975	GCTACCTCTTCTTGTGGCTTGTGCTTAGCTTTCGGGCCACCTTACTATGAAGGAATGGCT	6034
Db	4895	CAGTCTACGTTAGACGCGCACCGTGCAGGAAACCTCGAGACTTCGGTGAAGGGCCCTTATC	4954	QY	6580	AGAAGGGGAAATCAATGTGACAAAAGAACATAGAGACCAATGCAATGGGGATCCCAA	6639
QY	5563	TCGTAATTTTGAACACCAACCGCTGTGAAAGTTCGAAGGAATCTCAACCTGGATTCATG	5622	Db	6035	AGAGGGGGAATTCATGTGACAAAGGACATAGAGACCAATGATACATGGGATCCCAA	6094
Db	4955	ACGTACTTTTGAACACCAACCGCTGTGAAAGTTCGAAGGAATCTCAACCTGGATTCATG	5014	QY	6640	AATAAGCTTACCTTACTGAGGTTTTCGAAAAAGGCACTCTGCATAGAAAGGTTCCCCCA	6699
QY	5623	CATCCAGCTTAAACCGGCGCACTCCCGATTGGGGTGAAGCGGAAGACTGAA	5682	Db	6095	AATAAGCTTACCTTACTGAGGTTTTCGAAAAAGGCACTCTGCATAGGATGGTTCCCCCA	6154
Db	5015	CATCCAGCTTAAACCGGCGCACTCCCGATTGGGGTGAAGCGGAAGACTGAA	5074	QY	6700	TCCACCAACACCTTTGTAACCACTGAAAGCCTTTAATCAACCTCTGAGAGTCAATAT	6759
QY	5683	ATCCCTTAAAGCTTGCCTCCATCGCGTGGTTTCTTACTCTGTCAATAACCTCTCAGACT	5742	Db	6155	TCCACCAACACCTTTGTAACCACTGAAAGCCTTTAATGAAACCTCTGAGAGTCAATAT	6214
Db	5075	ATCCCTTAAAGCTTGCCTCCATCGCGTGGTTTCTTACTCTGTCAATAACCTCTCAGATT	5134				

QY 6760 CTGGTACCTGGTTATACAGAGTGGTGGCATGTAATACTGGATTAAACCCCTTGTGTCTCC 5819
DB 6215 CTGGTACCTGGTTATACAGAGTGGTGGCATGTAATACTGGATTAAACCCCTTGTGTCTCC 6274
QY 6820 ACCTTGTTTAAACCAAACTAAAGATTTTTCATTATGGTCCAAATTTGTTCCCGAGTG 6879
DB 6275 ACCTTGTTTAAACCAAACTAAAGACTTTTGGTTATGGTCCAAATTTGTTCCCGGGTG 6334
QY 6880 TATTACTATCCGAAAGCAATCCTTGTATGATATGACTACAGAAATCATCGACAAAAG 6939
DB 6335 TACTACTATCCGAAAGCAGTCCCTTGTATGATATGACTATAGATATATATCGGCCAAA 6394
QY 6940 AGAAGACCATATCTCTGACACTTGTCTGATGCTCGACTTGGAGTGGCAGAGGTGTA 6999
DB 6395 AGAGAGCCATATCCCTGACACTAGCTGTAATGCTCGGATTTGGAGTGGCTGCGAGCGTG 6454
QY 7000 GGAACAGGACAGCTCCCTGGTTCAGGGACACAGCAGCAGTACAGACAGACTTAGTAAC 7059
DB 6455 GGAACAGGACAGCTGCCCTTAATCACAGGACCGCAACAGCTGGAGAAAGACTTAGTAAC 6514
QY 7060 CTACATCGAATTGTAAACAGAAATCTCCAAGCCCTAGAAAAATCTGTCAAGTAACCTGGAG 7119
DB 6515 CTACATCGAATTGTAAACGGAAGATCTCCAAGCCCTAGAAAAATCTGTCAAGTAACCTGGAG 6574
QY 7120 GAATCCCTAACCTCTTATCTGAAGTAGTCTTACAGAAATAGAGGGTTAGATTATTA 7179
DB 6575 GAATCCCTAACCTCTTATCTGAAGTGGTTCTACAGAAACAGAGGGGTTAGATCTGTTA 6634
QY 7180 TTTCTAAAGAGGAGGATATGTGTAGCTTGAAGGGAATGCTGTTTTTATGTGGAT 7239
DB 6635 TTTCTAAAGAGGAGGATATGTGTAGCTTGAAGGGAATGCTGTTTTTATGTGGAT 6694
QY 7240 CATTCAGGGGCCATCAGAGACTCCATGAACA ----- 7270
DB 6695 CATTCAGGGGCCATCAGAGACTCCATGAACAGCTTAGAGAAAGGACTGGAGCGCCCG 6754
QY 7271 ----- 7270
DB 6755 CGGGTCTCGAACCAACCCAGACAGTTGCTTGTTCATTTAAAGAACTGTGCGAAGTAACCG 6814
QY 7271 -----AGCTTAGAGAAAGTTGGAGACGCTCGAAGGGAAGAAAGAACTACT 7317
DB 6815 CTGAGCTAAAGCAGCTTAGAGAAAGTTGGAGAGCGTTCGAAGGGAAGAAAGAACTACT 6874
QY 7318 CAAGGTGGTTTGAAGGATGGTTCAACAGGTCTCTTTGGTTGGCTACCCCTACTTTCTGCT 7377
DB 6875 CAAGGTGGTTTGAAGGATGGTTCAACAGGTCTCTTTGGTTGGCTACCCCTACTTTCTGCT 6934
QY 7378 TTAACAGGACCCCTTAATAGTCTCTCTCTGTTACTCACAGTTGGGCCATGTATTATTAAC 7437
DB 6935 TTAACAGGACCCCTTAATAGTCTCTCTCTGTTACTCACAGTTGGGCCATGTATTATTAAC 6994
QY 7438 AAGTTAATTCCTTCAATAGAGAACGAATAAGTGCAGTCCAGATCATGTACTTAGACAA 7497
DB 6995 AAGTTAATTCCTTCAATAGAGAACGAATAAGTGCAGTCCAGATCATGTACTTAGACAA 7054
QY 7498 CAGTACCAAGCCGCTAGCAGGGAGCTGGCCGCTAGCTCTACAGTTCTTAAGATTAG 7557
DB 7055 CAGTACCAAGCCGCTAGCAGAGAAAGCTGGCCGCTAGCTCTACAGTTCTTAAGATTAG 7114
QY 7558 AACTATTAAACAGAGAAAGTGGGAATGAAAGGATGAAATACAACCT----- 7607
DB 7115 AACTATTAAACAGAGAAAGTGGGAATGAAAGGATGAAATGCAACCTGACTCTCCCA 7174
QY 7608 -----AAGCTAATGAGAGCTTAAATTTGTTCTGAATTCAGAGTTTGTCTTAT 7658
DB 7175 GAACCCAGAGGTTAATAGAAAGCTCTAAATGCCCTCGAATTCAGACCCCTGTCCCTAT 7234
QY 7659 AGGTAAAGATTAGTTTTTGTGTTTTTAAATATGC----- 7696
DB 7235 AGGTAAAGATTATATCTTTTGTCTTTTGTAGGGCTGCTTTCTGCTCTGACAAACTTT 7294
QY 7697 -----GGAAGTAAATAGGCCCTTGAGTACATGTCTCTAGGCATGAAACTTCTTGAAC 7750

DB 7295 GTGGAAGGGGAAAAACAGGCCCTGAGTATGTCCTCTATGCTGAAACTTCTTGAAC 7354
QY 7751 ATTTGAGATAAACAGAAAAAGGAGTTTCTAACTGCTTGTGTTA----- 7792
DB 7355 GCTCCTAACTGCTTGTGTTGGCTTCTGTAACCTGCTTGCATTAAGATAAAAAAGAGAGA 7414
QY 7793 -----GCTTCTGTAATACTGGTTGGCCATAAAGATGTTGAATGTTGATACATATC 7846
DB 7415 TCAATTGCTTAACGACCCAGTAAGATCGGGGTGTAACCAAAATGTTGAAACACATATC 7474
QY 7847 TTGGTGACAACTGCTCCCCACCCGAAACATGCGCAAACTGTGTAACCTTAAACAAT 7906
DB 7475 TTGGTGACAACTGCTCCCCACCCGAAACATGCGCAAACTGTGTAACCTTAAACAAT 7534
QY 7907 TTAATTAATTTGGTCCACGAAGCGGGCTCTCGAAGTTTTTAAATGACTGCTGTTGTGAT 7966
DB 7535 TTAATTAATTTGGTCCACGAAGCGGGCTCTCGAAGTTTTTAAATGACTGCTGTTGTGAT 7594
QY 7967 ATTTTGAATGATTTGTTTAAAGCGGGCTTTTGTGTGAACCCCATATAAAGCTGTCC 8026
DB 7595 ATTTTGAATGATTTGTTTAAAGCGGGCTTTTGTGTGAACCCCATATAAAGCTGTCC 7654
QY 8027 CGACTCCACACTCGGGCGCGAGTCTCTACCCCTGCGTGTGTAGTGTGGGCCCCA 8086
DB 7655 CGACTCCACACTCGGGCGCGAGTCTCTACCCCTGCGTGTGTAGTGTGGGCCCCA 7714
QY 8087 GGGCGCTTGGATAAAAAATCCTTCTGCTGTTTGCATCAAA 8127
DB 7715 GCGCGCTTGGATAAAAAATCCTTCTGCTGTTTGCATCAAGA 7755
RESULT 8
ABQ76884
ID ABQ76884 standard; DNA; 8763 BP.
XX
AC ABQ76884;
XX
DT 06-MAR-2003 (first entry)
XX
DE PERV clone PK15-PERV-B(213) DNA.
XX
KW PERV; porcine; env; gag; infection; vaccine; virucide; immunization;
KW pig breeding; chromosome mapping; protection; ds.
XX
OS Porcine endogenous retrovirus.
XX
PN DE1011433-A1.
XX
PD 19-SEP-2002.
XX
PF 09-MAR-2001; 2001DE-01011433.
XX
PR 09-MAR-2001; 2001DE-01011433.
XX
PA (BUND) BUNDESREPUBLIK DEUT PAUL-EHRLICH-INST.
XX
PI Toenjes RR, Krach U;
XX
DR WPI; 2002-699548/76.
XX
PT Replication-competent molecular clones of porcine endogenous retrovirus,
PT useful as sources of env peptides for vaccination and for viral
PT detection.
XX
PS Claim 5; Fig 15; 52pp; German.
XX
CC This invention describes novel replication-competent molecular clones of
CC porcine endogenous retrovirus (PERV) isolated from a porcine BAC
CC (bacterial artificial chromosome) library which are replication competent
CC after transfer into permissive cells. The invention also discloses (a)
CC env and gag polyptides encoded by the molecular clones of the invention
CC ; (b) porcine nucleic acids that represent the 5' and 3' flanking

sequences of the integration site of a replication competent molecular
CC clone in the porcine genome; (c) oligonucleotides for detecting
CC integrated PERV; (d) a method for detecting appearance of infectious PERV
CC particles in a sample; (e) a vaccine for immunization against replication
CC -competent PERV, comprising an env protein and (f) a method for isolating
CC the molecular clones of the invention. The products of the invention are
CC have virulence activity. The clones are from native PERV and make possible
CC comparisons of proviral sequences of different origins at the molecular,
CC structural and cellular levels, and mapping of proviral sequences at
CC chromosomal positions in specific breeds of pigs. Also different breeds
CC of pigs can be screened for presence of specific infectious PERV, i.e. to
CC identify PERV-free animals. Also vaccines that contain the env
CC polypeptides encoded by the clones of the invention are useful for
CC protection against replication-competent PERV. The products of the
CC invention are functional, replication-competent, full-length, proviral
CC clones isolated directly from the pig genome, i.e. they are 'native',
CC PERV. This sequence represents a PERV clone fragment described in the
CC disclosure of the invention

XX
SQ Sequence 8763 BP; 2301 A; 2200 C; 2287 G; 1974 T; 0 U; 1 Other;

Query Match 77.7%; Score 6319; DB 6; Length 8763;
Best Local Similarity 87.0%; Pred. No. 0;
Matches 7159; Conservative 0; Mismatches 941; Indels 126; Gaps 15;

QY 1 GCGTGGTACGACTGTGGGCCCCAGCGCGCTTGGAAATAAAATCCTTGTCTTTGCA 60
DB 488 GCGTGGTACGACTGTGGGCCCCAGCGCGCTTGGAAATAAAATCCTTGTCTTTGCA 547
QY 61 TCAAGACCGCTTCTCGTGAAGTAAAGGGAGTTCGCTTTTCGAGCCTGGAGG----- 115
DB 548 TCAAGACCGCTTCTGTGAGTGAT--TGGGGTTCGCTCTTCCGAGCCGAGAGGGG 606
QY 116 -----TTCTTTTGTGCTTACATTTTGGGGGCTCGTCGGGGATCTGTGGGGCCACCCC 171
DB 607 GATTGTTCTTTTACTGGCCCTTCAATTTGGTGGCTTGGCCGGGAAATCCTTGCACACCCC 666
QY 172 TAACACCGGAGAACGCTTGGAGTAAAGAGATCCTCTTTTAAAGTGTATCATGTA 231
DB 667 TTACACCGGAGAACGCTTGGAGT--AAAGGATCCCTTTGGAAGTGTG--TGTG 723
QY 232 CCGGCCCGCGTCTCTGTCTCAGTGTCTGTCTTTCAGTGTGTGGCGCTTTCGGTTTGCAGC 291
DB 724 TCGGCCCGCGTCTATGTCTCAGTGTCTGTCTTTCGGTAATCGCGCTTTCGGTTTGCAGC 783
QY 292 TGTCTCTCAGCCCGTAAGGCTGTGGGACTGTGATCAGCAGACGTGTCTAGGAGATCAC 351
DB 784 TGTCTCTCAGACCGTAAGGACTGTGGAGCTGTGATCAGCAGACGTGTCTAGGAGATCAC 843
QY 352 AGGCTGTGCTTGGGAGACCCCGGAGGTGAGGAGCCGAGCGCTTGGTGTCT 411
DB 844 AGGCTGTGCTTGGGAGACCCCGGAGGTGAGGAGCCGAGCGCTTGGTGTCT 903
QY 412 GCTACTGTGCTGAGAGACCGAATTCGTGTGCTGAAGCGAAAGCTTCCCGCTCCGGAC 471
DB 904 CCTACTGTGCTGAGAGTCCGAGTTCGTGTGCTGAAGCGAAGAGCTTCCCGCTCCGGAC 963
QY 472 CGTCCGACTCTTTTGCCTCTTGTGGAAGACGTGGACGGGTCACTGTGTCTGAGATCTGT 531
DB 964 CGTCCGACTCTTTTGCCTCTTGTGGAAGACGTGGACGGGTCACTGTGTCTGAGATCTGT 1023
QY 532 TGGTTTCTGTTGTGTCTTGTCTTGTGTGTCTTGTCTACAGTTTAAATATGGAC 591
DB 1024 TGGTTTCTGTTGTGTCTTGTCTTGTGTGTCTTGTCTACAGTTTAAATATGGAC 1083
QY 592 AGACGCTGACGACCCCTCTTGTGTTGACTCTCGACATTGGACTGAAGTAAATCCAGGG 651
DB 1084 AGACGCTGACGACCCCTCTTGTGTTGACTCTCGACATTGGACTGAAGTAAATCCAGGG 1143
QY 652 CTCATAAATTTGTGCTCAGGTTAAGAGGGACCTTGGCAGACTTTTGTGTCTCTGAAT 711
DB 1144 CTCATAAATTTGTGCTCAGGTTAAGAGGGACCTTGGCAGACTTTTGTGTCTCTGAAT 1203

QY 712 GGCCGACATTCGATGTTGGATGCCATCAGAGGGGACCTTTAATTTCTGAGATTTATCCTGG 771
DB 1204 GGCCAAATTCGATGTTGGATGCCATCAGAGGGGACCTTTAATTTCTGAAATTTATCCTGG 1263
QY 772 CTGTTAAAGCAGTTATTTTTCAGACTGGACCCGGCTCTCATCCGATCAGAGAGCCCTATA 831
DB 1264 CTGTTAAGCAATCAATTTTTCAGACTGGACCCGGCTCTCATCTGTATCAGAGAGCCCTATA 1323
QY 832 TCCTTACGTGGCAAGATTGGCAGAGATCCTCCGCCATGGTTAAACCATTGGCTGAATA 891
DB 1324 TCCTTACGTGGCAAGATTGGCAGAGAACCTCCGCCATGGTTAAACCATTGGCTGAATA 1383
QY 892 AGCCAAAGAACAGGTCCCGGAATTTCTGCTCTTGGAGAGAAACCAACACCTCGGCTG 951
DB 1384 AACCAAGAAAGCAGGTCCCGGAATCCTGGCTCTTGGAGAGAAACCAACACCTCGGCTG 1443
QY 952 AAAAGTCAAGCCCTCTCTCATATCTACCCCGAGATTGAGGAGCACCAGCTTGGCGGG 1011
DB 1444 AAAAGTCAAGCCCTCTCTGGTATCTACCCCGAGATCGAGAGCCCGCACTTGGCGGG 1503
QY 1012 AACCCCAATCTGTTCCCGCACCCCTTATCTGGCACAGGGTGGCGGAGGGGACCTTTTG 1071
DB 1504 AACCCCAATCTGTTCCCGCACCCCTTATCCAGCACAGGGTGTGTGAGGGGACCTCTG 1563
QY 1072 CCCCTCTGTGAGCTCCGGCGGTGGAGGACCTGTCTGAGGAGACTCGAGAGCCGAGGGGCG 1131
DB 1564 CCCCTCTGTGAGCTCCGGTGTGGAGGACCTGTCTCGGGGACTCGAGAGCCGAGAGGCG 1623
QY 1132 CCACCCGAGCGGACAGACAGATCGGACATTTACCGCTCGCACAGCTGACGGCCCTCCCA 1191
DB 1624 CCACCCGAGCGGACAGACAGATCGGATATTTACCGCTCGCACAGCTTATGGCCCTCCCA 1683
QY 1192 CACCGGGGGCCAAATTCAGCCCCCTCCAGTATTTGGCCCTTTTCTTCTGCAGATCTCTATA 1251
DB 1684 TGCAGGGGGCCAAATTCAGCCCCCTCCAGTATTTGGCCCTTTTCTTCTGCAGATCTCTATA 1743
QY 1252 ATTGGAATACTAACCATCTCCCTTTCTCGAGAGATTCGCCAAGCGCTCACGGGGTGTGG 1311
DB 1744 ATTGGAATACTAACCATCTCCCTTTCTCGAGAGATTCGCCAAGCGCTCACGGGGTGTGG 1803
QY 1312 AGTCCCTTATGTTCTCTCAGCGCTACTTGGGATGATTTGTCACAGCTGCTGCAGACAC 1371
DB 1804 AGTCCCTTATGTTCTCTCAGCGCTACTTGGGATGATTTGTCACAGCTGCTGCAGACAC 1863
QY 1372 TCTTCAACAACGAGGAGCGAGAGAATTTCTATTAGAGGCTAGAAAAAATGTTCTCTGGGG 1431
DB 1864 TCTTCAACAACGAGGAGCGAGAGAATTTCTATTAGAGGCTAGAAAAAATGTTCTCTGGGG 1923
QY 1432 CCGACGGGCGACCCACCGGTTGCANAATGAGATTGACATGGGATTTTCCCTTAACTCGCC 1491
DB 1924 CCGACGGGCGACCCACCGGTTGCANAATGAGATTGACATGGGATTTTCCCTTAACTCGCC 1983
QY 1492 CCGGTTGGGACTACAACACCGCTGAAGTAGGAGAGCTTGAANAATCTATCGCAGGCTC 1551
DB 1984 CCGGTTGGGACTACAACACCGCTGAAGTAGGAGAGCTTGAANAATCTATCGCAGGCTC 2043
QY 1552 TGGTGGGGGCTCTCCGGGGCGCTCAAGACGGCCCACTAAATTTGGCTAAGGTAAAGAGAG 1611
DB 2044 TGGTGGGGGCTCTCCGGGGCGCTCAAGACGGCCCACTAAATTTGGCTAAGGTAAAGAGAG 2103
QY 1612 TGATGACAGGAGCCGAATGAACCCCTCTGTCTTCTTGGAGAGGCTTTGGAAGCTTCA 1671
DB 2104 TGATGACAGGAGCCGAATGAACCCCTCTGTCTTCTTGGAGAGGCTTTGGAAGCTTCA 2163
QY 1672 GCGGTTACACCCCTTTGATCTCCACCTCAGAGGGCCAAAAAGCCTCAGTGGCTTTGGCT 1731
DB 2164 GCGGTTACACCCCTTTGATCTCCACCTCAGAGGGCCAAAAAGCCTCAGTGGCTTTGGCT 2223
QY 1732 TTATAGGACAGCTCAGCTTGGATATAGAAAAGAGCTTCAGAGACTTGAAGGTTTACAGG 1791
DB 2224 TCAATGGGACAGCTCAGCTTGGATATCAGAAAAGAACTTCAGAGACTTGAAGGTTTACAGG 2283
QY 1792 AGGCTGAGTTACGTGATCTAGTGAAGGAGGAGAGAAAGTATATTTACAAAAGGAGACAG 1851

Qy	4012	TTGAGGAGACTGGGGTCCGCAAGACCTTTACAGACATACCGCTCACTGGAGAAAGTGCTAA	4071	5092	GTCCAGGACCTGGCCAAAGATATTGGGGATTGATTGGAACTGCAATGTGTCATACAGACCCC	5151
Db	4504	TTGAGGAGACTGGGGTCCGCAAGACCTTTACAGACATACCGCTCACTGGAGAAAGTGCTAA	4563	5584	GTCCAGGACCTGGCCAAAGATATTGGGGATTGATTGGAACTGCAATGTGTCATACAGACCCC	5643
Qy	4072	CCTGGTTCACTGACGGAAGCAGCTATATGTGTGGAAGTAAAGAGATGGCTGGGGCGGCGG	4131	5152	AAAGCTCAGACAGCTGAGAGAGTGAATAGAACCAATTAAGAGAGCCCTTACTTAAATTGA	5211
Db	4564	CCTGGTTCACTGACGGAAGCAGCTATATGTGTGGAAGTAAAGAGATGGCTGGAGCGGCGG	4623	5644	AAAGCTCAGACAGCTGAGAGAGTGAATAGAACCAATTAAGAGAGCCCTTACCAATTGA	5703
Qy	4132	TGGTGGACGGACCCGCAACCATCTGGGCCAGCAGCTGCGGAGGAACATTCACGACAAA	4191	5212	CCGCGGAGACTGGCGTTAATGATTGGATAGCTCTCTCGCCCTTTGTCTTTTAGGGTTA	5271
Db	4624	TGGTGGACGGACCCGCAACCATCTGGGCCAGCAGCTGCGGAGGAACATTCACGCGAAA	4683	5704	CCACAGAGACTGGCAATTAATGATTGGATAGCTCTCTCGCCCTTTGTGCTTTTAGGGTTA	5763
Qy	4192	AGGCTGAGCTCATGGCCCTCAAGCAAGCTTTGCGGCTGGCGAAGGAAATCCATAAACA	4251	5272	GGAAACCCCTGGACAGTTTGGGTGACCCCTCTAGAAATTACTCTACGGGGGACCCCCC	5331
Db	4684	AGGCTGAGCTCATGGCCCTCAAGCAAGCTTTGCGGCTGGCGAAGGAAATCCATAAACA	4743	5764	GGAAACCCCTGGACAGTTTGGGTGACCCCTCTAGAAATTAAGTCTACGGGGGACCCCCC	5823
Qy	4252	TTTATACGACAGCAGTATGCCCTTTCGCACTGACACATGAGGGGCCATCTATAAAC	4311	5332	CAATGGTAGAAATTGCTCTGTACATAGTGTGACGCTGTGCTTTCCAGCCCTTTGTCTCT	5391
Db	4744	TTTATACGACAGCAGTATGCCCTTTCGCACTGACACATGAGGGGCCATCTATAAAC	4803	5824	CGTTGGTAGAAATTGCTCTGTACATAGTGTGCTGTGCTTTCCAGCCCTTTGTCTCT	5883
Qy	4312	AAAGGGGTGCTTACCTCAGCAGGGAGGGAATTAAGAACAAAGAGGAATTTCTAAGCC	4371	5392	CTAGGCTCAAGGCACTTGAGTGGGTGAGACAACGACGCTGGAGGCAACTCCGGAGGCGCT	5451
Db	4804	AAAGGGGTGCTTACCTCAGCAGGGAGGGAATTAAGAACAAAGAGGAATTTCTAAGCC	4863	5884	CTAGGCTCAAGGCGCTCGAGTGGGTGAGCAACGAGCGTGGAGAGCACTCCGGAGGCGCT	5943
Qy	4372	TATTAGAAGCCGTACATTACCAAAAGGCTAGCTATTATACACTGCTCTGGACATCAGA	4431	5452	ACTCAGAGAGAGACTTTGCAGATCCCAATCGTTTCCAAGTGGAGATTCAGTCTACG	5511
Db	4864	TATTAGAAGCCCTTACATTGGCCAAAAGGCTAGCTATTATACACTGCTCTGGACATCAGA	4923	5944	ACTCAGAGAGAGAGACTTTGCAAGTTTCCAATCGCTTCCAAGTGGAGATTCAGTCTATG	6003
Qy	4432	AAGCTAAAGATCTCATATCCAGAGGAAACAGATGGCTGACCGGGTTGCCAAGCAGCAG	4491	5512	TTAGACGCCACCGTGCAGGAAACCTCGAGACTCGGTGGAGGGCCCTTATCTCGTACTTT	5571
Db	4924	AAGCTAAAGATCTCATATCCAGAGGAAACAGATGGCTGACCGGGTTGCCAAGCAGCAG	4983	6004	TTAGACGCCACCAATGAGGAAACCTCGAGACTCGGTGGAGGGCCCTTATCTCGTACTTT	6063
Qy	4492	CCAGGGTGTTAACTTCTGCTTAATAGAAATGCCCAAGCCCAAGACCCAGACAGCAG	4551	5572	TGACCAACCAACCGGCTGTGAAAGTCCGAAGGAATCTCCACTCGGATCCCATGCCAAG	5631
Db	4984	CCAGGGTGTTAACTTCTGCTTAATAGAAATGCCCAAGCCCAAGACCCAGACAGCAG	5043	6064	TGACCAACCAACCGGCTGTGAAAGTCCGAAGGAATCTCCACTCGGATCCCATGCCAAG	6123
Qy	4552	AGTACACCTTAGAAGACTGGCAAGAGATATAAAGATAGACCACTTCTTGAGACTCCGG	4611	5632	TTAAACCGGGCCCACTCCCGATTCGGGGTGGAAAGCCGGAAGAGACTGAAAAATCCCTTA	5691
Db	5044	AGTACACCTTAGAAGACTGGCAAGAGATATAAAGATAGACCACTTCTTGAGACTCCGG	5103	6124	TTAAGCTGGCGCCCACTCCCGACTCGGGGTGGAGAGCCGGAAGAGACTGGAATTCCTCTTA	6183
Qy	4612	AAGGGACCTGCTATACCTCAGATGGGAAGGAATCTCTGCCCCACAAAGAGGGTTAGAAT	4671	5692	AGCTTCGCTCCATCGGTGGTTCTTACTCTGCTCAATACCTCTCAGACTTAATGGTATG	5751
Db	5104	AGGGACCTGCTATACCTCATATGGGAAGGAATCTCTGCCCCACAAAGAGGGTTAGAAT	5163	6184	AGCTTCGCTCCATCGCTGGTTCTTACTCTAACCAATTAATCTCCAGGCCAGTAGTAAA	6243
Qy	4672	ATGTCCAACAGATACATGCTTAACCCACCTAGAACTTAAACACTCGCAGCAGTTGGTCA	4731	5752	CGCATAGGAGACAGCCTGAACTCCCATAAACCCCTTATCTCTCACTGGTTAAATTAAGTAC	5811
Db	5164	ATGTCCAACAGATACATGCTCTACCCACCTAGAACTTAAACACTCGCAGCAGTTGGTCA	5223	6244	CGCTTATAGACAGCTCGAACCCCACTAGACCTTTATCCCTTACCTGGCTGATTAATTGAC	6303
Qy	4732	GAAACATCCCTTTATCATGTTCTGAGGCTTACCAGAGTGGCTGACTCCGTGGTCAAAAT	4791	5812	TCCGGCACAGGATTAATATCAACAACACTCAAGGGGAGGCTCTTTAGGAACTGGTGG	5871
Db	5224	GAAACATCCCTTTATCATGTTCTGAGGCTTACCAGAGTGGCTGACTCCGTGGTCAAAAT	5283	6304	CCTGATACGGGTGCTCATCTGTAAATAGCACTCGAGGTGTGTCTCTAGAGGCACTGGTGG	6363
Qy	4792	GTGTGCCCTGCGAGCTGTTAATGCTAATCTCTCAGAAATGCTCCAGAGGAAGAGACTAA	4851	5872	CCTGATCTATACGTTTGGCTTCAGATCAGTTATTTC---CTAGTCTGACCTCAACCCCAAGAT	5928
Db	5284	GTGTGCCCTGCGAGCTGTTAATGCTAATCTCTCAGAAATGCTCCAGAGGAAGAGACTAA	5343	6364	CCTGAACTGCAATTTCTGCTCCCGATTAACCCCGCTGTAAAGGCAACCTCCCAAC	6423
Qy	4852	GGGGAAGCCACCGGCGCTCACTGGGAGTGGACTTCACTGAGGTAAAGCCGCTAAAT	4911	5929	ATCCTCCATCCTCAACGGATTTTATGTTTGGCCAGGACCAACAAATTAATGAAACCAATTGC	5988
Db	5344	GGGGAAGCCACCGGCGCTCACTGGGAGTGGACTTCACTGAGGTAAAGCCGCTAAAT	5403	6424	CTAGTCCGTAGTTATGGTCTCTATTCGTCGCCAG---CACAGAGAAAGAGAAATACTGT	6480
Qy	4912	ACGGAAACAATACCTATTTGTTTTGTAGACACTTTTCAGGATGGGTAGAGGCTTATC	4971	5989	GGAAATCCCAAGAGATTTCTTTTGTAAACAATAGAACTGTGTAACTCTAATGATGATAT	6048
Db	5404	ACGGAAACAATATCTATTTGTTTTGTAGACACTTTTCAGGATGGGTAGAGGCTTATC	5463	6481	GGGGTTCTGGGGAATCCTTCTGTAGGAGATGGAGCTGCGCTCACTCAACGATGGAGAC	6540
Qy	4972	CTACTAAGAAAGAGACTTCAACCGTGGTGTGCTTAAAAAATACTGGAAAGAAATTTTCCAA	5031	6049	TGGAAATGGCCAACTCTCAGCAGGATAGGGTAAAGTTTCTTTATGTCACACCTATACC	6108
Db	5464	CTACTAAGAAAGAGACTTCAACCGTGGTGTGCTTAAAAAATACTGGAGGAAATTTTCCGA	5523	6541	TGGAAATGGCCGATCTCTCTCCAGGACCGGGTAAAAATCTCTCTTTGTCAA-----	6590
Qy	5032	GATTTGGAATACCTTAAGGTAAATAGGGTCAGACAATGTGTCAGCTTTTGTGCCCAGGTAA	5091	6109	AGCTCTGCAACAATTTAATTAACCTGACCTGGATTAGAACTGGAAAGCC	

DT 06-MAR-2003 (first entry)
XX PERV clone PK15-PERV-B (Bac-192B9) DNA.
DE
XX PERV; porcine; env; gag; infection; vaccine; virucide; immunization;
KW pig breeding; chromosome mapping; protection; ds.
XX Porcine endogenous retrovirus.
OS
XX
XX
XX DE10111433-Al.
XX
XX 19-SEP-2002.
XX
XX 09-MAR-2001; 2001DE-01011433.
XX
XX 09-MAR-2001; 2001DE-01011433.
XX
XX (BUND) BUNDESREPUBLIK DEUT PAUL-EHRLICH-INST.
XX
XX Toenjes RR, Krach U;
XX
XX WPI; 2002-699548/76.
XX
XX Replication-competent molecular clones of porcine endogenous retrovirus,
PT useful as sources of env peptides for vaccination and for viral
PT detection.
XX
XX Claim 8; Fig 17; 52pp; German.
XX
XX This invention describes novel replication-competent molecular clones of
CC porcine endogenous retrovirus (PERV) isolated from a porcine BAC
CC (bacterial artificial chromosome) library which are replication competent
CC after transfer into permissive cells. The invention also discloses (a)
CC env and gag polypeptides encoded by the molecular clones of the invention
CC ; (b) porcine nucleic acids that represent the 5' and 3' flanking
CC sequences of the integration site of a replication competent molecular
CC clone in the porcine genome; (c) oligonucleotides for detecting
CC integrated PERV; (d) a method for detecting appearance of infectious PERV
CC particles in a sample; (e) a vaccine for immunization against replication
CC -competent PERV, comprising an env protein and (f) a method for isolating
CC the molecular clones of the invention. The products of the invention are
CC have virucide activity. The clones are from native PERV and make possible
CC comparisons of proviral sequences of different origins at the molecular,
CC structural and cellular levels, and mapping of proviral sequences at
CC chromosomal positions in specific breeds of pigs. Also different breeds
CC of pigs can be screened for presence of specific infectious PERV, i.e. to
CC identify PERV-free animals. Also vaccines that contain the env
CC polypeptides encoded by the clones of the invention are useful for
CC protection against replication-competent PERV. The products of the
CC invention are functional, replication-competent, full-length, proviral
CC clones isolated directly from the pig genome, i.e. they are 'native'
CC PERV. This sequence represents a PERV genome fragment described in the
CC disclosure of the invention
XX
XX Sequence 8840 BP; 2307 A; 2227 C; 2315 G; 1991 T; 0 U; 0 Other;
XX
XX
XX Query Match 77.3%; Score 6288.8; DB 6; Length 8840;
XX Best Local Similarity 86.8%; Pred. No. 0;
XX Matches 7173; Conservative 0; Mismatches 932; Indels 155; Gaps 17;
XX
XX 1 CGGTGGTGTACAGCTGTGGGCCCCAGCGCGCTTGGATATAAAATCCTCTGCTGTTGCA 60
XX
XX 526 CGGTGGTGTACAGCTGTGGGCCCCAGCGCGCTTGGATATAAAATCCTCTGCTGTTGCA 585
XX
XX 61 TCAAGACCGCTTCTCGTGTAGTGATTAAAGGGAGTGCCTTTTCCGAGCTCGAGG----- 115
XX
XX 586 TCAAGACCGCTTCTCGTGTAGTGATT-TGGGGTGTGCGCTCTCCGAGCCCGAGAGGGG 644
XX
XX 116 -----TTCTTTTGTGCTTACATTTGGGGGCTCGTCCGGGATCTGTCCGGGCCACCCC 171
XX
XX 645 GATTGTTCTTTTACTGGCTTTTCATTTGTTGGTGGCGCGGAAATCTTCGCGACACCCC 704
XX
XX 172 TAAACCCGAGAACCGACTTGGAGGTAAAGGATCCTCTTTTAAACGTGTATGATGTA 231

Db 705 TTACACCCGAGAACCGACTTGGAGGT-AAAGGGATCCCCTTTTGAACGTGTGTG--TGTG 761
Qy
Db 232 CGGGCCGGCGTCTCTGTCTGTAGTGTCTGTTTTCAGTGGTGCCTGCTTTCGGTTCGAGC 291
Db 762 TCGGCCGGCGTCTCTGTCTGTAGTGTCTGTTTTCGGTGTATCGCGCTTTCGGTTCGAGC 821
Qy 292 TGTCTCTCTCAGGCCGTAAGGGCTTGGGGAGCTGTGATCAGCAGAGCTGTCTAGGAGGATCAC 351
Db 822 TGTCTCTCTCAGACCGTAAAGGACTGGAGGACTGTGATCAGCAGAGCTGTCTAGGAGGATCAC 881
Qy 352 AGGCTGCTGCTGCGGGAGCGCCCGGGAGGTGAGGAGCCAGGAGCGCTGTGTGTCT 411
Db 882 AGGCTGCTGCTGCGGGAGCGCCCTGGGAGGTGGGAGAGCCAGGAGCGCTGTGTGTCT 941
Qy 412 CTTACTGTGCTGCTCAGAGGACCGAAATCTGTGTCTGTAAGCGAAAGCTTCCCTCCCGGAC 471
Db 942 CTTACTGTGCTGCTCAGAGGACCGAGTCTGTGTGTAAGCGAAAGCTTCCCTCCCGGAC 1001
Qy 472 CGTCCGACTCTTTTGTCTGCTGTGAAGACGTGGACGGGTCACTGTGTCTGTGATCTGT 531
Db 1002 CGTCCGACTCTTTTGTCTGCTGTGAAGACGTGGACGGGTCACTGTGTCTGTGATCTGT 1061
Qy 532 TGTGTTCTGTTTGTGTGTCTTGTGTGTGTCTTGTGTGTCTGTGTGTGTGTGTGTGTGTGT 591
Db 1062 TGTGTTCTGTTTGTGTGTCTTGTGTGTGTCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1121
Qy 592 AGACGGTGTGACGCCCTCTTGT 651
Db 1122 AGACGGTGTGACGCCCTCTTGT 1181
Qy 652 CTCATAATTTGTGTCAGTTTGTGTTAAGAGGAGCTTGGCAGACTTTCGTGTCTCTGAAT 711
Db 1182 CTCATAATTTGTGTCAGTTTGTGTTAAGAGGAGCTTGGCAGACTTTCGTGTCTCTGAAT 1241
Qy 712 GGCGCAGTTCGATTTGGATGGCCATCAGAGGGGACTTAAATCTTGAGATTAATCTCGG 771
Db 1242 GGCGCAGTTCGATTTGGATGGCCATCAGAGGGGACTTAAATCTTGAGATTAATCTCGG 1301
Qy 772 CTGTTAAGCAGTATTTTTCAGACTGCGACCGCGCTCTCATCCCGATCAGAGGCGCTTATA 831
Db 1302 CTGTTAAGCAGTATTTTTCAGACTGCGACCGCGCTCTCATCCCGATCAGAGGCGCTTATA 1361
Qy 832 TCCTTACGTGCGCAAGATTGTCGAGAGGATCTCCGCCATGGGTTAAACCAATGGCTGAATA 891
Db 1362 TCCTTACGTGCGCAAGATTGTCGAGAGGATCTCCGCCATGGGTTAAACCAATGGCTGAATA 1421
Qy 892 AGCCAAAGAAAGCCAGGTCCCGAATTCGGCTCTTTGGAGAGAAACAAACACTCGGCTG 951
Db 1422 AACCAAGAAAGCCAGGTCCCGAATTCGGCTCTTTGGAGAGAAACAAACACTCGGCTG 1481
Qy 952 AAAAGTCAAGCCCTCTCTCATATCTACCCCGAGATTGAGGAGCCACCGCTTTGGCCGG 1011
Db 1482 AAAAGTCAAGCCCTCTCTCATATCTACCCCGAGATTGAGGAGCCACCGCTTTGGCCGG 1541
Qy 1012 AACCCCAATCTGTTCCTCCCGACCGCTTATCTGGCAGAGGGTGCCTGAGGGGAGCCCTTTG 1071
Db 1542 AACCCCAATCTGTTCCTCCCGACCGCTTATCCAGCAGAGGGTGTCTGTGAGGGGAGCCCTCTG 1601
Qy 1072 CCCCTCTCTGAGTCTCCCGCGGTGGAGGAGCTGTGTGAGGAGCTTCGGAGCCGAGGGGCG 1131
Db 1602 CCCCTCTCTGAGTCTCCCGGTGGAGGAGCTGTGTGAGGAGCTTCGGAGCCGAGGGGCG 1661
Qy 1132 CCACCCCGAGCGAGCAGACGAGATCGGACATTTACCGCTGCGCAGCTGACCGGCTCCCA 1191
Db 1662 CCACCCCGAGCGAGCAGACGAGATCGGACATTTACCGCTGCGCAGCTTATGGCCCTCCCA 1721
Qy 1192 CACCGGGGGCGCAATTGCGAGCCCTCCAGTATTGGCCCTTTTCTTCTGAGATCTCTATA 1251
Db 1722 TGCCGGGGGGCAATTGCGAGCCCTCCAGTATTGGCCCTTTTCTTCTGAGATCTCTATA 1781
Qy 1252 ATTGGAAACCTAACCATCCCCCTTTCTCGGAGGATCCCAACCGCTTACCGGGTGTGTGG 1311

Db 1782 ATTGGAATACTAACCAATCCCTTTCTCGAGGATCCCAACGCCTCACGGGGTTGGTG 1841
QY 1312 AGTCCCTTATGTTCTCTCAACAGCCTACTTGGGATGATTTGTAACAGCTGCTGCAGACAC 1371
Db 1842 AGTCCCTTATGTTCTCTCAACAGCCTACTTGGGATGATTTGTAACAGCTGCTGCAGACAC 1901
QY 1372 TCTTCAACACCGAGGAGCGAGAGAAATTTCTATTAGAGCTAGAAAAATGTTCTGGGG 1431
Db 1902 TCTTCAACACCGAGGAGCGAGAGAAATTTCTGTTAGAGCTAGAAAAATGTTCTGGGG 1961
QY 1432 CCGACGGGCGACCCACGGTTCGCAAAATGAGATTTGACATGGATTTCCCTTAACCTGCC 1491
Db 1962 CCGACGGGCGACCCACGGTTCGCAAAATGAGATTTGACATGGATTTCCCTTAACCTGCC 2021
QY 1492 CCGGTTGGGACTACAAACGGCTGAAGGTAGGAGAGCTTGAAAATCTATCGCCAGGCTC 1551
Db 2022 CCGGTTGGGACTACAAACGGCTGAAGGTAGGAGAGCTTGAAAATCTATTCGCCAGCTC 2081
QY 1552 TGGTGGCGGTCTCCGGGGCGCTCAAGACGGCCCACTAATTTGGCTAAGGTAAGAGAAG 1611
Db 2082 TGGTGGCGGTCTCCGGGGCGCTCAAGACGGCCCACTAATTTGGCTAAGGTAAGAGAAG 2141
QY 1612 TGAATCAGGACCGAATGAACCCCTCTGTTTCTTGAGAGGCTCTTGGAGCCTTCA 1671
Db 2142 TGAATCAGGACCGAATGAACCCCTCTGTTTCTTGAGAGGCTCATGGAAGCCTTCA 2201
QY 1672 GCGGTTACACCCCTTTTGATCCACCTCAGAGGCCCAAAAGCCTCAGTGGCTTTGGCCT 1731
Db 2202 GCGGTTACACCCCTTTTGATCTTACCTCGAGGCCCAAGAGCCTCAGTGGCCTGBCCT 2261
QY 1732 TTATAGGACAGTCAGCCTTTGGATATTAGAAAGAGCTTCAGAGACTGGAAGGTTACAGG 1791
Db 2262 TCATTGGGAGTCGGCTCGGATATCAGAAAGAACTTCAGAGACTTGAAGGTTACAGG 2321
QY 1792 AGCTCAGTTACGTGATCTAGTGAAGGAGCAGAGAAAGTATATTACAAAAGGAGACAG 1851
Db 2322 AGGCTGAGTTACGTGATCTAGTGGGAGGCGAGAGAGGTGATTATCAGAAAGGAGACAG 2381
QY 1852 AAGAAGAAAGGGAACAAAGAAAGAGAGAAAGAGAGAAAGGAGGAAGACGCTAATA 1911
Db 2382 AAGAGAGAGGAAACAGAGAAAGAAAGAAAGAGAGAGAAAGGAGGAAGACGTGATA 2441
QY 1912 AACGCAAGAGAGAAATTTGACTAAGATCTTGGCTGCTAGTGGTTGAAGGGAAGCAATA 1971
Db 2442 GACGCAAGAGAGAAATTTGACTAAGATCTTGGCCGCTGTTGAAGGGAAGAGCAGCA 2501
QY 1972 CCGAAAGAGAGAGATTTTAGAAAATTTAGTTCAGGCCCTAGACAGTCAGGGAACCTGG 2031
Db 2502 GGGAGAGAGAGAGATTTTAGAAAATTTAGTTCAGGCCCTAGACAGTCAGGGAACCTGG 2561
QY 2032 GCAATAGGACCCCACTCGAACAGGACCAATGTGCATATTGTAAGAAAGAGGACACTGG 2091
Db 2562 GCNATAGGACCCCACTCGAACAGGACCAAGTGTGCGTATTGTAAGAAAGAGGACACTGG 2621
QY 2092 CAAGGAACCTGCCCAAGAGGGAACAAAGGACCGAAGGTCTCTAGTAGAAGAGATA 2151
Db 2622 CAAGGAACCTGCCCAAGAGGGAACAAAGGACCGAAGGTCTCTAGTAGAAGAGATA 2681
QY 2152 AAGATTAGGGGAGACGGGGTTCGGACCCCTCCCGAGCCAGGGTAACTTTGAAGGTGG 2211
Db 2682 AAGATTAGGGGAGACGGGGTTCGGACCCCTCCCGAGCCAGGGTAACTTTGAAGGTGG 2741
QY 2212 AGGGGCAACAGTTGAGTTCTCGTTGATACCGGAGCAACATTCAGTGTCTACTACAGC 2271
Db 2742 AGGGGCAACAGTTGAGTTCTCGTTGATACCGGAGCGAGCAATTCAGTGTCTACTAAC 2801
QY 2272 CATTTAGGAAAATAAAGATAAAAAATCTCTGGGTGATGGGTGCCACAGGCGCAACACAGT 2331
Db 2802 CATTTAGGAAAATAAAGATAAAAAATCTCTGGGTGATGGGTGCCACAGGCGCAACAGT 2861
QY 2332 ATCCATGGACTACCCGAAGAACAGTTGACTTGGGAGTGGGACGGGTAAACCCACTCGTTTC 2391
Db 2862 ATCCATGGACTACCCGAAGAACAGTTGACTTGGTGTGGGACGGGTAAACCCACTCGTTTC 2921

QY 2392 TGGTCATACCTGAGTGCCCGACACCCCTCTTTAGGTAGAGACTTATTTGACCAAGATGGGAG 2451
Db 2922 TGGTCATCCCTGAGTGCCCGAGTACCCCTTCTTAGGTAGAGACTTACTGACCAAGATGGGAG 2981
QY 2452 CACAAATTTCTTTTGAACNAGGGAACCGAAGTGTCTGCAAAATACAAACCTATCAGCTG 2511
Db 2982 CTCAAATTTCTTTTGAACNAGGGAACCGAAGTGTCTGCGATTAACAAACCATCAGCTG 3041
QY 2512 TGGTGACCTCCAAATTTAGATGACGAATATCGACTATCTCTCCCTAGTAAAGCCCTGATC 2571
Db 3042 TGGTGACCTCCAAATTTAGATGATGATATCGACTATTTCTCCCAAGTAAAGCCCTGATC 3101
QY 2572 AAAATATACAAATTTGGTTGGAACTTTCCCAAGCCTGGCGCAGAAAACCGCAGGATGG 2631
Db 3102 AAGATATACAGTCTCTGGTTGGAGCAGTTTCCCAAGCCTGGCGCAGAAAACCGCAGGATGG 3161
QY 2632 GTTTGGCAAAAGCAAGTTCCCCCACAAGATTATTTCACTGAAGGCCAGTGCACACCACTGT 2691
Db 3162 GTTTGGCAAAAGCAAGTTCCCCCACAAGTTATTTCACTGAAGGCCAGTGTCTACACCACTAT 3221
QY 2692 CAGTCAGACAGTACCCCTTTGAGTAAAGAGCTCAAGAAAGAAATTCGGCCGCAATGTCCAAA 2751
Db 3222 CAGTCAGACAGTACCCCTTTGAGTAAAGAGCTCGAAGAGAAATTTGGCCGCAATGTTCAAA 3281
QY 2752 GATTAATCCAAACAGGCGCATCTAGTTTCTGTCCAAATCTCCCTGGAAATCTCCCTCTGTAC 2811
Db 3282 GATTAATCCAAACAGGCGCATCTAGTTTCTGTCCAAATCTCCCTTTGGAATACTCCCTCTGTAC 3341
QY 2812 CGGTTAGAAAGCCTGGGACTAATGATATCGACCAAGTACAGGACTTTGAGAGAGGTCAATA 2871
Db 3342 CGGTTAGGAAGCCTGGGACCAATGATATCGACCAAGTACAGGACTTTGAGAGAGGTCAATA 3401
QY 2872 AAGGGTGCAGGATATACACCCCAACAGTCCCGAAACCTTTATTAACCTTTGTGTCTCTCC 2931
Db 3402 AAGGGTGCAGGATATACACCCCAACAGTCCCGAAACCTTTATTAACCTTTGTAGCGCCTCC 3461
QY 2932 CACCCCAACCGGAGCTGTATACAGATTGGGACTTAAAGGATGCTTTCTCTGCTGAGAT 2991
Db 3462 CGCCTGAACGGAACTGGTACACAGATTGGACTTAAAGATGCCTTCTTCTGCTGAGAT 3521
QY 2992 ATACCCCACTAGGCAACCACTTTTGGCTTCGAATGGAGAGATCCAGGTACGGGAGAA 3051
Db 3522 ATACCCCACTAGGCAACCACTTTTGGCTTCGAATGGAGAGATCCAGGTACGGGAGAA 3581
QY 3052 CCGGCGAGCTCACCTGGACCCGACTGCCCCAAGGGTTCAAGAACTCCCGACCATCTTTG 3111
Db 3582 CCGGCGAGCTCACCTGGACCCGACTGCCCCAAGGGTTCAAGAACTCCCGACCATCTTTG 3641
QY 3112 ACGAAGCCCTACACAGAGACCTGGCCAACTTCAGGATCAACAACCTTCAGGTGACCCCTCC 3171
Db 3642 ACGAAGCCCTACACAGGAGACCTGGCCAACTTCAGGATCAACAACCTTCAGGTGACCCCTCC 3701
QY 3172 TCAGTACGTGATGACCTGCTTGGCGGGAGCCCAACAGGACTCTCTTAGAAGGCA 3231
Db 3702 TCAGTACGTGATGACCTGCTTGGCGGGAGCCCAACAGGACTCTCTTAGAAGGTA 3761
QY 3232 CGAAGCACTACTGCTGGAAATTTGCTGACCTTAGGCTTACAGAGCTCTCTTAAGAGGCC 3291
Db 3762 CGAAGCACTACTGCTGGAAATTTGCTGACCTTAGGCTTACAGAGCTCTCTTAAGAGGCC 3821
QY 3292 AGATTTGACGAGAGAGAGGTAAACATACTTGGGGTACAGTTTGGGGGACGGGACGATGGC 3351
Db 3822 AGATTTGACGAGAGAGAGGTAAACATACTTGGGGTACAGTTTGGGGGACGGGACGATGGC 3881
QY 3352 TGAACGAGGCAACGGAAGAAAACTGTAGTCCAGATCCGGCCCAACCAACAGCCCAACAAA 3411
Db 3882 TGAACGAGGCAACGGAAGAAAACTGTAGTCCAGATCCGGCCCAACCAACAGCCCAACAAA 3941
QY 3412 TCAGAGAGTTTGTGGGACAGCTGGATTTTGCAGACTGTGGATCCCGGGGTTTGGCAGCCT 3471
Db 3942 TGAGAGAGTTTGTGGGACAGCTGGATTTTGCAGACTGTGGATCCCGGGGTTTGGCAGCCT 4001

Qy	3472	TAGCAGCCCACTTACCCGCTAACCAAGAGAAAGGGGAATTCCTCTGGGCTCTTGAGC	3531		Db	5082	AGTACACCCCTAGAAGCTGGCAAGAGATAAAAAGATAGACCAGTTCTCTGAGACTCCGG	5141	
Db	4002	TAGCAGCCCACTTACCCGCTAACCAAGAGAAAGGGGAATTCCTCTGGGCTCTTGAGC	4061		Qy	4612	ACGGGACCTGCTATACCTCAGATGGGAAGGAAATCTCTGCCCCCAAAAGAGGGTTAGAAT	4671	
Qy	3532	ACCAAGAGGCAATTTGATGCTATCAAAAGGCCCTGCTGAGGCACTCTGCTCTGGCCCTCC	3591		Db	5142	AGGGGACCTGCTATACCTCATATGGGAAGAAATCTCTGCCCCCAAAAGAGGGTTAGAAT	5201	
Db	4062	ACCAAGAGGCAATTTGATGCTATCAAAAGGCCCTGCTGAGCGCACCTGCTCTGGCCCTCC	4121		Qy	4672	ATGTCCAAACAGATACATCGTCTAACCCACCTAGGAATAAAACCTCGAGAGTTGTGTCA	4731	
Qy	3592	CTGAGCTAACTTAACCCCTTTACCCCTTTATGTGGATGAGCGTAAAGGAGTAGCCCGGGGAG	3651		Db	5202	ATGTCCAAACAGATACATCGTCTCACCCACCTAGGAATAAAACCTGTAGCAGTTGGTCA	5261	
Db	4122	CTGAGCTAACTTAACCCCTTTACCCCTTTATGTGGATGAGCGTAAAGGAGTAGCCCGAGAG	4181		Qy	4732	GAACATCCCTTATCATGTTCTGAGGCTACCGAGAGTGGCTGACTCGGTGGTCAAAACATT	4791	
Qy	3652	TTTTAAACCCAAACCTTAGGACCATGAGAGAACCTGTGCGCTACTCTGTCAAGAGAGCTCG	3711		Db	5262	GAACATCCCTTATCATGTTCTGAGGCTACCGAGAGTGGCTGACTCGGTGGTCAAAACATT	5321	
Db	4182	TTTTAAACCCAAACCTTAGGACCATGAGAGAACCTGTGCGCTACTCTGTCAAGAGAGCTTG	4241		Qy	4792	GTGTGCCCTGCCAGCTGGTTAATGTCTTCCAGAAATGCTCTCCAGGAAAGAGACTAA	4851	
Qy	3712	ATCCTGTAGCCAGTGTGTGGCCCATATGCTGTGAAGGCTATGCGAGCTGTGGCCATCTGG	3771		Db	5322	GTGTGCCCTGCCAGCTGGTTAATGTCTTCCAAAGTACCTCCAGGGAAGAGACTAA	5381	
Db	4242	ATCCTGTAGCCAGTGTGTGGCCCATATGCTGTGAAGGCTATGCGAGCTGTGGCCATCTGG	4301		Qy	4852	GGGGAAGCCACCCAGGCGCTCACTGGGAAGTGACTTTCACTGAGGTAAAGCCGGCTAAAT	4911	
Qy	3772	TCAAGGACGCTGACAAATTTGACTTTGGGACAGAAATATACTGTAAATAGCCCCCATGCAT	3831		Db	5382	GGGGAAGCCACCCAGGCGCTCACTGGGAAGTGACTTTCACTAAAGTAAAGCCGGCTAAAT	5441	
Db	4302	TCAAGGACGCTGACAAATTTGACTTTGGGACAGAAATATACTGTAAATAGCCCCCATGC	4361		Qy	4912	ACGGAACAAATACCTATTTGTTTGTAGACACCTTTTTCAGGATGGGTAGAGGCTTATC	4971	
Qy	3832	TGGAGAACATCGTTTCGGCAGCCCGCAGACCGATGGATGACCAACGCGCGCATGACCCACT	3891		Db	5442	ACGGAACAAATACCTATTTGTTTGTAGACACCTTTTTCAGGATGGGTAGAGGCTTATC	5501	
Db	4362	TGGAGAACATCGTTTCGGCAGCCCGCAGACCGATGGATGACCAACGCGCGCATGACCCACT	4421		Qy	4972	CTACTAAGAAAGAGACTTCAACCGTGTGGTGTCTAAAAAATACTCTGGAAGAAATTTTTC	5031	
Qy	3892	ATCAAGCCTGCTTCTCAGAGAGGGTCACTGTTGCTTCCACAGCGCGCTCTCAACCCCTG	3951		Db	5502	CTACTAAGAAAGAGACTTCAACCGTGTGGTGTCTAAAAAATACTCTGGAAGAAATTTTTC	5561	
Db	4422	ATCAAGCCTGCTTCTCAGAGAGGGTCACTGTTGCTTCCACAGCGCGCTCTCAACCCCTG	4481		Qy	5032	GATTTGGAATACCTTAAGGTAAATAGGGTACAGCAATGGTCCAGCTTTTGTGCCCCAGGTAA	5091	
Qy	3952	CCACTCTTCTGCTGAAGAGACTGATGAACCAAGTACTCATGATGGCATCAACTATTGA	4011		Db	5562	GATTTGGAATACCTTAAGGTAAATAGGGTACAGCAATGGTCCAGCTTTTGTGCCCCAGGTAA	5621	
Db	4482	CCACTCTTCTGCTGAAGAGACTGATGAACCAAGTACTCATGATGGCATCAACTATTGA	4541		Qy	5092	GTACAGGACTGGCCCAAGATATTGGGGATTTGATTGGAAACCTGTCATTTGTCATACAGCCCC	5151	
Qy	4012	TTGAGGAGACTGGGCTCGCAAGGACCTTACAGACATACCGCTGACTGGGAAGTGTCTAA	4071		Db	5622	GTACAGGACTGGCCCAAGATATTGGGGATTTGATTGGAAACCTGTCATTTGTCATACAGCCCC	5681	
Db	4542	TTGAGGAGACTGGGCTCGCAAGGACCTTACAGACATACCGCTGACTGGGAAGTGTCTAA	4601		Qy	5152	AAAGCTCAGACAGGTAGAGAGGATGAATAGAACCATTTAAAGAGACCTTACTAAATTTGA	5211	
Qy	4072	CTCTGTTCACTACGCGAAGCAGCTATGTGTGGAGGTAAAGAGATGGCTGGGCGGCGG	4131		Db	5682	AAAGCTCAGACAGGTAGAGAGGATGAATAGAACCATTTAAAGAGACCTTACTAAATTTGA	5741	
Db	4602	CTCTGTTCACTACGCGAAGCAGCTATGTGTGGAGGTAAAGAGATGGCTGGGCGGCGG	4661		Qy	5212	CCGCGGAGACTGGCGTTAATGATTTGGATAGCTCTCTCGCCCTTTGTGCTTTTAAAGGTTA	5271	
Qy	4132	TGGTGAACGCGACCGACGATCTGGGCCAGCAGCTGCGGAGAGAACTTCAGACAAA	4191		Db	5742	CCAGAGACTGGCATTTAATGATTTGGATAGCTCTCTCGCCCTTTGTGCTTTTAAAGGTTA	5801	
Db	4662	TGGTGAACGCGACCGACGATCTAGGCCAGCAGCTGCGGAAAGAACTTCAGCGCAAA	4721		Qy	5272	GGAAACCCCTGGACAGTTTGGGCTGACCCCTTATGAATTACTCTACGGGGAGACCCCGCC	5331	
Qy	4192	AGGCTGAGCTCATGSCCTCAGCAAGCTTTTGGGCTGGCCGAAAGGAAATCCCATAAACA	4251		Db	5802	GGAAACCCCTGGACAGTTTGGGCTGACCCCTTATGAATTTGCTCTACGGGGAGACCCCGCC	5861	
Db	4722	AGGCTGAGCTCATGSCCTCAGCAAGCTTTTGGGCTGGCCGAAAGGAAATCCCATAAACA	4781		Qy	5332	CATTGGTGAATTTGCTTCTGTACATAGTGTGACGTGCTCTTTTCCAGCGCTTTGTCT	5391	
Qy	4252	TTTATACGGACAGCAGGTATGCTTTTGGACTGCAACGTATAGGGGCCATCTATAAC	4311		Db	5862	CGTTGGTAGAAATTTGCTTCTGTACATAGTGTGATGTGCTCTTTCCAGCGCTTTGTCT	5921	
Db	4782	TTTATACGGACAGCAGGTATGCTTTTGGACTGCAACGTATAGGGGCCATCTATAAC	4841		Qy	5392	CTAGGCTCAAGGCATTTGAGTGGGTGAGACAAACAGCGGTGGAGGCAATCCCGGAGGCGCT	5451	
Qy	4312	AAAGGGGTGCTTACCTCAGCAGGAGGAAATAAAGAACAAAGAGAAATTTCTAAGCC	4371		Db	5922	CTAGGCTCAAGGCCTCGAGTGGGTGAGGACGAGCGGTGGAAGCAGCTCCCGGAGGCGCT	5981	
Db	4842	AAAGGGGTGCTTACCTCAGCAGGAGGAAATAAAGAACAAAGATGAAATTTCTAAGCC	4901		Qy	5452	ACTCAGGAGGAGAGACTTGCAGATGCCACATCGTTTCCAAAGTGGGAGATTCAGTCTACG	5511	
Qy	4372	TATTAGAGCCGTACATTTACMAAAGGCTAGCTATTATACCTGCTCGACATCAGA	4431		Db	5982	ACTCAGGAGGAGAGACTTGCAGATGCCACATCGCTTCCAAAGTGGGAGATTCAGTCTATG	6041	
Db	4902	TATTAGAGCCCTACATTTGCAAAAGGCTAGCTATTATACCTGCTCGACATCAGA	4961		Qy	5512	TTAGACGCCACCGTGCAGGAAACCTCGAGACTCGGTGGAAGGGCCCTTATCTCGTACTTT	5571	
Qy	4432	AAGCTTAAAGATCTCATATCCAGAGGAAACAGATGGCTGACCGGTTGCCAAGCAGGCGAG	4491		Db	6042	TTAGACGCCACCGTGCAGGAAACCTCGAGACTCGGTGGAAGGGCCCTTATCTCGTACTTT	6101	
Db	4962	AAGCCAAAGATCTCATATCTAGAGGGAACAGATGGCTGACCGGATTTGCCAAGCAGGCGAG	5021		Qy	5572	TGACCAACAAACGCGCTGTGAAAGTCTCGAAGAAATCTCCACCTGGATCCATGCATCCACG	5631	
Qy	4492	CCCAGGGTGTAACTTCTGCTTATAATAGAAATGCCCAAGCCCGAGAACCCAGACGAC	4551		Db	6102	TGACCAACAAACGCGCTGTGAAAGTCTCGAAGAAATCTCCACCTGGATCCATGCATCCACG	6161	
Db	5022	CCCAGGGTGTAACTTCTGCTTATAATAGAAACGCCCAAGCCCGAGAACCCAGACGAC	5081		Qy	5632	TTAAACCGGCGCCACTCTCCGATTTGGGGTGGAAAGCCGAAAGACTGAAAATCCCTTTA	5691	
Qy	4552	AGTACACCCCTAGAGACTGGGCAAGAGATAAAAAGATAGACCAAGTTCTCTGAGACTCCGG	4611						

D	b	6162	TTAAGCTGGGGCCACCTCCGACTCGGGTGGAGAGCCGAAAGACGTGAGAAATCCCTTTA	6221	6700	TCCACCACACACCTTTGTAAACCACTGAAGCCTTTAATCAAACTCTGAGAGTCAATAT	6759		
Q	y	5692	AGCTTCGCTCCATCCGCTGGTTCCTTACTCTGTCAATAACCTCTCAGACTAATGGTATG	5751	D	b	7284	TCCACCACACCTTTGTAGTACTGTGGTTATGAGAGCCCTCAGAAAAATCAGTAT	7343
D	b	6222	AGCTTCGCTCCATCCGCTGGTTCCTTACTCTAACAATAACTCCCCAGGCCAGTAGTAAA	6281	Q	y	6760	CTGGTACCTGGTTATGACAGGTGGGCATGTAACTACTGGAATTAACCCCTTGTGTTTC	6819
Q	y	5752	CGCATAGGAGACAGCCTGAACCTCCATAAACCTTATCTCTACCTGGTTAATTACTGAC	5811	D	b	7344	TTAGTACCTGGTTATAACAGGTGGTGGCATCAATACCTGCGGTTAACCCCTGTGTTTC	7403
D	b	6282	CGCTTTATAGACAGCTCGAAACCCCATAGACCTTTATCCCTTACCTGGCTGATTATTGAC	6341	Q	y	6820	ACCTTGGTTTTTAAACCAACTAAAGATTTTTCATTTATCGTCCAAATTTGTTCCCGAGTG	6879
Q	y	5812	TCCGGCACAGGTATTAAATCAACAACACTCAAGGGAGGCTCTCTTTAGGAACTCGTGG	5871	D	b	7404	ACCTCAGTCTTCAACCAATCCAAAGATTTCTGTGTCATGTCCTCAAAATCGTCCCGGAGTG	7463
D	b	6342	CTGTATACGGGTGCTACTGTAAATAGCACTCGAGGTGTGCTCTTAGAGGCACTCGGTGG	6401	Q	y	6880	TATTACTATCCGAAAAAGCAATCTCTTGATGAATATGACTACAGAAATCATCGACAAAAG	6939
Q	y	5872	CCTGATCTTATACGTTTGGCTCAGATCAGTTATTTC---CTAGTCTGACCTCACCCCCAGAT	5928	D	b	7464	TACTACCACTCTGAGGAAGTGGTCTTGATGAATATGACTATCGGTATAACCGACCGAAA	7523
D	b	6402	CCTGAACCTGCAATTTCTGCTCCGCTCCGATTGAATTAACCCCGCTGTTAAAGACACACTCCCAAC	6461	Q	y	6940	AGAGAACCATATCTCTGACACTTGTCTGTGATGCTCGGACTTGGAGTGGCAGCAGGTGTA	6999
Q	y	5929	ATCCTCCATGCTCACGGATTTTANGTTTGGCCAGGACCAACCAATAATGAAGAAACATTCG	5988	D	b	7524	AGAGAACCCGTATCCCTTACCTAGCTGTAAATGCTCGGATTAGGGACGGCCGTTGGCATA	7583
D	b	6462	CTAGTCCGTAGTTATGGGTTCCTTCTGTAGAGATGGAGCTGGCTCACCTCCAAACAATGGAGAC	6518	Q	y	7000	GGAAACAGGAAACAGCTGCCCTGTACCGGACCAACAGCAGCTAGAAAAACAGGACTTAGTAAC	7059
Q	y	5989	GGAAATCCAGAGATTTCTTTGTAAACAATGGAACGTGTAACTCTTAATGATGATAT	6048	D	b	7584	GGAAACAGGACAGCTGCCCTGATCACAGGACCAACAGCAGCTAGAGAAAGGACTTGGTGAG	7643
D	b	6519	GGGGTCTTGGGGAATCCTTCTGTAGAGATGGAGCTGGCTCACCTCCAAACAATGGAGAC	6578	Q	y	7060	CTACATCGAATTTGTAAACAGAGATCTCCAAGCCCTAGAAAAATCTGTCTAGTAACCTGGAG	7119
Q	y	6049	TGAAATGCGCAACCTCTCAGCAGGATAGGGTAAGTTTCTTATGTATCAACACCTATACC	6108	D	b	7644	CTACATCGCGCCATCAGAGAAGATCTCCGAGCTTAGAGGAGTCTGTATTAGCAACCTAGAA	7703
D	b	6579	TGGAATGCGCGATCTCTCCAGGACCGGTAAATTTCTCCTTTGTAAA-----	6628	Q	y	7120	GAATCCCTAACCTCTTATCTGAAGTAGTCCTACAGATAGAGAGGGTTAGATTTATTAA	7179
Q	y	6109	AGCTCTGGACAATTTAATTAACCTGACCTGGATTAGAACTGGAAAGCCCAAGTGTCTCTCT	6168	D	b	7704	GAGTCCCTGACTTCTTTGTCTGAAGTGGTCTACAGAACCGGAGGGGATTAGATCTGCTG	7763
D	b	6629	--TTCCGGCCCGGCAAGTACAAAGTGATGAACATATATAAAGATTAAGAGCTGCTCCCA	6686	Q	y	7180	TTTCTAAAAAGAGGAGGATTATGTGTAGCTTTGAAAGGAGGAATGCTGTGTTTTATGTGGAT	7239
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D	b	6687	TCAGACTTAGATTATCTAAGATAAGTTTCACGTGAAGAAAGGAAACAGGAAATATTCAA	6746	Q	y	7240	CAATCAGGGGCCATCAGAGATCCATGAAACAAGCTTAGAGAAAGGTTGGAGAACCTCGA	7299
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D	b	6747	NAGTGATAAATGGTATGAGCTGGGGAATAGTTTTTTATAA---TATGGCGGGAGCA	6803	Q	y	7300	AGGAAAAGGAAACTACTCAAGGTGGTTTGAAGGATGGTTCAACAGGTCTCTTTGGTTG	7359
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D	b	6804	GGGTCCACTTAAACCATTCGCTTAGGATAGAGCGGGGACAGAAACCCCTGTGGCAGTG	6863	Q	y	7360	GCTACCTACTTCTGCTTTAAACAGGACCTTAAATAGTCTCTCTCTCTGTACTCAAGTT	7419
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D	b	6924	CCGGTCCCAATTAACTCGCTCGGCGCTGACATAACACAGCCGCTAGCAACGGTACC	6983	Q	y	7480	ATCATGGTACTTAGACAACAGTACCAAGCCCGCTTAGC---AGGAACTGGCCCTAG	7536
Q	y	6415	TTGTGATCAGACCCCACTGAGTCTAACAGCA-----CGACTAAATGGGG	6459	D	b	8064	ATCATGGTACTTAGACAACAGTACCAAGCCCTTCTGAGCCAAAGGAGAACTGACCTCTAG	8123
D	b	6984	ACTGGATTGATTCCTACCAACACGCTAGAAAACCTCCCAAGGTGTTCTGTTAAGACAGGA	7043	Q	y	7537	CTCTACAGTCTTAAGATTAGAACTATTAAACAAGAGAAGTGGGGAATGAAAGATGA	7596
Q	y	6460	GCMAACTTTTAGCTCATCCAGGAGCTTTTCAAGCTTTAACTCCAGCTCCAGAG	6519	D	b	8124	CCTTCCAGTCTTAAGATTAGAACTATTAAACAAGACAGAGTGGGGAATGAAAGATGA	8183
D	b	7044	CAGAGACTCTTCACTCTCAGGAGCTTTTCCAAGCCATCAACTCCACCGACCTGAT	7103	Q	y	7597	AAATCAACCT-----AAGCTAATCAGAGGCTTAAATTTGTTCTGA	7637
Q	y	6520	GCTACCTCTTCTTGTGGGTATGCTTAGCTTCGGGCCCACTTACTATGAAGAAATGGCT	6579	D	b	8184	AAATGCAACTAAACCTCCAGAACCCAGGAAGTTAATAAAAGCTCTAAATGCCCCCGA	8243
D	b	7104	GCACCTCTCTTGTGGCTTGTCTATCCTCAGGCTCTTATTTATGAGGGATGGCT	7163	Q	y	7638	ATTCAGAGTGTGTTCCCTT-----ATAGCTAAAGATTAGGTTTTTGTCTGTTTTAA	7689
Q	y	6580	AGAAGAGGAAATTCATGTGACAAAGAACATAGAGACCAATGCAATGGGATCCCAA	6639	D	b	8244	ATTCAGAGCCCTGCTGGCTGCCAGTAAATAGGTAGAGGTACACACTTCTCTATTGTTCCAG	8303
D	b	7164	AAAGAGGAAATTCATGTGACAAAGACGCTAGAAATCAATGTACATGGGGGTCCCGA	7223	Q	y	7690	AAATGCGGAAGT----AAAAATAGGCCCTGAGTACATGTCTCTAGGCATCAAACTTTCTTG	7745
Q	y	6640	ATAAGCTTACCTTACTGAGTTTCTGGAAGGCACTGCATAGGAAGTTTCCCCCA	6699	D	b	8304	GGCTGCTACTCTGGCCCTAAGTAAGATAACAGGAATAGTTGACTAATTTGCTTATCTGG	8363
D	b	7224	ATAAGCTTACCTTACTGAGTTTCTGGAAGGCACTGCATAGGAAGTTTCCCCCA	7283					

XX Polynucleotide encoding porcine retrovirus expression product - useful to
PT develop products for use in vaccines, diagnosis and xeno-transplantation.
XX
XX PS
XX Claim 4; Fig 3; 69pp; English.
XX This DNA sequence encodes the porcine retrovirus (poEV) virion core
CC polypeptide (GAG), polymerase (pOL) and envelope (ENV) proteins and also
CC includes the Long Terminal Repeat (LTR). These proteins can be used to
CC develop viral vaccines, antisense nucleic acids, ribozymes and other
CC antiviral agents. They can also be used in xeno-transplantation
CC technology and as diagnostic tools. (Updated on 27-AUG-2003 to correct OS
CC field.)
XX
SQ Sequence 8209 BP; 2168 A; 2064 C; 2154 G; 1823 T; 0 U; 0 Other;
Query Match 77.3%; Score 6282.4; DB 2; Length 8209;
Best Local Similarity 87.1%; Pred. No. 0;
Matches 7165; Conservative 0; Mismatches 931; Indels 134; Gaps 19;
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1 GTGGTGTACGACTGTGGGCCCCAGCGCGCTTGGAAATAAAATCCTCTTGTGTGTGATC 60
63 AAGACCGCTTCTCGTGAAGTGAATTAAGGGAGTGCCTTTTCGAGCGCTGGAGS----- 115
61 AAGACCGCTTCTCGTGAAGTGAAT-TGGGGTGTGCGCTCTTCGAGCCCGAGCGAGGGGA 119
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1316 GTCCCTTATGTTCTCTCACCAGCTACTTGGAGATGATTTGTCAACAGCTCTGACAGACT 1375
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KW Porcine retrovirus; PoEV; POL protein; ENV protein; GAG protein; vaccine;
 KW diagnosis; xenotransplantation; prophylactic; therapeutic; ds.
 XX
 OS piq endogenous retrovirus.

Key	Location/Qualifiers
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WO9740167-A1.

30-OCT-1997.

18-APR-1997; 97WO-GB001087.

19-APR-1996: 96GB-00008164

TU-FEB-1997; 9/GB-00002668.

(QONE-) Q-ONE BIOTECH LTD.
(IMUT-) IMUTRAN LTD.

Galbraith DN, Hawor

WPI: 1997-535851/49.

Polynucleotide encod

Claim 4; Fig 2; 69pp; English.

This DNA sequence encodes the

polymerase (Nuc), polymerase (Pol), and envelope (Env) proteins can be used to develop viral vaccines, antisense nucleic acids, ribozymes and other antiviral agents. They can also be used in xenotransplantation technology and as diagnostic tools. (Updated on 27-AUG-2003 to correct QS field.)

Sequence 8196 BP; 2165 A; 2061 C; 2147 G; 1820 T; 0 U; 3 Other;

Query Match	76.8%;	Score 6248.8;	DB 2;	Length 8196;
Best Local Similarity	87.0%;	Pred. No. 0;		
Matches 7151; Conservative	2;	Mismatches 929;	Indels 136;	Gaps 21;

QY 15 TGTGGCCCCAGCGGCTTGGAATAAAATCCTCTTGCTGTTTGCATCAAGACCGCTTCT 74

Db
1 TGTGGCCCCAGCGCGCTTGGAATAAAAAATCCTCTTGCTGTTGCATCAAGACCGCTTCT 60

QV 75 CGTGAGTGATTAAAGGGAGTCGCCCTTTTCCGAGCCTGGAGG-----TTCTTTTTC 125

Db
61 CGTGAGTGATT-TGGGGTGTGCGCCTCTTCCGAGCCCGACGAGGGGATGTTCTTTTAC 119

QY 126 TGGTCTTACATTTGGGGGCTCGTCCGGGATCTGTGCGGCCACCCCTAACACCCGAGAAC 185

Db 120 TGGCCTTTCATTGGTGGCTGGCCGGGAAATCCTGCGACCACTTACCCGAGAAC 179

Qy 186 CGACTTGGAGGTAAAGGATCCTCTTTTAAAGTGATGCA TGACCGCGCGGTCTC 245

Db 180 CGACTTGGAGGT-AAAGGGATCCCCCTTTGGAACTGTGTG--TGTGTCGGCCGGCGTCTC 236

QY 246 TGTTCTGAGTGTCTGTTTTCAGTGTGCGCGCTTTCGGTTTGCAGCTGTCTCTCAGGCC 305

Db 237 TGTTCTGAGTGCTGTTTTCGGTGATGCGGCTTTCGGTTTGCAGCTGTCTCTCAGACC 296

Qy	306	GTAAAGGCTGGGGACATGTGATCAGCAGACGTCCTAGGAGGATCAGAGGCTGCTGCCCTG	365
Db	297	GTAAAGCACTGGAGGACTGTGATCAGCAGACGTCCTAGGAGGATCAGAGGCTGCCACCCCTG	356
Qy	366	GGGACGCCGCCGGAGGTGAGGAGAGCAGGGACGCTTGGTGTCTCTACTCTCGGTCA	425
Db	357	GGGACGCCGCCGGAGGTGGGAGAGCAGGGACGCTTGGTGTCTCTACTCTCGGTCA	416
Qy	426	GAGGACCGAATCTTGTTCTGAAGCGAAGCTTCCCTCCCGGACCGTCCGACTCTTTT	485
Db	417	GAGGACCGAGTCTTGTTGTTGAACGAAAGCTTCCCTCCCGCGCGCTCCGACTCTTTT	476
Qy	486	GCCTGCTTGTGGAAGACGTGGACGGGTCACGTGTGCTGATCTGTGTGTTTCTGTGTTTG	545
Db	477	GCCTGCTTGTGGAAGACCGGACGGGTGCGGTGTGCTGGATCTGTGTGTTTCTGTCTCG	536
Qy	546	TGTGTCTTTGTCTTGTGTGTCCTTGTCTACAGTATTTAATATGGGACAGACGGTGACGACC	605
Db	537	TGTGTCTTTGTCTTGTGCGTCTTGTCTACAGTATTTAATATGGGACAGACAGTGACTACC	596
Qy	606	CCTCTTAGTTTGACTCTCGACCAATTGGACTGAAGTTAAATCCAGGGCTCATATTTGTCA	665
Db	597	CCCTTTAGTTTGACTCTCGACCAATTGGACTGAAGTTAGATCCAGGGCTCATATTTGTCA	656
Qy	666	GTTTCAGGTTAAGAAGGACCTTGGCAGACTTTCGTGTCTCTGAATGGCCGACATTCGAT	725
Db	657	GTTTCAGGTTAAGAAGGACCTTGGCAGACTTTCGTGTCTCTGAATGGCCAAATTCGAT	716
Qy	726	GTTTGGATGGCCATCAGAGGGGACCTTTAAATTCGAGATTAATCTCGCTGTGTTAAGCAGTT	785
Db	717	GTTTGGATGGCCATCAGAGGGGACCTTTAAATTCGAAATTAATCTCGCTGTGTTAAGGCAATC	776
Qy	786	ATTTTTTCAGACTCGACCCGGCTCTACCCGATCCGATCAGAGCCCTATATCTTACGTGGCAA	845
Db	777	ATTTTTTCAGACTCGACCCGGCTCTACTCTGATCAGAGCCCTATATCTTACGTGGCAA	836
Qy	846	GATTTGGCAGAGGATCCTCCGCCATGGGTTAAACCAATGGCTGAATGAAGCCAAAGAACCA	905
Db	837	GATTTGGCAGAGATCCTCCGCCATGGGTTAAACCAATGGCTGAATGAAGCAAGAACCA	896
Qy	906	GGTCCCGGAATCTTGGCTTTGGAGAGAAAAACAACATCCGCTGAAAAGTCAAGCCC	965
Db	897	GGTCCCGGAATCTTGGCTTTGGAGAGAAAAACAACATCCGCGCCGAAAAGTCAAGCCC	956
Qy	966	TC-TCCTCATATCTACCCCGAGATTCAGGAGCCACCGGTTGGCCGGAAACCCCAATCTGT	1024
Db	957	TCCTTCTGTATCTACCCCGAGATTCAGGAGCCGCGGACTTGGCCGGAAACCCCAACCTGT	1016
Qy	1025	TCCCCCAACCCCTTATCTGCGCA CAGGGTGGCGAGGGAGACCTTTTGCCCTCTCTGGAGC	1084
Db	1017	TCCCCCAACCCCTTATCCAGCA CAGGGTGTGTGTGAGGGGA-CTCTGTGCCCTCTCTGGAGC	1075
Qy	1085	TCCGGGGGTGGAGGACCTGCTCAGGGACTCCGAGCCGAGGGGGCCACCCCGGAGCG	1144
Db	1076	TCCGGGTGTGGAGGGACCTGCTGCCGGGACTCCGAGCCGAGAGGGCCACCCCGGAGCG	1135
Qy	1145	GACAGACGAGATCCGCACATTACCGCTGCGCAGGTACGGCCCTCCACACCGGGGGGCCA	1204
Db	1136	GACAGACGAGATCGCGATATTA CCGCTGCGCACTATGGCCCTCCCATGCCAGGGGGCCA	1195
Qy	1205	ATTGCAAGCCCTCCAGTATTTGGCCCTTTTCTTCTGCAGATCTCTATTAATTGGAAAACTAA	1264
Db	1196	ATTGCAAGCCCTCCAGTATTTGGCCCTTTTCTTCTGCAGATCTCTATTAATTGGAAAACTAA	1255
Qy	1265	CCATCCCCCTTCTCTCGAGGATCCCAACGCCCTCAGCGGTTGGTGAGTCCCTTATGTT	1324
Db	1256	CCATCCCCCTTCTCTCGAGGATCCCAACGCCCTCAGCGGTTGGTGAGTCCCTTATGTT	1315
Qy	1325	CTCTCACAGCCCTACTTTGGGATGATTGTCAACAGCTGCTGCAGACACTCTTCAACAACCGA	1384
Db	1316	CTCTCACAGCCCTACTTTGGGATGATTGTCAACAGCTGCTGCAGACACTCTTCAACAACCGA	1375

1385 GGAGCGAGAGAGAAATTCATTAGAGGCTAGAAAAATGTTCTGGGCCGACGGCGACC 1444
1376 GGAGCGAGAGAGAAATTCGTTAGAGGCTAGAAAAATGTTCTGGGCCGACGGCGACC 1435
1445 CACGGGTTGCCAAAATGAGATTGACATGGGAATTCCTTAACTCGCCCCGGTTGGGACTA 1504
1436 CACGCAGTTGCCAAAATGAGATTGACATGGGAATTCCTTGACTCGCCCCGGTTGGGACTA 1495
1505 CAACACGGCTGAAGGTAGGAGAGCTTGAATAATCTATCGCCAGGCTCTGGTGGCGGTCT 1564
1496 CAACACGGCTGAAGGTAGGAGAGCTTGAATAATCTATCGCCAGGCTCTGGTGGCGGTCT 1555
1565 CCGGGGCGCTCAAGACGGCCCACTAATTTGGCTAAGGTAAAGAAAGTGAAGAGGAGC 1624
1556 CCGGGGCGCTCAAGACGGCCCACTAATTTGGCTAAGGTAAAGAGGTGATGAGGAGC 1615
1625 GAATGAACCCCTCTGTTTCTTGGAGAGGCTCTTGGAAAGCCTTCAAGGCGGTACACCCC 1684
1616 GAACGAACCTCTCCCTCGGTATTTCTTGGAGAGGCTCATGGAAGCCTTCAGGCGGTAC 1675
1685 TTTTGTATCCCACTCAGAGGCCCAAAAGCCTCAGTGGCTTTGGCCCTTTATAGGACAGTC 1744
1676 TTTTGTATCCCACTCAGAGGCCCAAAAGCCTCAGTGGCCCTTCAATGGGCAAGTC 1735
1745 AGCCTTGGATATAGAAAGAGCTTCAAGAGACTGGAAAGGCTTACAGAGGCTGAGTTACG 1804
1736 GGCTCTGGATATCAGGAGAACTTCAAGAGCTTGAAGGCTTACAGAGGCTGAGTTACG 1795
1805 TGATCTAGTGAAGGAGCAGAGAAAGTATATTACAAAGGGAGACAGAAAGAAAGGGA 1864
1796 TGATCTAGTGAAGGAGCAGAGAAAGTATATTACAAAGGGAGACAGAAAGGAGAGGA 1855
1865 ACAAGAAAAGAGAGAGAGAGAAAGGAGGAAGCTGAATAAAGCGGCAAGAGAA 1924
1856 ACAGAGAAAAGAAAGAGAGAGAGAAAGGAGGAAGCTGATAGACGGCAAGAGAA 1915
1925 GAATTTCACTAAGATCTTGGCTGAGTGGTTGAAGGGAAGAAAGCAATACGGAAAGAGAG 1984
1916 GAATTTGACTAAGATCTTGGCCGAGTGGTTGAAGGGAAGAGCAGCAGGAGAGAGAG 1975
1985 AGATTTTAGGAAAATTAGGTCAGGCCCTAGACAGTCAAGGGAACCTGGGCAATAGGACCC 2044
1976 AGATTTTAGGAAAATTAGGTCAGGCCCTAGACAGTCAAGGGAACCTGGGCAATAGGACCC 2035
2045 ACTCGACAGGACCAATGTGATATTGTAAGAAAGAGGACACTGGGCAAGGAACTGCC 2104
2036 ACTCGACAGGACCAAGTGTGCTATTGTAAGAAAGAGGACACTGGGCAAGGAACTGCC 2095
2105 CAAGAAGGGAACAAAGACCAAGGATCCTAGCTCTAGAAGAGATAAAGATTAGGGGAG 2164
2096 CAAGAAGGGAACAAAGAGCCGAAG - TCCTAGCTCTAGAAGNAGATAAAGNTTAGGGGAG 2154
2165 ACGGGGTTTCGACCCCTCCCGAGCCGAGGGTAACTTTGAAGGTGAGGGGCAACCACT 2224
2155 AC - GGGTTTCGACCCCTCCCGAGCCGAGGGTAACTTTGAAGGTGAGGGGCAACCACT 2213
2225 TGAGTCTCTGTTGATACCGGAGCGAAACATTTCAGTGTACTACAGCCATTAGGAAACT 2284
2214 TGAGTCTCTGTTGATACCGGAGCGGACATTTCAGTGTCTGTACAAACCATTTAGGAAACT 2273
2285 AAAAGATAAAAAATCCTGGGTGATGGGTGCCACAGGGCAACAAAGATTCCATGACTAC 2344
2274 AAAAGATAAAAAATCCTGGGTGATGGGTGCCACAGGGCAACCGCATTCATGACTAC 2333
2345 CCGAAGAACAGTTGACTTTGGGAGTGGGACGGGTAAACCACTCGTTTCTGGTCAATCCTGA 2404
2334 CCGAAGAACAGTTGACTTTGGGAGTGGGACGGGTAAACCACTCGTTTCTGGTCAATCCTGA 2393
2405 GTGCCACGACACCCCTCTTGGGTAGAGACTTATGACCAAGATGGGAGCAAAATTTCTTT 2464
2394 GTGCCACGATACCCCTCTTGGGTAGAGACTTATGACCAAGATGGGAGCTCAAAATTTCTTT 2453
2465 TGAACAAGGGAAACAGAGAGTGTCTGCAAAATAACAAACCTATCACTGTGTTGACCCCTCA 2524

2454 TGAAACAAGGAAGACCAAGAGTGTCTGTGAATTAACAAACCCATCACTGTGTTGACCTCCA 2513
2525 ATTAGATGACGAATATCGACTATACCTCTCCCTAGTAAAGCCCTGATCAAAATATACAATT 2584
2514 ATTAGATGATGAATATCGACTATATCTCCCAAGTAAAGCCCTGATCAAGATATACAGTC 2573
2585 CTGGTTGGAAACAGTTCCTCCCAAGCCTGGGAGAAACCGCAGGGATGGGTTGGCAAGCA 2644
2574 CTGGTTGGAGCAGTTCCTCCCAAGCCTGGGAGAAACCGCAGGGATGGGTTGGCAAGCA 2633
2645 AGTTCCCCCAACAGTTTATTAACCTGAAGCCAGTGCACACAGTGTCACTGACAGACGTA 2704
2634 AGTTCCCCCAACAGTTTATTAACCTGAAGCCAGTGTCAACCAAGTATCACTGACAGACGTA 2693
2705 CCCTTTGAGTAAAGAGCTCAAGAGGAATTCGCGCGCATGTCCAAAGATTAATCCAACA 2764
2694 CCCTTTGAGTAGAGAGCTCGAGAGGAATTTGGCCGCAATGTTCAAAGATTAATCCAACA 2753
2765 GGGCATCTAGTTCCTGTCCTCCCTGGAATATCTCCCTGCTACCGGTTAGAAAGCC 2824
2754 GGGCATCTAGTTCCTGTCCTCCCTGGAATATCTCCCTGCTACCGGTTAGAAAGCC 2813
2825 TGGGACTAATGACTATCGACCACTACAGGACTTGAAGAGGTCAATAAAGGGTGCAGGA 2884
2814 TGGGACCAATGATTTATCGACCACTACAGGACTTGAAGAGGTCAATAAAGGGTGCAGGA 2873
2885 TATACACCCCAACAGTCCCGAAACCTTATAACCTCTTGTGTGCTCTCCCAACCCCAACGGAG 2944
2874 CATACACCCCAACAGTCCCGAAACCTTATAACCTCTTGAAGGCCCTCCCGCTGAACGGA 2933
2945 CTGGTATACAGTATTGGACTTAAAGGATGCTTCTTCTGCTGAGATTACACCCCACTAG 3004
2934 CTGGTACACAGTATTGGACTTAAAGGATGCTTCTTCTGCTGAGATTACACCCCACTAG 2993
3005 CCAACCACTTTTTCCTTTCGAATGGAGAGATCCAGGTACGGGAGAACCCGGGCACTCAC 3064
2994 CCAACCACTTTTTCCTTTCGAATGGAGAGATCCAGGTACGGGAGAACCCGGGCACTCAC 3053
3065 CTGGACCCGACTCCCGCAAGGTTCAAGAACTCCCGCAACCATCTTTGACGAAGCCCTACA 3124
3054 CTGGACCCGACTCCCGCAAGGTTCAAGAACTCCCGCAACCATCTTTGACGAAGCCCTACA 3113
3125 CAGAGACCTTGGCCCAACTTCAGGATCCAAACCCCTCAGGTGACCTCTCCAGTACGTGGA 3184
3114 CAGGACCTTGCCCAACTTCAGGATCCAAACCCCTCAGGTGACCTCTCCAGTACGTGGA 3173
3185 TGACCTGCTTCTGGCGGGAGCCAAACAGGACTGCTTGAAGGTACGAAGGCACTACT 3244
3174 TGACCTGCTTCTGGCGGGAGCCAAACAGGACTGCTTGAAGGTACGAAGGCACTACT 3233
3245 GCTGGAAATTCCTGACCTTAGCTACAGAGCTCTGCTAAGAGGCCCAAGATTTCGAGGAG 3304
3234 GCTGGAAATTCCTGACCTTAGCTACAGAGCTCTGCTAAGAGGCCCAAGATTTCGAGGAG 3293
3305 AGAGGTAAACATACCTTGGGGTACAGTTTGGCGGAGCGGCGAGCGATGGCTGACGGAGCACG 3364
3294 AGAGGTAAACATACCTTGGGGTACAGTTTGGCGGAGCGGCGAGCGATGGCTGACGGAGCACG 3353
3365 GAAGAAAATCTGATGTCAGATACCGGCCCAACACAGCCCAACAAATAGAGAGATTTTT 3424
3354 GAAGAAAATCTGATGTCAGATACCGGCCCAACACAGCCCAACAAATAGAGAGATTTTT 3413
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3414 GGGGACAGCTGGATTTTTCAGACTGTGGATCCCGGGGTTTCGCACTTTAGCAGCCCCACT 3473
3485 CTACCCCTTAACAAAGAAAAGGGGAATTTCTCTGGGCTCCTGAGCAACCAAGAGGCAATT 3544
3474 CTACCCCTTAACAAAGAAAAGGGGAATTTCTCTGGGCTCCTGAGCAACCAAGAGGCAATT 3533
3545 TGATGCTATCAAAAAGGCCCTGCTGAGCGCACTGTGCTGCGCCCTCCCTGACGTAACATAA 3604

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QY 3605 ACCCTTTACCCCTTATGTGGATGAGCGTAAAGGAGTAGCCCGGGAGTTTAAACCCAAAC 3664
Db 3594 ACCCTTTACCCCTTATGTGGATGAGCGTAAAGGAGTAGCCCGGGAGTTTAAACCCAAAC 3653
QY 3665 CTTAGACCATGGAGAAGACCTGTGCGCTTACCTGTCAAAAGAGCTCGATCCTGTGAGCCAG 3724
Db 3654 CTTAGACCATGGAGAGACCTGTGCGCTTACCTGTCAAAAGAGCTTGATCCTGTGAGCCAG 3713
QY 3725 TGGTTGGCCCATATGCTGAAGCTATCGAGCTGTGGCCATACCTGGTCAAGGACGCTGA 3784
Db 3714 TGGTTGGCCCGTATGTTCAAGGCTATCGAGCTGTGGCCATACCTGGTCAAGGACGCTGA 3773
QY 3785 CAAATTGACTTTGGGACAGATATTAATCTGTAAATAGCCCCCATGATCGATGGAGAAATCGT 3844
Db 3774 CAAATTGACTTTGGGACAGATATTAATCTGTAAATAGCCCCCATGATCGATGGAGAAATCGT 3833
QY 3845 TCGGAGCCCCCAGACCGGATGGATGACCAACGCCCGCATGACCCACTATCAAAAGCCTGCT 3904
Db 3834 TCGGAGCCCCCAGACCGGATGGATGACCAACGCCCGCATGACCCACTATCAAAAGCCTGCT 3893
QY 3905 TCTCAGAGAGGGTCACTTTCGCTCCACAGCGCGCTCTCAACCTTGCCACTCTTCTGCC 3964
Db 3894 TCTCAGAGAGGGTCACTTTCGCTCCACAGCGCGCTCTCAACCTTGCCACTCTTCTGCC 3953
QY 3965 TGAAGAGACTGATGAACCACTGACTCATGATTTGCCATCAACTATTTGATTGAGGAGACTGG 4024
Db 3954 TGAAGAGACTGATGAACCACTGACTCATGATTTGCCATCAACTATTTGATTGAGGAGACTGG 4013
QY 4025 GGTCCGCAAGGACCTTTACAGACATACCGCTGACTGGAGAAGTCTAACTGGTTCACTGA 4084
Db 4014 GGTCCGCAAGGACCTTTACAGACATACCGCTGACTGGAGAAGTCTAACTGGTTCACTGA 4073
QY 4085 CGGAAGCAGCTATGTGGTGGAGGTAAAGAGTAAAGAGTGGCTGGCGCGGCAAGTGGTGGAGCGGAC 4144
Db 4074 CGGAAGCAGCTATGTGGTGGAGGTAAAGAGTAAAGAGTGGCTGGCGCGGCAAGTGGTGGAGCGGAC 4133
QY 4145 CGGCAGATCTGGCCAGCAGCCTCGCGGAAGAACTTCAGACACAAAGGCTGAGCTCAT 4204
Db 4134 CGGCAGATCTGGCCAGCAGCCTCGCGGAAGAACTTCAGGCACAAAGGCTGAGCTCAT 4193
QY 4205 GGCCTTCAGCAAGCTTTGCGGTGCGCGGAAGGAAATCCATAAAATTTATACGGACAG 4264
Db 4194 GGCCTTCAGCAAGCTTTGCGGTGCGCGGAAGGAAATCCATAAAATTTATACGGACAG 4253
QY 4265 GAGGTATGCTTTGCGACTGCACACGTACATGGGGCCATCTATAACAAAGGGGTGCT 4324
Db 4254 CAGGTATGCTTTGCGACTGCACACGTACACGGGGCCATCTATAACAAAGGGGTGCT 4313
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Db 4314 TACCTCAGCAGGAGGGAATTAAGAAACAAAGAGAAATTTAAAGCCTATTAGAAGCCGT 4373
QY 4385 ACATTTACAAAGGCTAGCTATTATACACTGTCTCGACATCAGAAAGCTAAAGATCT 4444
Db 4374 ACATTTGCCAAAGGCTAGCTATTATACACTGTCTCGACATCAGAAAGCTAAAGATCT 4433
QY 4445 CATATCCAGAGNAACAGATGGCTGACCGGGTTGCCAAGCAGGAGCCCGAGGGTTTAA 4504
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Db 4494 CTTTCTGCTTAAATAGAAACCGCCCAAGCCCAAGCCCAAGACAGTACACCTCTAG 4553
QY 4565 AGACTGGCAAGATATAAAGATAGACCAAGTCTCTGAGACTTCGGAAAGGACCTTGCTA 4624
Db 4554 AGACTGGCAAGATATAAAGATAGACCAAGTCTCTGAGACTTCGGAGGGACCTTGCTA 4613
QY 4625 TACCTCAGATGGGAAGGAATTCCTGCCCAAAAGAGGGTTAGAAATATGTCCAAAGAT 4684
Db 4614 TACCTCATATGGGAAGGAATTCCTGCCCAAAAGAGGGTTAGAAATATGTCCAAAGAT 4673

QY 4685 ACATCGTCTAAACCCACCTAGGAACTAAACACCTGCGAGAGTTGGTCAGAAACATCCCTTTA 4744
Db 4674 ACATCGTCTAAACCCACCTAGGAACTAAACACCTGCGAGCAGTTGGTCAGAAACATCCCTTTA 4733
QY 4745 TCATGTTCTGAGGCTACAGGAGTGGCTGACTCGGTGGTCAACATTTGTGCGCCCTGCCA 4804
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QY 4805 GCTGGTTAATGCTAATCTCTCCAGATGCTCTCAGGGAAGAGACTAAGCGGAAGCCACCC 4864
Db 4794 GCTGGTTAATGCTAATCTCTCCAGATGCTCTCAGGGAAGAGACTAAGCGGAAGCCACCC 4853
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Db 4854 AGCGCTCACTGGGAAGTGAAGTCTTCACTGAGGTAAAGCCGGCTAAATACGGAACAAATA 4913
QY 4925 CCTATTGGTTTTGTAGACACCTTTTTCAGGATGGGTAGAGGCTTATCTCTACTAAGAAAGA 4984
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QY 5045 TAAAGTAAATAGGGTCAAGCAATGGTCCAGCTTTTGTGCCAGGTAAAGTCAGGACTGGC 5104
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Db 5094 CAAAGATATTTGGGGATTTGTTGGAATCTGATTTGTGCATACAGACCCCAAGCTCAGGACA 5153
QY 5165 GGTAGAGAGATTAATAGAACCATTAAGAGACCCCTTACTAAATTACACCGGAGACTGG 5224
Db 5154 GGTAGAGAGATTAATAGAACCATTAAGAGACCCCTTACTAAATTACACCGGAGACTGG 5213
QY 5225 CGTTAATGATTTGGATAGCTCTCTGCCCCCTTGTGCTTTTGTAGGTTTGAAGAACCCCTGG 5284
Db 5214 CATTAATGATTTGGATAGCTCTCTGCCCCCTTGTGCTTTTGTAGGTTTGAAGAACCCCTGG 5273
QY 5285 ACAGTTTGGGCTGACCCCTTATGAATTAATCTACGGGGGACCCCCCTTATGTTAGAAAT 5344
Db 5274 ACAGTTTGGGCTGACCCCTTATGAATTTGCTCTACGGGGGACCCCCCTTGGCAGAAAT 5333
QY 5345 TGCCTCTGTACATAGTGTGCTGCTTTTCCAGCCTTTTCTTAGGCTCAAGGC 5404
Db 5334 TGCCTTTGCACATAGTGTGCTGCTTTTCCAGCCTTTTCTTAGGCTCAAGGC 5393
QY 5405 ACTTGAGTGGGTGAGACAAACGAGCGTGAGGCAACTCCGGGAGGCTTACTCAGGAGGAGG 5464
Db 5394 GCTCGAGTGGGTGAGGACGAGCGTGGAAGCAGCTCCGGGAGGCTTCTC --- AGGAGG 5450
QY 5465 AGACTTGCAGATCCACATCGTTTTCAAGTGGAGATTGAGTCTAGTTAGCGCCACCG 5524
Db 5451 AGACTTGCAGATCCACATCGTTTTCAAGTGGAGATTGAGTCTATGTTAGCGCCACCG 5510
QY 5525 TGCAGGAAACCTCGAGCTCGGTGGAGGGCCCTTATCTCTGACTTTTGAACACACCAAC 5584
Db 5511 TGAGGAAACCTCGAGCTCGGTGGAGGGACCTTATCTGTAATTTTGAACACCAAC 5570
QY 5585 GCGTGTGAAAGTCGAAGGAATCTCCACCTGGATCCATGATCCACGTTTAAACCGCGCC 5644
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QY 5645 ACCTCCGATTCGGGGTGGAAAGCCGAAAGACTGAAATCCCTTTAAGCTTCGCTCCA 5704
Db 5631 ACCTCCGATTCGGGGTGGAGAGCCGAAAGACTGGAATCCCTTTAAGCTTCGCTCCA 5690
QY 5705 TCGCGTGGTTCTTACTCTGTCAATAACCTCTCAGACTTAATGATTCGTCATAGGAGACA 5764
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Db 7885 ACTGCAATCTGTCACTCTGTCGCCAGGAGCCACGCCAGATCGGGACCTCCGGAGCTATTTTA 7944
QY 7910 AATTAATTGGTCCACGAAGCGCGGCTCTCGAAGTTTAAATTTGAAGTGGT----- 7959
Db 7945 AATGATTGGTCCACGAGCGGGCTCTCGATATTTTAAATGATTGGTCCATGGAGCG 8004
QY 7960 -----TTGTGATATTTTGAATGATTGGTTTGAAGCGGGCTTTGTTGTAACCCCA 8014
Db 8005 CGGGCTCTCGATATTTTAAATGATTGGTTTGTGACGACAGGCTTTGTTGTAACCCCA 8064
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Db 8065 TAAAGCTGTCGCGACTTCGCGACTCGGGCGCGCAGTCTCTACCCCTGGGTGTGACGA 8124
QY 8075 CTGTGGGCCCCAGCGGGCTTGGAAATAAAATCCTTGTGCTTTGGCATCAAAAAAAA 8132
Db 8125 CTGTGGGCCCCAGCGGCTTGGAAATAAAATCCTTGTGCTTTGGCATCAAAAAAAA 8182
RESULT 12
AAC67019
ID AAC67019 standard; DNA; 7362 BP.
AC AAC67019;
XX
DT 27-MAR-2001 (first entry)
XX
DE PERV env protein coding sequence SEQ ID NO: 19.
XX
KW Xenotransplantation; infectious agent; vaccine; ds.
XX
OS Porcine endogenous retrovirus.
XX
PN WO200071726-A1.
XX
PD 30-NOV-2000.
XX
PF 24-MAY-2000; 2000WO-US014296.
XX
PR 24-MAY-1999; 99US-0135631P.
XX
PA (MAYO-) MAYO MEDICAL VENTURES.
XX
PI Federspiel MJ;
XX
DR WPI; 2001-032041/04.
XX
PT Inhibiting or preventing infectious agent transmission in mammalian
PT transplant recipients, by introducing recombinant DNA comprising DNA
PT encoding extracellular proteins of the agent into donor cells, such as
PT swine cells.
XX
PS Claim 16; Page 101-104; 144pp; English.
XX
CC The present invention provides a method to prevent the transmission of
CC infectious agents during xenotransplantation. This involves introducing
CC to donor swine cells a recombinant DNA encoding a peptide fragment from
CC the infectious agent, and then introducing these cells into the
CC transplant recipient
XX
SQ Sequence 7362 BP; 1997 A; 1821 C; 1881 G; 1663 T; 0 U; 0 Other;
Query Match 75.9%; Score 6174.6; DB 4; Length 7362;
Best Local Similarity 95.7%; Pred. No. 0;
Matches 6412; Conservative 0; Mismatches 224; Indels 63; Gaps 4;
QY 1 GCCTGGTGACGACTGTGGCCCCCAGCGGCTTTGGAATAAAATCCTTGTGCTGTTGCA 60
Db 664 GCCTGGTGACGACTGTGGCCCCCAGCGGCTTTGGAATAAAATCCTTGTGCTGTTGCA 723
QY 61 TCNAGACCGCTTCTGTGAGTGATTAAGGGAGTCGCTTTCCGAGCCTGGAGGTTCTT 120
Db 724 TCAAGACCGCTTCTGTGAGTGATTAAGGGAGTCGCTTTCCGAGCCTGGAGGTTCTT 783

QY 121 TTTGTGCTGCTTACATTTGGGGGCTGTCCTCGGATCTGTGCGGCCACCCCTAAACCCCG 180
Db 784 TTTGTGCTGCTTACATTTGGGGGCTGTCCTCGGATCTGTGCGGCCACCCCTAAACCCCG 843
QY 181 AGAACCGACTTGGAGGTAAAGGATCCTCTTTTAAACGTGTATGATGTACCGGCGGC 240
Db 844 AGAACCGACTTGGAGGTAAAGGATCCTCTTTTAAACGTGTATGATGTACCGGCGGC 903
QY 241 GTCTCTGTTCTCAGTGTCTGTTTTCAAGTGGTGGCGCTTTCGGTTTGCAGCTGTCTCTC 300
Db 904 GTCTCTGTTCTCAGTGTCTGTTTTCAAGTGGTGGCGCTTTCGGTTTGCAGCTGTCTCTC 963
QY 301 AGGCGGTAAAGGCTGGGGAATGTGATCAGCAGACGTGTAGAGGATCACAGGCTGCTG 360
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Db 1024 CCTGGGGGACGCCCCGGGAGGTGGGGAGAGCCAGGACGCTGGTGGTCTCTCTCTGTC 1083
QY 421 GGTCAAGACACCGAATTTCTGTTGCTGAAGCGAAAGCTTCCCTCCGCGACCGTCCGACT 480
Db 1084 GGTCAAGACACCGAATTTCTGTTGTTGAAGCGAAAGCTTCCCTCCGCGCGCTCGACT 1143
QY 481 CTTTTCCTGCTTGTGGAAAGACGTGGACGCGGTCACTGTGTCTGGATCTGTGGTTTCTG 540
Db 1144 CTTTTCCTGCTTGTGGAAAGACGCGGAGCGGTGGTGTGTCTGGATCTGTGGTTTCTG 1203
QY 541 TTTTGTGTCTTGTGCTTGTGTCCTTGTCTACAGTTTTTAATATGGACACAGCGTGA 600
Db 1204 TTTTGTGTCTTGTGCTTGTGTCCTTGTCTACAGTTTTTAATATGGACACAGCGTGA 1263
QY 601 CGACCCCTCTTAGTTTGACTCTCGACCATTTGGACCTGAAGTTAAATCCAGGGCTCAATA 660
Db 1264 CGACCCCTCTTAGTTTGACTCTCGACCATTTGGACCTGAAGTTAAATCCAGGGCTCAATA 1323
QY 661 TGTCAAGTTTAAAGAGGACCTTGGCAGACTTTCTGTGTCTCTGTAATGCGCGACAT 720
Db 1324 TGTCAAGTTTAAAGAGGACCTTGGCAGACTTTCTGTGTCTCTGTAATGCGCGACAT 1383
QY 721 TCGATGTTGGATGGCCATCAGAGGGACCTTTAAATCTGAGATTATCTGGCTGTTAAAG 780
Db 1384 TCGATGTTGGATGGCCATCAGAGGGACCTTTAAATCTGAGATTATCTGGCTGTTAAAG 1443
QY 781 CAGTTATTTTTCAGACTGGACCCGCTCTCATCCCATCAGAGCGCTATATCCTTTACGT 840
Db 1444 CAATATTTTTCAGACTGGACCCGCTCTCATCCCATCAGAGCGCTATATCCTTTACGT 1503
QY 841 GGCAAGATTGGCAGAGGATCCTCCGCCATGGGTTAAACCATGGCTGAATAAGCCCAAGAA 900
Db 1504 GGCAAGATTGGCAGAGGATCCTCCGCCATGGGTTAAACCATGGCTGAATAAGCCCAAGAA 1563
QY 901 AGCAGGTCCCCGAATTTGGCTCTTGGAGAGAAAAACAAACACTCGGCTGAAAAAGTCA 960
Db 1564 AGCAGGTCCCCGAATTTGGCTCTTGGAGAGAAAAACAAACACTCGGCTGAAAAAGTCA 1623
QY 961 AGCCCTCTCCTCATATCTACCCCGAGATTGAGGAGCCACCGCTTCGCGGACCCCAAT 1020
Db 1624 AGCCCTCTCCTCATATCTACCCCGAGATTGAGGAGCCCGGCTTGGCGGAACCCCAT 1583
QY 1021 CTGTTCCCCCACCCCTTATCTGGCACAGGCTGCCCGAGGGAGCCCTTTTGGCCCTCTTG 1080
Db 1684 CTGTTCCCCCACCCCTTATCTGGCACAGGCTGCTGCGAGGGAGCCCTCTGCCCCCTCTG 1743
QY 1081 GAGCTCGGCGGTGAGGAGCACTGTGAGGAGACTCGGAGCGGAGGGGCGCCACCCCG 1140
Db 1744 GAGCTCGGCGGTGAGGAGCACTGTGAGGAGACTCGGAGCGGAGGGGCGCCACCCCG 1803
QY 1141 AGCGGACACACGAGATCGCGCATTACCGCTCGCACGTTACGGCCCTCCACACCGGGGG 1200
Db 1804 AGCGGACACACGAGATCGCGCATTACCGCTCGCACGTTACGGCCCTCCACACCGGGGG 1863

Qy	1201	GCCTATGCGAGCCCTCCAGTATGCGCCCTTTTCTTCTGCGAGTCTCTAATTTGAAAA	1260	Db	2944	AACTAAAGATAAAAATCTTGGGTGATGGTGCCACAGGGCAACACAGTATCCATGGA	3003
Db	1864	GCCAAATGCGAGCCCTCCAGTATGCGCCCTTTTCTTCTGCGAGTCTCTAATTTGAAAA	1923	Qy	2341	CTACCCGAAGAACAGTGTGACTTTGGGAGTGGGACGGGTAAACCCACTCGTTTCTGGTCAATC	2400
Qy	1261	CTAAACATCCCTTTCTCGGAGGATCCCAACGCTCAGCGGTTGGTGGAGTCCCTTA	1320	Db	3004	CTACCCGAAGAACAGTGTGACTTTGGGAGTGGGACGGGTAAACCCACTCGTTTCTGGTCAATC	3063
Db	1924	CTAAACATCCCTTTCTCGGAGGATCCCAACGCTCAGCGGTTGGTGGAGTCCCTTA	1983	Qy	2401	CTGAGTCCCGACACCCCTCTTAGGTAGAGACTTATTGACCAAGATGGGAGCAAAATTT	2460
Qy	1321	TGTTCTCTACAGCCCTACTTTGGGATGATTTGTCACAGCTGCTGACAGACTCTTACAA	1380	Db	3064	CTGAGTCCCGACACCCCTCTTAGGTAGAGACTTATTGACCAAGATGGGAGCAAAATTT	3123
Db	1984	TGTTCTCTACAGCCCTACTTTGGGATGATTTGTCACAGCTGCTGACAGACTCTTACAA	2043	Qy	2461	CTTTTGAACAAGGGAACCAAGAGTGTCTGCAATTAACAACCTATCACCTGTGTGACCC	2520
Qy	1381	CCGAGGAGCGAGAGAAATTTCTATTAGAGCTAGAAAAATGTTCTCGGGCCGACGGGC	1440	Db	3124	CTTTTGAACAAGGGAACCAAGAGTGTCTGCAATTAACAACCTATCACCTGTGTGACCC	3183
Db	2044	CCGAGGAGCGAGAGAAATTTCTATTAGAGCTAGAAAAATGTTCTCGGGCCGACGGGC	2103	Qy	2521	TCCAAATAGATGACGAATATCGACTATCTCTCCCTTAGTAAAGCCCTGATCAAAATATAC	2580
Qy	1441	GACCCAGCGGTTGCAAAATGAGATTGACATGGGATTTCCCTTAACTCGGCCCGGTTGGG	1500	Db	3184	TCCAAATAGATGACGAATATCGACTATCTCTCCCTTAGTAAAGCCCTGATCAAAATATAC	3243
Db	2104	GACCCAGCGGTTGCAAAATGAGATTGACATGGGATTTCCCTTAACTCGGCCCGGTTGGG	2163	Qy	2581	AATTCTGGTTGGAAACAGTTTCCCAAGCTTGGGCGAGAAACCGCAGGGATGGGTTGGCAA	2640
Qy	1501	ACTACACAGGCTGAAGGTAGGAGAGCTTGAATCTATCGCAGGCTCTGTTGGCGG	1560	Db	3244	AATTCTGGTTGGAAACAGTTTCCCAAGCTTGGGCGAGAAACCGCAGGGATGGGTTGGCAA	3303
Db	2164	ACTACACAGGCTGAAGGTAGGAGAGCTTGAATCTATCGCAGGCTCTGTTGGCGG	2223	Qy	2641	AGCAAGTTCCTCCCAAGTTTCACTGAAGGCCAGTGCACACAGTGTCTAGTCAAGC	2700
Qy	1561	GTCTCCGGGGCGCTCAAGACGGCCCACTAATTTGGCTAAGGTAAGAGAAAGTATGCAGG	1620	Db	3304	AGCAAGTTCCTCCCAAGTTTCACTGAAGGCCAGTGCACACAGTGTCTAGTCAAGC	3363
Db	2224	GTCTCCGGGGCGCTCAAGACGGCCCACTAATTTGGCTAAGGTAAGAGAAAGTATGCAGG	2283	Qy	2701	AGTACCCCTTGAAGTAAAGAGCTCAAGAGGAATTTGGCGCGCATGTCCAAAGATTAATCC	2760
Qy	1621	GACCGAATGAACCCCTCTGTTTCTTGAGAGGCTCTTGGAAAGCTTCAAGGCGGTACA	1680	Db	3364	AGTACCCCTTGAAGTAAAGAGCTCAAGAGGAATTTGGCGCGCATGTCCAAAGATTAATCC	3423
Db	2284	GACCGAATGAACCCCTCTGTTTCTTGAGAGGCTCTTGGAAAGCTTCAAGGCGGTACA	2343	Qy	2761	AACAGGCGATCTCTGTTCTCAATCTCCCTGGAAATATCTCCCTGCTACCGGTTAGAA	2820
Qy	1681	CCCTTTTGATCCCACTCAGAGCCCAAGAGCTCAGTGGCTTTGGCCCTTTATAGGAC	1740	Db	3424	AACAGGCGATCTCTGTTCTCAATCTCCCTGGAAATATCTCCCTGCTACCGGTTAGAA	3483
Db	2344	CCCTTTTGATCCCACTCAGAGCCCAAGAGCTCAGTGGCTTTGGCCCTTTATAGGAC	2403	Qy	2821	AGCTGGGACTAATGACTATCGACAGTACAGGACTTGAAGAGGTCAATAAAGCGGTGC	2880
Qy	1741	AGTCAGCTTTGGATATTAGAAAGAGCTTCAAGAGCTGGAAGGTTTACAGAGGCTGAGT	1800	Db	3484	AGCTGGGACTAATGACTATCGACAGTACAGGACTTGAAGAGGTCAATAAAGCGGTGC	3543
Db	2404	AGTCAGCTTTGGATATTAGAAAGAGCTTCAAGAGCTGGAAGGTTTACAGAGGCTGAGT	2463	Qy	2881	AGGATATACACCCCAAGTCCGAACTTAACTTAACTTGTGTGCTCTCCACCCCAAC	2940
Qy	1801	TAGCTGATCTAGTGAAGAGGACAGAGAAAGTATTATCAAAAGGGAGACAGAGAGAAA	1860	Db	3544	AGGATATACACCCCAAGTCCGAACTTAACTTAACTTGTGTGCTCTCCACCCCAAC	3603
Db	2464	TAGCTGATCTAGTGAAGAGGACAGAGAAAGTATTATCAAAAGGGAGACAGAGAGAAA	2523	Qy	2941	GGAGCTGGTATACAGTATTGGACTTAAAGGATGCTTTCTGCTCGATGATTAACCCCA	3000
Qy	1861	GGGAACAAAGAAAGAGAGAAAGAGAGAAAGGAGGAGGAGGAGGAGGAGGAGGAGG	1920	Db	3604	GGAGCTGGTATACAGTATTGGACTTAAAGGATGCTTTCTGCTCGATGATTAACCCCA	3663
Db	2524	GGGAACAAAGAAAGAGAGAAAGAGAGAAAGGAGGAGGAGGAGGAGGAGGAGGAGG	2583	Qy	3001	CTAGCCCAACCACTTTTTCCTTGAATTTGAGAGATCCAGGTACCGGAGAGACCGGGCAGC	3060
Qy	1921	AGAGAAATTTGACTTAAGATCTTGGCTGAGTGGTTGAAGGAAAGCAATACGGAAGAG	1980	Db	3664	CTAGCCCAACCACTTTTTCCTTGAATTTGAGAGATCCAGGTACCGGAGAGACCGGGCAGC	3723
Db	2584	AGAGAAATTTGACTTAAGATCTTGGCTGAGTGGTTGAAGGAAAGCAATACGGAAGAG	2643	Qy	3061	TCACCTGGAGCCGACTGCCCCCAAGGTTCAAGAACTCCCGACCATCTTTGACGAAGGCC	3120
Qy	1981	AGAGAGATTTTGAAGAAATTAGGTCAAGCCCTAGACAGTCAAGGAACTTGGGCAATAGGA	2040	Db	3724	TCACCTGGAGCCGACTGCCCCCAAGGTTCAAGAACTCCCGACCATCTTTGACGAAGGCC	3783
Db	2644	AGAGAGATTTTGAAGAAATTAGGTCAAGCCCTAGACAGTCAAGGAACTTGGGCAATAGGA	2703	Qy	3121	TACACAGAGACTCTGGCCAACTTCAAGGATCCAAACCCCTCAGGTGACCCCTCTCCAGTACG	3180
Qy	2041	CCCCCTCGACAAAGCAATTTGCTATTTGTAAGAAAGAGGAGGAGGAGGAGGAGGAGG	2100	Db	3784	TACACAGAGACTCTGGCCAACTTCAAGGATCCAAACCCCTCAGGTGACCCCTCTCCAGTACG	3843
Db	2704	CCCCCTCGACAAAGCAATTTGCTATTTGTAAGAAAGAGGAGGAGGAGGAGGAGGAGG	2763	Qy	3181	TGGATGACCTGCTTCTGGCGGAGCCACCAAGAGGACTGTTAGAGGAGGAGGAGGAGGAGG	3240
Qy	2101	GCCCCAAGAGGGAACCAAGGACCAAGGATCTTAGCTCTAGAGAGAGATAAAGATTAGG	2160	Db	3844	TGGATGACCTGCTTCTGGCGGAGCCACCAAGAGGACTGTTAGAGGAGGAGGAGGAGGAGG	3903
Db	2764	GCCCCAAGAGGGAACCAAGGACTGAAGGCTTTAGCTCTGAAAGAGATTAAGACTAGG	2823	Qy	3241	TACTGCTGGAAATGCTGCTAGCTAGCTAGGCTCTGCTAAAGGCGCCAGATTTCGA	3300
Qy	2161	GGAGACGGGGTTCGGACCCCTCCCGAGCCGAGGTAACCTTTGAAGGTGGAGGGGCAAC	2220	Db	3904	TACTGCTGGAAATGCTGCTAGCTAGCTAGGCTCTGCTAAAGGCGCCAGATTTCGA	3963
Db	2824	GAAAGCGGGTTCGGACCCCTCCCGAGCCGAGGTAACCTTTGAAGGTGGAGGGGCAAC	2883	Qy	3301	GGAGAGAGGTAACACTTCTGGGGTACAGTTTTCGGGGAGCGGCGAGCGATGGCTGACGAGG	3360
Qy	2221	CAGTTGAGTTCCTGGTGTGATACCGGAGCGAAACATTTAGTGTCTACTACAGCCATTAGGAA	2280	Db	3964	GGAGAGAGGTAACACTTCTGGGGTACAGTTTTCGGGGAGCGGCGAGCGATGGCTGACGAGG	4023
Db	2884	CAGTTGAGTTCCTGGTGTGATACCGGAGCGAAACATTTAGTGTCTACTACAGCCATTAGGAA	2943	Qy	3361	CACGGAGAGAAACTGTAGTCCAGATACCGGCGCCCAACACACAGGCCAAACAAATGAGAGAGT	3420
Qy	2281	AACTAAAGATAAAAATCTTGGGTGATGGGTGCCACAGGGCAACACAGTATCCATGGA	2340				

Db 4024 CACGGAAGAAACTGTAGTCCAGATACCGGCCCAACACAGCCAAACAAGTGAGAGGT 4083
Qy 3421 TTTTGGGGACAGCTGGATTTTGAGACTGTGGATCCCGGGGTTTGCACTTTAGCAGCCC 3480
Db 4084 TTTTGGGGACAGCTGGATTTTGAGACTGTGGATCCCGGGGTTTGCACTTTAGCAGCCC 4143
Qy 3481 CACTCTACCGCTAACCAAGAAAGGGGAATTTCTCGGGTCTCTGAGCACCAGAGG 3540
Db 4144 CACTCTACCGCTAACCAAGAAAGGGGAATTTCTCGGGTCTCTGAGCACCAGAGG 4203
Qy 3541 CATTTGATGCTATCAAAAAGGCCCTGCTGAGCGCACTGCTCTGGCCCTCCCTGACGTAA 3600
Db 4204 CATTTGATGCTATCAAAAAGGCCCTGCTGAGCGCACTGCTCTGGCCCTCCCTGACGTAA 4263
Qy 3601 CTAAACCCCTTTACCTTTTATGTGGATGAGCGTAAGGGAGTAGCCCGGGGAGTTTAAACCC 3660
Db 4264 CTAAACCCCTTTACCTTTTATGTGGATGAGCGTAAGGGAGTAGCCCGGGGAGTTTAAACCC 4323
Qy 3661 AAACCTAGGACCATGGAGAAGCCTGTGCGCTTACTGTCAAGAAAGCTCGATCTGTGTAG 3720
Db 4324 AAACCTAGGACCATGGAGAGACCTGTTGCCCTACCTGTCAAGAAAGCTCGATCTGTGTAG 4383
Qy 3721 CGAGTGGTTGGCCCATATGCCCTGAAGCTATCGCAGCTGTGGCCATCTGCTCAAGGAGG 3780
Db 4384 CGAGTGGTTGGCCCGTATGCTTGAAGGCTATCGCAGCTGTGGCCATCTGCTCAAGGAGG 4443
Qy 3781 CTGACAAATTTGACTTTGGGACAGAAATATACTGTAATAGCCCCCATGCAATTTGGAGAA 3840
Db 4444 CTGACAAATTTGACTTTGGGACAGAAATATACTGTAATAGCCCCCATGCTTTGGAGAA 4503
Qy 3841 TCGTTCCGAGCCCCCAGACCCGATGATGACCAACGCCCGCATGACCCCATATCAAAAGCC 3900
Db 4504 TCGTTCCGAGCCCCCAGACCCGATGATGACCAACGCCCGCATGACCCCATATCAAAAGCC 4563
Qy 3901 TGCCTTCCAGAGAGGGTCAAGTTGCTTCCAGCAGCGCTCTCAACCCCTGCCACTCTTC 3960
Db 4564 TGCCTTCCAGAGAGGGTCAAGTTGCTTCCAGCAGCGCTCTCAACCCCTGCCACTCTTC 4623
Qy 3961 TGCCTGAAGAGACTGATGAACCAAGTGACTCATGATTTGCCATCAACTATTGATTGAGGAGA 4020
Db 4624 TGCCTGAAGAGACTGATGAACCAAGTGACTCATGATTTGCCATCAACTATTGATTGAGGAGA 4683
Qy 4021 CTGGGTCCGCAAGACCTTACAGACATACCGCTGACTGGAGAAGTCTAAACCTGTTTCA 4080
Db 4684 CTGGGTCCGCAAGACCTTACAGACATACCGCTGACTGGAGAAGTGTAAACCTGTTTCA 4743
Qy 4081 CTGACCGAAGCAGCTATGTGGTGAAGGTAAAGGATGCTGGGGCGCGGTGGTGGACG 4140
Db 4744 CTGACCGAAGCAGCTATGTGGTGAAGGTAAAGGATGCTGGGGCGCGGTGGTGGACG 4803
Qy 4141 GGACCCGACGATCTGGGCAGCAGCTTGCAGGAAGGAACCTTCAGCACAAAGGCTGAGC 4200
Db 4804 GGACCCGACGATCTGGGCAGCAGCTTGCAGGAAGGAACCTTCAGCACAAAGGCTGAGC 4863
Qy 4201 TCATGGCCCTCAGCAGCTTTTCGGCTGGCCGGAAGGGAATCCATAAACATTTATACGG 4260
Db 4864 TCATGGCCCTCAGCAGCTTTTCGGCTGGCCGGAAGGGAATCCATAAACATTTATACAG 4923
Qy 4261 ACAGCAGGTATGCTTTTGAGCTGACACATCATGCGGGCCATCTATAACAAAGGGGT 4320
Db 4924 ACAGCAGGTATGCTTTTGAGCTGACACATCATGCGGGCCATCTATAACAAAGGGGT 4983
Qy 4321 TGCCTTACCTCAGCAGGGGGAATTAAGAAACAGAGGAATTTCTAAGCCTATTAGAAG 4380
Db 4984 TGCCTTACCTCAGCAGGGGGAATTAAGAAACAGAGGAATTTCTAAGCCTATTAGAAG 5043
Qy 4381 CCGTACATTTACCAAAAAGCTAGCTATTATACATGTCTCTGGACATCAAGAAAGCTAAAG 4440
Db 5044 CCTTACATTTGCCCCAAAAGGCTAGCTATTATACATGTCTCTGGACATCAAGAAAGCCAAAG 5103
Qy 4441 ATCTCATATCCAGAGAAACCCAGATGGCTGACCGGGTTGCCAAGCAGGACGCCCGGCTG 4500
Db 5104 ATCCCATATCCAGAGGAACCCAGATGGCTGACCGGGTTGCCAAGCAGGACGCCCGGCTG 5163

Qy 4501 TTAAACCTTCTGCTATATATAGAAATGCCCCAAAGCCCCAGAACCCAGACGACGACTACACCC 4560
Db 5164 TTAAACCTTCTGCTATATATAGAAACACCCAAAGCCCCAGAACCCGACGACGACTACACCC 5223
Qy 4561 TAGAAGACTGGCAAGAGATATAAAGATAGACAGTTCTCTGAGACTCCGGAAGGACCT 4620
Db 5224 TAGAAGACTGGCAAGAGATATAAAGATAGACAGTTCTCTGAGACTCCGGAAGGACCT 5283
Qy 4621 GCTTATACCTCAGATGGGAAGGAAATCCTGCCCCACAAGAAAGGTTAGAAATATGTCCAAC 4680
Db 5284 GCTTATACCTCAGATGGGAAGGAAATCCTGCCCCACAAGAAAGGTTAGAAATATGTCCAAC 5343
Qy 4681 AGATACATCGTCTAAACCCACCTAGGAACTAAACACCTGCAGCAGTTGGTCAGAAACATCCC 4740
Db 5344 AGATACATCGTCTAAACCCACCTAGGAACTAAACACCTGCAGCAGTTGGTCAGAAACATCTC 5403
Qy 4741 CTTATCATGTTCTGAGGCTACCAAGAGTGGCTGACTCGGTGGTCAACACATTTGTGTGCCCT 4800
Db 5404 CTTATCATGTTCTGAGGCTACCAAGAGTGGCTGACTCGGTGGTCAACACATTTGTGTGCCCT 5463
Qy 4801 GCCAGCTGTTAATGCTAATCTTCCAGAAATGCTCCAGGAAGAGACTAAAGGGGAAGCC 4860
Db 5464 GCCAGCTGTTAATGCTAATCTTCCAGAAATGCTCCAGGAAGAGACTAAAGGGGAAGCC 5523
Qy 4861 ACCCAGGCGCTCACTGGGAAGTGGACTTCACTGAGTAAAGCCGGCTAAATACGGAAACA 4920
Db 5524 ACCCAGGCGCTCACTGGGAAGTGGACTTCACTGAGTAAAGCCGGCTAAATACGGAAACA 5583
Qy 4921 AATACCTATTTGTTTGTAGACACCTTTTTCAGGATGGGTAGAGGCTTATCTCTACTAAGA 4980
Db 5584 AATATCTATTTGTTTGTAGACACCTTTTTCAGGATGGGTAGAGGCTTATCTCTACTAAGA 5643
Qy 4981 AAGAGACTTCAACCGTGTGGCTTAAAGAAATCTGGAAGAAATTTTTCAGAAATTTGGAA 5040
Db 5644 AAGAGACTTCAACCGTGTGGCTTAAAGAAATCTGGAAGAAATTTTTCAGAAATTTGGAA 5703
Qy 5041 TACTAAAGTAATAGGGTCAGACAAATGTCAGCTTTTGTGCCAGGTAAGTCAGGAC 5100
Db 5704 TACTAAAGTAATAGGGTCAGACAAATGTCAGCTTTTGTGCCAGGTAAGTCAGGAC 5763
Qy 5101 TGCCCAAGATATTTGGGATTTGATTTGGAATCTGATTTGTCATACAGACCCCAAGCTCAG 5160
Db 5764 TGCCCAAGATATTTGGGATTTGATTTGGAATCTGATTTGTCATACAGACCCCAAGCTCAG 5823
Qy 5161 GACAGTACAGAGGATGAATAGAACCATTAAGAGAGACCTTACTAAATTTGACCGCGGAGA 5220
Db 5824 GACAGTACAGAGGATGAATAGAACCATTAAGAGAGACCTTACTAAATTTGACCGCGGAGA 5883
Qy 5221 CTGGCGTTAATGATTGGATAGCTCTCTGCCCCCTTTGTGCTTTTATAGGGTTAGGAAACACCC 5280
Db 5884 CTGGCGTTAATGATTGGATAGCTCTCTGCCCCCTTTGTGCTTTTATAGGGTTAGGAAACACCC 5943
Qy 5281 CTGGACAGTTTGGCTGACCCCTATGAATTAATCTACGGGGGACCCCCCTTGTGGTAG 5340
Db 5944 CTGGACAGTTTGGCTGACCCCTATGAATTAATCTACGGGGGACCCCCCTTGTGGTAG 6003
Qy 5341 AATATTGCTTCTGTACATAGTGTGACGTCTGCTTTCCAGACCTTTGTTCTCTAGGCTCA 5400
Db 6004 AATATTGCTTCCGTACATAGTGTGACGTCTGCTTTCCAGACCTTTGTTCTCTAGGCTCA 6063
Qy 5401 AGGCACCTTGAAGTGGGTGAGACCAACGAGCGTGGAGGCACTCCGGGAGGCTACTCAGGAG 5460
Db 6064 AGGCACCTTGAAGTGGGTGAGACCAACGAGCGTGGAGGCACTCCGGGAGGCTACTCAGGAG 6123
Qy 5461 GAGGAGACTTTGAGATCCCAATCGTTTCCAGTGGGAGATTCAGTCTACGTTAGAGCC 5520
Db 6124 GAGGAGACTTTGAGATCCCAATCGTTTCCAGTGGGAGATTCAGTCTACGTTAGAGCC 6183
Qy 5521 ACCGTGACGAAACCTTCGAGACTTCGTTGGAAGGGCCCTTATCTCTGACTTTTTCACACAC 5580
Db 6184 ACCGTGACGAAACCTTCGAGACTTCGTTGGAAGGGCCCTTATCACGTACTTTTTCACACAC 6243

Matches 5521; Conservative 0; Mismatches 10; Indels 5; Gaps 5;

QY 1 GCGTGTGTACGACTGTGGGCCCCACGCGCTTGGAAATAAAATCCTCTTGTCTGTGCA 60
DB |||||
2528 GCGTGTGTACGACTGTGGGCCCCACGCGCTTGGAAATAAAATCCTCTTGTCTGTGCA 2587
QY 61 TCAAGACCGCTTCTCGTGTAGTGATTAAGGGAGTCGCGCTTTTCCGAGCCCTGAGGTTCTT 120
DB |||||
2588 TCAAGACCGCTTCTCGTGTAGTGATTAAGGGAGTCGCGCTTTTCCGAGCCCTGAGGTTCTT 2647
QY 121 TTTGCTGTCTTACATTTGGGGGCTCGTCGGGATCTGTGCGGCCACCCCTAAACCCG 180
DB |||||
2648 TTTGCTGTCTTACATTTGGGGGCTCGTCGGGATCTGTGCGGCCACCCCTAAACCCG 2707
QY 181 AGAACCGACTTGGAGGTAAAGAGATCCTCTTTTAAACGTGTATGATGTACCGGCCGC 240
DB |||||
2708 AGAACCGACTTGGAGGTAAAGAGATCCTCTTTTAAACGTGTATGATGTACCGGCCGC 2767
QY 241 GTCTCTGTCTGAGTGTCTGTCTTTCAGTGTGCGCGCTTTTCGGTTTGCAGCTGTCTCTC 300
DB |||||
2768 GTCTCTGTCTGAGTGTCTGTCTTTCAGTGTGCGCGCTTTTCGGTTTGCAGCTGTCTCTC 2827
QY 301 AGGCCGTAAAGGCTGGGGAATCTGTATCAGCAGACGTGTAGGAGATCACAGGCTGCTG 360
DB |||||
2828 AGGCCGTAAAGGCTGGGGAATCTGTATCAGCAGACGTGTAGGAGATCACAGGCTGCTG 2887
QY 361 CCTGGGGACGCCCGGAGGTGAGGAGCGCAGGAGCGCTTGGTGTCTCTACTGTC 420
DB |||||
2888 CCTGGGGACGCCCGGAGGTGAGGAGCGCAGGAGCGCTTGGTGTCTCTACTGTC 2947
QY 421 GGTTCAGAGGACCGAAATCTGTCTGTAAGCGAAGCTTCCCGTCGCGACCGTCCGACT 480
DB |||||
2948 GGTTCAGAGGACCGAAATCTGTCTGTAAGCGAAGCTTCCCGTCGCGACCGTCCGACT 3007
QY 481 CTTTTCGCTGTGTGGAGAGACGTGGAACGGGTCACTGTGTCTGTGATCTGTGGTTCTG 540
DB |||||
3008 CTTTTCGCTGTGTGGAGATACTGTGACCGGTCACTGTGTCTGTGATCTGTGGTTCTG 3067
QY 541 TTTTGTGTGTCTTGTGTGTCTTGTGTCTTGTGTCTTGTGTCTTGTGTCTTGTGTCTTGT 600
DB |||||
3068 TTTTGTGTGTCTTGTGTGTCTTGTGTCTTGTGTCTTGTGTCTTGTGTCTTGTGTCTTGT 3127
QY 601 CGACCCCTCTTAGTCTTGTGACTCTCGACCAITGGACTGAAGTTAAATCCAGGGCTCAAT 660
DB |||||
3128 CGACCCCTCTTAGTCTTGTGACTCTCGACCAITGGACTGAAGTTAAATCCAGGGCTCAAT 3187
QY 661 TGTCACTTCAGTTAAGAGGACCTTGGCAGACTTTCTGTGTCTCTGATGTCGACAT 720
DB |||||
3188 TGTCACTTCAGTTAAGAGGACCTTGGCAGACTTTCTGTGTCTCTGATGTCGACAT 3247
QY 721 TCGATCTTGGATGGCCATCAGAGGGACCTTTTAAATCTCAGATTTATCTCGGCTGTTAAAG 780
DB |||||
3248 TCGATCTTGGATGGCCATCAGAGGGACCTTTTAAATCTCAGATTTATCTCGGCTGTTAAAG 3307
QY 781 CAGTTATTTTTCAGACTTGGACCGCGCTCTCATCCCGATCAGAGGCCCTATATCTTTACGT 840
DB |||||
3308 CAATTATTTTTCAGACTTGGACCGCGCTCTCATCCCGATCAGAGGCCCTATATCTTTACGT 3367
QY 841 GGCAGATTTGGCAGAGGATCTCTCGGCATGGGTTAAACCATGGCTGAATTAAGCCAGAA 900
DB |||||
3368 GGCAGATTTGGCAGAGGATCTCTCGGCATGGGTTAAACCATGGCTGAATTAAGCCAGAA 3427
QY 901 AGCCAGGTCCCGAAATCTGGCTCTTGGAGAGAAAAACAAACACTCGGCTGAAAAAGTCA 960
DB |||||
3428 AGCCAGGTCCCGAAATCTGGCTCTTGGAGAGAAAAACAAACACTCGGCTGAAAAAGTCA 3487
QY 961 AGCCCTCTCTCATATCTACCCGAGATTGAGAGGCCACCGGCTTGGCCGGAAACCCCAAT 1020
DB |||||
3488 AGCCCTCTCTCATATCTACCCGAGATTGAGGAAACCCCGGCTTGGCCGGAAACCCCAAT 3547
QY 1021 CTGTTCCCGACCCCTTATCTGGCAGAGGTCGCGGAGGAGACCTTTGGCCCTCTCTG 1080
DB |||||
3548 CTGTTCCCGACCCCTTATCTGGCAGAGGTCGCGGAGGAGACCTTTGGCCCTCTCTG 3607

1081 GAGCTCCGCGGTGGAGGACCTGTGCAAGGACTCGGAGCCGAGGGCGCAACCCCG 1140
DB |||||
3608 GAGCTCCGCGGTGGAGGACCTTCTGCAAGGACTCGGAGCCGAGGGCGCACCCCG 3667
QY 1141 AGCGGACAGACGAGATCGGACATTTACCGCTCGGCACGTACGGCCCTCCACACCCGGGG 1200
DB |||||
3668 AGCGGACAGACGAGATCGGACATTTACCGCTCGGCACGTACGGCCCTCCACACCCGGGG 3727
QY 1201 GCCAATTGCAAGCCCTCCAGTATTGGCCCTTTTCTTGCAGATCTCTATAATTGAAAA 1260
DB |||||
3728 GCCAATTGCAAGCCCTCCAGTATTGGCCCTTTTCTTGCAGATCTCTATAATTGAAAA 3787
QY 1261 CTAAACCATCCCCCTTTCTCGGAGGATCCCAACGCTCAACGGGTTGGTGGAGTCCCTTA 1320
DB |||||
3788 CTAAACCATCCCCCTTTCTCGGAGGATCCCAACGCTCAACGGGTTGGTGGAGTCCCTTA 3847
QY 1321 TGTCTCTCACAGCCTACTTGGGATGATTGTCAACAGCTGCTGCAGACACTCTTTCACAA 1380
DB |||||
3848 TGTCTCTCACAGCCTACTTGGGATGATTGTCAACAGCTGCTGCAGACACTCTTTCACAA 3907
QY 1381 CCGAGGAGCGAGAGAAATTTCTATTAGAGGCTAGAAAAATGTTCTTGGGGCGCAGCGGC 1440
DB |||||
3908 CCGAGGAGCGAGAGAAATTTCTATTAGAGGCTAGAAAAATGTTCTTGGGGCGCAGCGGC 3967
QY 1441 GACCCACGCGTTGCAAAATGAGATTGACATGGGATTTCCCTTAACTCGCCCGGTTGG 1500
DB |||||
3968 GACCCACGCGTTGCAAAATGAGATTGACATGGGATTTCCCTTAACTCGCCCGGTTGG 4027
QY 1501 ACTCAACAGCGCTAGGATAGGAGCTTGAAAAATCTATCGCAGGCTCTTGGTGGCG 1560
DB |||||
4028 ACTCAACAGCGCTAGGATAGGAGCTTGAAAAATCTATCGCAGGCTCTTGGTGGCG 4087
QY 1561 GTCCTCGGGCGCTCAAGACGCGCCACTAAATTTGGCTAAGGTAAAGAAAGTATGATCAGG 1620
DB |||||
4088 GTCCTCGGGCGCTCAAGACGCGCCACTAAATTTGGCTAAGGTAAAGAAAGTATGATCAGG 4147
QY 1621 GACCGAAATGAACCCCTCTGTTTTTTCTTGAGAGGCTCTTGAAGCCTTCAGCGGTACA 1680
DB |||||
4148 GACCGAAATGAACCCCTCTGTTTTTTCTTGAGAGGCTCTTGAAGCCTTCAGCGGTACA 4207
QY 1681 CCGCTTTTGTATCCCACTCAGAGGCCCAAAAAGCCTCAGTGGCTTTGGCTTTATAGGAC 1740
DB |||||
4208 CCGCTTTTGTATCCCACTCAGAGGCCCAAAAAGCCTCAGTGGCTTTGGCTTTATAGGAC 4267
QY 1741 AGTCAGCCTTTGGATATTAGAAAAGAGCTTCAGAGACTGGAAGGTTTACAGGAGGCTGAGT 1800
DB |||||
4268 AGTCAGCCTTTGGATATTAGAAAAGAGCTTCAGAGACTGGAAGGTTTACAGGAGGCTGAGT 4327
QY 1801 TACGTGATCTAGTGAAGGAGGAGAGAAAGTATATTAACAAAAGGAGACAGAAAGAAA 1860
DB |||||
4328 TACGTGATCTAGTGAAGGAGGAGAGAAAGTATATTAACAAAAGGAGACAGAAAGAAA 4387
QY 1861 GGGAAACAAAGAAAGAGAGAGAAAGGAGAAAGGAGAAAGACGTATTAACGCGCAAG 1920
DB |||||
4388 GGGAAACAAAGAAAGAGAGAGAAAGGAGAAAGGAGAAAGACGTATTAACGCGCAAG 4447
QY 1921 AGAAGAAATTTGACTTAAGATCTTGGCTGAGTGTGTAAGGGAAAAAGCAATACGGAAGAG 1980
DB |||||
4448 AGAAGAAATTTGACTTAAGATCTTGGCTGAGTGTGTAAGGGAAAAAGCAATACGGAAGAG 4507
QY 1981 AGAGAGATTTTAGGAAAAATTAGTTCAGGCCCTAGACAGTCAGGAAACCTGGGCAATAGGA 2040
DB |||||
4508 AGAGAGATTTTAGGAAAAATTAGTTCAGGCCCTAGACAGTCAGGAAACCTGGGCAATAGGA 4567
QY 2041 CCCCCTCGACAGAGCCAAATGTGCAATTTTAAAGAAAGAGACACTGGGCAAGGAACT 2100
DB |||||
4568 CCCCCTCGACAGAGCCAAATGTGCAATTTTAAAGAAAGAGACACTGGGCAAGGAACT 4627
QY 2101 GCCCCAAGAGGAAAAACAAAGGACCAAGGATCCTAGCTCTAGAAAGAGATAAAGATTAGG 2160
DB |||||
4628 GCCCCAAGAGGAAAAACAAAGGACCAAGGATCCTAGCTCTAGAAAGAGATAAAGATTAGG 4687

QY 2161 GGAGACGGGGTTCGGACCCCTCCCGAGCCAGGGTAACTTTGAAGGTGGAGGGCAAC 2220
Db 4688 GGAGACGGGGTTCGGACCCCTCCCGAGCCAGGGTAACTTTGAAGGTGGAGGGCAAC 4747
QY 2221 CAGTTGAGTTCCTGGTTGATACCGGAGCGAAACAATTGAGTGTCTATACAGCCATTAGGAA 2280
Db 4748 CAGTTGAGTTCCTGGTTGATACCGGAGCGAAACAATTGAGTGTCTATACAGCCATTAGGAA 4807
QY 2281 AACTAAAGATAAATAATCTGGGTGATGGTGCACAGGCGCAACACAGTATCCATGGA 2340
Db 4808 AACTAAAGATAAATAATCTGGGTGATGGTGCACAGGCGCAACACAGTATCCATGGA 4866
QY 2341 CTACCCGAAGACAGTTGACTTGGGAGTGGGACGGGTAAACCCACTCGTTTCTGGTCAATC 2400
Db 4867 CTACCCGAAG-ACAGTTGACTTGGGAGTGGGACGGGTAAACCCACTCGTTTCTGGTCAATC 4925
QY 2401 CTGAGTCCGAGCACCCCTCTTAGGTAGAGACTTATTTGACAGAGTGGGAGCAAAATTT 2460
Db 4926 CTGAGTCCGAGCACCCCTCTTAGGTAGAGACTTATTTGACAGAGTGGGAGCAAAATTT 4985
QY 2461 CTTTGAAGGGAACAGAGTGTCTGCAATACAAACCTTATCACTGTGTGACCC 2520
Db 4986 CTTTGAAGGGAACAGAGTGTCTGCAATACAAACCTTATCACTGTGTGACCC 5045
QY 2521 TCCAAATTAGATGACGAATATCGACTATCTCTCCCTAGTAAAGCCTGATCAAAATATAC 2580
Db 5046 TCCAAATTAGATGACGAATATCGACTATCTCTCCCTAGTAAAGCCTGATCAAAATATAC 5105
QY 2581 AATTCTGGTTGGAAACAGTTTCCCAAGCCTGGGAGAAACCGCAGGAGTGGTTGGCAA 2640
Db 5106 AATTCTGGTTGGAAACAGTTTCCCAAGCCTGGGAGAAACCGCAGGAGTGGTTGGCAA 5165
QY 2641 AGCAAGTTCGCCCAACAGTTTATCACTGAAGGCCAGTGCACACAGTGTCACTGACAC 2700
Db 5166 AGCAAGTTCGCCCAACAGTTTATCACTGAAGGCCAGTGCACACAGTGTCACTGACAC 5225
QY 2701 AGTACCCCTTGAGTAAAGAGCTCAAGAGGAATTCGGCCGCATGTCCAAAGATTAATCC 2760
Db 5226 AGTACCCCTTGAGTAAAGAGCTCAAGAGGAATTCGGCCGCATGTCCAAAGATTAATCC 5285
QY 2761 AACAGGGCATCTAGTTCTCTGTCCAAATCTCCCTGGAATATCTCCCTGTACCCGTTAGAA 2820
Db 5286 AACAGGGCATCTAGTTCTCTGTCCAAATCTCCCTGGAATATCTCCCTGTACCCGTTAGAA 5345
QY 2821 AGCCTGGGACTAATGACTATCGACAGTACAGGACTTGAAGAGGTCAATAAACGGGTGC 2880
Db 5346 AGCCTGGGACTAATGACTATCGACAGTACAGGACTTGAAGAGGTCAATAAACGGGTGC 5405
QY 2881 AGGATATACCCCAACAGTCCGAAACCTTATAACCTCTGTGTGCTCTCCACCCCAAC 2940
Db 5406 AGGATATACCCCAACAGTCCGAAACCTTATAACCTCTGTGTGCTCTCCACCCCAAC 5465
QY 2941 GGAGCTGGTATACAGTATGAGTAAAGGATGCTTCTTCTGCTGAGATTAACCCCA 3000
Db 5466 GGAGCTGGTATACAGTATGAGTAAAGGATGCTTCTTCTGCTGAGATTAACCCCA 5525
QY 3001 CTAGCCAAACCACTTTTGGCTTCGAAATGGAGAGATTCAGGTACGGGAAGAACCGGGCAGC 3060
Db 5526 CTAGCCAAACCACTTTTGGCTTCGAAATGGAGAGATTCAGGTACGGGAAGAACCGGGCAGC 5585
QY 3061 TCACCTGGACCGGACTGCCCAAGGGTTCAAGAACTCCCGACCATCTTTGACGAAGCCC 3120
Db 5586 TCACCTGGACCGGACTGCCCAAGGGTTCAAGAACTCCCGACCATCTTTGACGAAGCCC 5645
QY 3121 TACACAGAGACTGGCCAACTTCAGGATCCAAACCCCTCAGGTGACCCCTCTCCAGTACG 3180
Db 5646 TACACAGAGACTGGCCAACTTCAGGATCCAAACCCCTCAGGTGACCCCTCTCCAGTACG 5705
QY 3181 TGGATGACTGCTTCTGGCGGAGCCACCAACAGGACTGTTTGAAGGCAAGGAGGAC 3240
Db 5706 TGGATGACTGCTTCTGGCGGAGCCACCAACAGGACTGTTTGAAGGCAAGGAGGAC 5765
QY 3241 TACTGCTGGAAATTGCTGACCTAGGCTACAGGCTCTGTGAAGAGGCCCGCCAGATTGCA 3300

Db 5766 TACTGCTGGAAATTGCTGACCTAGGCTACAGAGCTCTGTGAAGAGGCCAGATTGCA 5825
QY 3301 GGAGAGAGGTAAACATACTTTGGGGTACAGTTTGGGACCGGACCGGATGCTCAGCGAGG 3360
Db 5826 GGAGAGAGGTAAACATACTTTGGGGTACAGTTTGGGACCGGACCGGATGCTCAGCGAGG 5885
QY 3361 CACGGAAGAAAACCTGATGTCAGATACCGGCCCCAAACACAGCCAAACAAATGAGAGGT 3420
Db 5886 CACGGAAGAAAACCTGATGTCAGATACCGGCCCCAAACACAGCCAAACAAATGAGAGGT 5945
QY 3421 TTTTGGGACAGCTGATTTTGCAGACTGTGGATCCGGGGTTTGGACCTTACAGACCC 3480
Db 5946 TTTTGGGACAGCTGATTTTGCAGACTGTGGATCCGGGGTTTGGACCTTACAGACCC 6005
QY 3481 CACTCTACCCGCTTAAACCAAGAAAAGGGGAAATCTCTGGGCTCTCTGAGCACCAGAGG 3540
Db 6006 CACTCTACCCGCTTAAACCAAGAAAAGGGGAAATCTCTGGGCTCTCTGAGCACCAGAGG 6065
QY 3541 CATTTGATGCTATCAAAAAGGCCCTGCTGAGCGCACTGCTCTGGCCCTCCCTGACGTAA 3600
Db 6066 CATTTGATGCTATCAAAAAGGCCCTGCTGAGCGCACTGCTCTGGCCCTCCCTGACGTAA 6125
QY 3601 CTAAAACTTTTACCTTTTATGCTGATGAGCGTAAAGGAGTAGCCCGGGAGTTTAAACC 3660
Db 6126 CTAAAACTTTTACCTTTTATGCTGATGAGCGTAAAGGAGTAGCCCGGGAGTTTAAACC 6185
QY 3661 AAACCTTAGACCACTTGGAGAGACCTGCTGCCCTACCTGTCAAGAGCTCGATCCTGTAG 3720
Db 6186 AAACCTTAGACCACTTGGAGAGACCTGCTGCCCTACCTGTCAAGAGCTCGATCCTGTAG 6245
QY 3721 CCAGTGTGTGGCCCATATGCTGAAGGCTATCGAGCTGTGGCCATATCTGTCGAAGACG 3780
Db 6246 CCAGTGTGTGGCCCATATGCTGAAGGCTATCGAGCTGTGGCCATATCTGTCGAAGACG 6305
QY 3781 CTGACAAATTTGACTTTTGGGAC-AGAAATATTAATGCTTAATAGCCCCCATATCGTGAAGAC 3839
Db 6306 CTGACAAATTTGACTTTTGGGACAAAGATATACTGTATAAGCCCCCATATCGTGAAGAC 6365
QY 3840 ATGCTTCGGCAGCCCCCAGACCGATGATGACCAACCGCCGATGACCCACTATCAAGC 3899
Db 6366 ATGCTTCGGCAGCCCCCAGACCGATGATGACCAACCGCCGATGACCCACTATCAAGC 6425
QY 3900 CTGCTTCTCAGAGAGGGTCACTGCTTCCGCTCCACAGCCGCTCTCAACCTGCCACTCTT 3959
Db 6426 CTGCTTCTCAGAGAGGGTCACTGCTTCCGCTCCACCAACCGCTCTCAACCTGCCACTCTT 6485
QY 3960 CTGCTTCAAGAGACTGATGAAACAGTGAATGCTGATGCTGATGCTGATGAGGAG 4019
Db 6486 CTGCTTCAAGAGACTGATGAAACAGTGAATGCTGATGCTGATGCTGATGAGGAG 6545
QY 4020 ACTGGGTCGCGAAGGACCTTACAGACATACCGCTGACTGGAGAGTGTAACTGGTTC 4079
Db 6546 ACTGGGTCGCGAAGGACCTTACAGACATACCGCTGACTGGAGAGTGTAACTGGTTC 6605
QY 4080 ACTGACGGAAGCAGCTATGTGGTGAAGGATGCTGGGGCGGCGGTGGTGCAC 4139
Db 6606 ACTGACGGAAGCAGCTATGTGGTGAAGGATGCTGGGGCGGCGGTGGTGCAC 6665
QY 4140 GGGACCCGCAAGATCTGGGCGCAGCAGCTGCGGGAAGAACTTCAGGCAAAAAGGCTGAG 4199
Db 6666 GGGACCCGCAAGATCTGGGCGCAGCAGCTGCGGGAAGAACTTCAGGCAAAAAGGCTGAG 6725
QY 4200 CTGATGGCCCTCAGCGAAGCTTTGCGGCTGGCCGAAGGGAATCCATAAACATTTATACG 4259
Db 6726 CTGATGGCCCTCAGCGAAGCTTTGCGGCTGGCCGAAGGGAATCCATAAACATTTATACG 6785
QY 4260 GACAGAGGTATGCTTTTGGGCTGCAACGCTCATGGGGCATCTATAAAACAAAGGGGG 4319
Db 6786 GACAGAGGTATGCTTTTGGGCTGCAACGCTCATGGGGCATCTATAAAACAAAGGGGG 6845
QY 4320 TTTGCTTACCTCAGCAGGAGGGGAATTAAGAACAAAGAGGAAATTTCTAAGCCTATTGAA 4379

Db 6846 TTGCTTAACTCTACGAGGGAGGAAATAAAGAAACAAAGAGGAAATTTCTAAGCCCTATTAGAA 6905

Qy 4380 GCGGTACATTTTACCAAAAAGGCTAGCTATTATATACACTGTCCTGGACATCAGAAAGCTAA 4439

Db 6906 GCGGTACATTTTACCAAAAAGGCTAGCTATTATATACACTGTCCTGGACATCAGAAAGCTAA 6965

Qy 4440 GATCTCATATCCAGAGGAAACAGATGGCTGACCGGGTTGCCAAGCAGGAGCCACAGGT 4499

Db 6966 GATCTCATATCCAGAGGAAACAGATGGCTGACCGGGTTGCCAAGCAGGAGCCACAGGT 7025

Qy 4500 GTTACCTTCTGCTTATATAGAAATGCCCAAGCCCAAGACCCAGACGACGATACACC 4559

Db 7026 GTTACCTTCTGCTTATATAGAAATGCCCAAGCCCAAGACCCAGACGACGATACACC 7085

Qy 4560 CTAGAAGACTGGCAAGAGATAAAAAAGATAGACCAAGTTCTCTGAGACTCCGGAAGGACC 4619

Db 7086 CTAGAAGACTGGCAAGAGATAAAAAAGATAGACCA-TTCTCTGAGACTCCGGAAGGACC 7144

Qy 4620 TGCTATACCTCAGATGGGAAGAAATCTCTGCCCAAAAGAGGGTTAGAAATATGTCCAA 4679

Db 7145 TGCTATACCTCAGATGGGAAGAAATCTCTGCCCAAAAGAGGGTTAGAAATATGTCCAA 7204

Qy 4680 C-AGATACATGCTTAACCCACTAGGAATAAAACACCTGCAGCAGTTGGTCAGAACATC 4738

Db 7205 CAAGATACATGCTTAACCCACTAGGAATAAAACACCTGCAGCAGTTGGTCAGAACATC 7264

Qy 4739 CCTTATCATGTTCTGAGGCTACAGGAGTGGCTGACTCGGTGCTCAAAATTTGTGTGC 4798

Db 7265 CCTTATCATGTTCTGAGGCTACAGGAGTGGCTGACTCGGTGCTCAAAATTTGTGTGC 7324

Qy 4799 CTGCCAGCTGGTTAATGCTAATCTTCCAGAAATGCTCCAGGGAAGAGACTAAGGGGAAG 4858

Db 7325 CTGCCAGCTGGTTAATGCTAATCTTCCAGAAATGCTCCAGGGAAGAGACTAAGGGGAAG 7384

Qy 4859 CCACCAGGCGCTCACTGGGAAGTGACATTCAGTAGGTAAAGCCGGCTAAATACGGAA 4918

Db 7385 CCACCAGGCGCTCACTGGGAAGTGACATTCAGTAGGTAAAGCCGGCTAAATACGGAA 7444

Qy 4919 CAAATACCTATTGGTTTTGTAGACACCTTTTCAGGATGGGTAGAGGCTTATCTACTAA 4978

Db 7445 CAAATACCTATTGGTTTTGTAGACACCTTTTCAGGATGGGTAGAGGCTTATCTACTAA 7504

Qy 4979 GAAAGAGACTTCAACCGTGGTCTAAAAAATATCTGGAAGAAATTTTCCAAAGATTGG 5038

Db 7505 GAAAGAGACTTCAACCGTGGTCTAAAAAATATCTGGAAGAAATTTTCCAAAGATTGG 7564

Qy 5039 AATACCTAAGTTAATAGGTCAGACAAATGGTCAGCTTTTGTGCCAGGTAAGTCAGG 5098

Db 7565 AATACCTAAGTTAATAGGTCAGACAAATGGTCAGCTTTTGTGCCAGGTAAGTCAGG 7624

Qy 5099 ACTGGCCAAAGATTTGGGGATTGATTGGAACTGCAATTGTGCATACAGACCCCAAGCTC 5158

Db 7625 ACTGGCCAAAGATTTGGGGATTGATTGGAACTGCAATTGTGCATACAGACCCCAAGCTC 7684

Qy 5159 AGGACAGGTAGAGAGTGAATAGAACCAATTAAGAGACCCCTTACTAAATTGACCCGGA 5218

Db 7685 AGGACAGGTAGAGAGTGAATAGAACCAATTAAGAGACCCCTTACTAAATTGACCCGGA 7744

Qy 5219 GACTGGCGTTAATGATGATAGTCTCTCTGCCCTTTGTGCTTTTAGGTTAGGAACAC 5278

Db 7745 GACTGGCGTTAATGATGATGATAGTCTCTCTGCCCTTTGTGCTTTTAGGTTAGGAACAC 7804

Qy 5279 CCTTGACAGATTTGGGCTGACCCCTATGAATTTACTCTAGGGGAGCCCCCCCATTTGT 5338

Db 7805 CCTTGACAGATTTGGGCTGACCCCTATGAATTTACTCTAGGGGAGCCCCCCCATTTGT 7864

Qy 5339 AGAAATTTGCTTCTGTATAGTGTGACCGTGTGCTTTTCCAGCCCTTTGTTCTCTAGGCT 5398

Db 7865 AGAAATTTGCTTCTGTATAGTGTGACCGTGTGCTTTTCCAGCCCTTTGTTCTCTAGGCT 7924

Qy 5399 CAAGGACATTTAGTGGGTGAGACAAACAGCGGTGGAGGCAACTCCGGGAGCCCTACTCAGG 5458

Db 7925 CAAGGACATTTAGTGGGTGAGACAAACAGCGGTGGAGGCAACTCCGGGAGCCCTACTCAGG 7984

Qy 5459 AGGAGGAGACTTTCAGATCCCAATCGTTTCCAAAGTGGAGATTCACTTACGTTAGACG 5518

Db 7985 AGGAGGAGACTTTCAGATCCCAATCGTTTCCAAAGTGGAGATTCACTTACGTTAGACG 8044

Qy 5519 CCACCGTGCAGGAAC 5534

Db 8045 CCACCGTGCAGGAAC 8060

RESULT 14

AAF77725

ID AAF77725 standard; cDNA; 8060 BP.

XX

AC AAF77725;

XX

DT 06-AUG-2003 (revised)

DT 23-MAY-2001 (first entry)

XX

Tsukuba-1 cDNA.

XX

Tsukuba-1; retrovirus; graft transplantation; xenotransplantation; ss.

XX

Porcine endogenous retrovirus.

XX

US6190861-B1.

XX

20-FEB-2001.

XX

13-DEC-1996; 96US-00766528.

XX

14-DEC-1995; 95US-00572645.

XX

(GEO) GEN HOSPITAL CORP.

XX

Fishman JA;

XX

WPI; 2001-256211/26.

XX

Assessing risk of endogenous retroviruses in clinical practice and in xenotransplantation, comprises using probe sequences derived from swine or miniature swine retroviral genome.

XX

Claim 1; Fig 1; 127pp; English.

XX

The present invention relates to a method for screening a cell or tissue for the presence or expression of a retrovirus (RV), comprising contacting a target nucleic acid from the cell or tissue with a second nucleic acid from the present invention (e.g. the present sequence or a fragment thereof). The method is useful for RV detection and to assess graft transplantation risk. Screening of animals allows the elimination of donors with active replication of known viruses. Inactive proviruses can be detected and inactivated, allowing identification and elimination of potential human pathogens derived from swine in a manner not possible in the outbred human organ donor population and is important to the development of human xenotransplantation. (Updated on 06-AUG-2003 to correct OS field.)

XX

Sequence 8060 BP; 2233 A; 1959 C; 2012 G; 1856 T; 0 U; 0 Other;

SQ

Query Match 67.1%; Score 5460; DB 4; Length 8060;

Best Local Similarity 99.7%; Pred. No. 0;

Matches 5521; Conservative 0; Mismatches 10; Indels 5; Gaps 5;

Qy 1 GCGTGGTGTACGACTGTGGGCCCCCAGCGCTTGGAAATAAAATCCTTGTGTTTGA 60

Db 2528 GCGTGGTGTACGACTGTGGGCCCCCAGCGCTTGGAAATAAAATCCTTGTGTTTGA 2587

Qy 61 TCAAGACCCGCTTCTCGTGAAGTAAAGGGAGTCGCCCTTTCCGAGCCTGGAGGTTCTT 120

Db 2588 TCAAGACCCGCTTCTCGTGAAGTAAAGGGAGTCGCCCTTTCCGAGCCTGGAGGTTCTT 2647

Qy 121 TTTGCTGGTCTTACATTTTGGGGGCTCGTCGGGATCTGTCGGGCCACCCCTAACCCG 180

Db	2648	TTTGTGCTTACATTTGGGGCTCGTCGGGATCTGTGCGGCCACCCCTAACCCCG	2707	Db	3728	GCCAAATTGACGCCCTCCAGTATTGGCCCTTTTCTTCTGCAGATCTCTATAATTGGAAA	3787
Qy	181	AGAACCGACTTGGAGTAAAGATCCTCTTTTAAACGTGTATGCATGTACCGCGCGC	240	Qy	1261	CTAACCATCCCCCTTTCTCGAGGATCCCAACGCCCTCACGGGTTGGTGGAGTCCCTTA	1320
Db	2708	AGAACCGACTTGGAGTAAAGATCCTCTTTTAAACGTGTATGCATGTACCGCGCGC	2767	Db	3788	CTAACCATCCCCCTTTCTCGAGGATCCCAACGCCCTCACGGGTTGGTGGAGTCCCTTA	3847
Qy	241	GTCTCTGTTCTGAGTGTCTGTTTCACTGGTGGCGCTTTCCGTTTGCAGCTGTCTCTC	300	Qy	1321	TGTTCTCTACAGCCTACTTGGGATGTTGTCAACAGCTGTCTGCAGACACTCTTCACAA	1380
Db	2768	GTCTCTGTTCTGAGTGTCTGTTTCACTGGTGGCGCTTTCCGTTTGCAGCTGTCTCTC	2827	Db	3848	TGTTCTCTACAGCCTACTTGGGATGTTGTCAACAGCTGTCTGCAGACACTCTTCACAA	3907
Qy	301	AGCCGTTAAGGCTTGGGGACTGTGTATCAGCAGAGTGTCTAGAGGATACAGGCTGCTG	360	Qy	1381	CCGAGAGCGAGAGAGAAATTTCTATTAGAGCTAGAAAAAATGTTCTTGGGGCCGACGGGC	1440
Db	2828	AGCCGTTAAGGCTTGGGGACTGTGTATCAGCAGAGTGTCTAGAGGATACAGGCTGCTG	2887	Db	3908	CCGAGAGCGAGAGAGAAATTTCTATTAGAGCTAGAAAAAATGTTCTTGGGGCCGACGGGC	3967
Qy	361	CCCTGGGGAGCGCCCGGAGGTGAGGAGCGCAGGACCGCTGTGTGCTCTCTACTGTC	420	Qy	1441	GACCCACCGGTTGCAAAATGAGATTGACATGGGATTTCCCTTAACTCGCCCCGGTTGGG	1500
Db	2888	CCCTGGGGAGCGCCCGGAGGTGAGGAGCGCAGGACCGCTGTGTGCTCTCTACTGTC	2947	Db	3968	GACCCACCGGTTGCAAAATGAGATTGACATGGGATTTCCCTTAACTCGCCCCGGTTGGG	4027
Qy	421	GGTCAGAGGACCGAAATTTCTGTGCTGAAGCGAAAGCTTTCCCTCCCGACCGCTCCGACT	480	Qy	1501	ACTTACACCGGCTGAAGGTAGGAGAGCTTTGAAAATCTATCGCAGGCTCTGTGTGGCG	1560
Db	2948	GGTCAGAGGACCGAAATTTCTGTGCTGAAGCGAAAGCTTTCCCTCCCGACCGCTCCGACT	3007	Db	4028	ACTTACACCGGCTGAAGGTAGGAGAGCTTTGAAAATCTATCGCAGGCTCTGTGTGGCG	4087
Qy	481	CTTTTGCTGCTGTGGAAGCGTGGACGGGTCAAGTGTCTGTGATCTGTGTGTTCTG	540	Qy	1561	GTCTCCGGGGCGCTCAAGACGGCCCACTAAATTTGGCTAAGGTAAAGAAAGTGTATGCAGG	1620
Db	3008	CTTTTGCTGCTGTGGAATACGTGGACGGGTCAAGTGTCTGTGATCTGTGTGTTCTG	3067	Db	4088	GTCTCCGGGGCGCTCAAGACGGCCCACTAAATTTGGCTAAGGTAAAGAAAGTGTATGCAGG	4147
Qy	541	TTTTGTGTCTTGTCTGTGTGCTCTGTCTACAGTCTTAAATATGGGACAGCGGTGA	600	Qy	1621	GACCGAATGAAACCCCTCTGTGTTTCTTGAGAGGCTCTTGGAAGCTTTCAGGCGGTACA	1680
Db	3068	TTTTGTGTCTTGTCTGTGTGCTCTGTCTACAGTCTTAAATATGGGACAGCGGTGA	3127	Db	4148	GACCGAATGAAACCCCTCTGTGTTTCTTGAGAGGCTCTTGGAAGCTTTCAGGCGGTACA	4207
Qy	601	GGACCCCTCTAGTTTGAACCTCTGACCATTTGCAATGGAATGGAATGGAATGGAATGGAAT	660	Qy	1681	CCCTCTTTGATGCCACCTCAGAGGCCCAAAAGCTCAGTGGCTTTGGCCCTTTATAGGAC	1740
Db	3128	GGACCCCTCTAGTTTGAACCTCTGACCATTTGCAATGGAATGGAATGGAATGGAATGGAAT	3187	Db	4208	CCCTCTTTGATGCCACCTCAGAGGCCCAAAAGCTCAGTGGCTTTGGCCCTTTATAGGAC	4267
Qy	661	TGTCAAGTTTCAAGAGGACCTTTGGCAGACTTTCTGTGCTCTGAAATGGCCGACAT	720	Qy	1741	AGTCAGCCTTGGATATTAGAAAGAGCTTTCAGAGACTGGAAGGTTTACAGAGGCTGAGT	1800
Db	3188	TGTCAAGTTTCAAGAGGACCTTTGGCAGACTTTCTGTGCTCTGAAATGGCCGACAT	3247	Db	4268	AGTCAGCCTTGGATATTAGAAAGAGCTTTCAGAGACTGGAAGGTTTACAGAGGCTGAGT	4327
Qy	721	TCGATGTTGATGTCATCAGAGGGACCTTTAAATCTGAGATTTATCTGGCTGTTAAAG	780	Qy	1801	TACGTGATCTAGTGAAGGAGCGAGAGAAAGTATATTTACAAAGGGAGACAGAGAGAAA	1860
Db	3248	TCGATGTTGATGTCATCAGAGGGACCTTTAAATCTGAGATTTATCTGGCTGTTAAAG	3307	Db	4328	TACGTGATCTAGTGAAGGAGCGAGAGAAAGTATATTTACAAAGGGAGACAGAGAGAAA	4387
Qy	781	CAGTATTTTTTCACTGGACCGGCTCTCATCCGATCAGAGGCTTATATCTTACGT	840	Qy	1861	GGGAAACAAAGAAAGAGAGAGAAAGAGAGAAAGGGAGAGAAAGCGTAAATAACGGCAG	1920
Db	3308	CAATATTTTTTCACTGGACCGGCTCTCATCCGATCAGAGGCTTATATCTTACGT	3367	Db	4388	GGGAAACAAAGAAAGAGAGAGAAAGAGAGAAAGGGAGAGAAAGCGTAAATAACGGCAG	4447
Qy	841	GGCAAGATTTGGCAGAGGATCCTCGCCATGGGTTAAACCAATGGCTGAATAAGCAAGAA	900	Qy	1921	AGAAGAAATTTGACTAAGATCTTGGCTCAGTGGTTGAAGGAAAGCAATACGGAAGAG	1980
Db	3368	GGCAAGATTTGGCAGAGGATCCTCGCCATGGGTTAAACCAATGGCTGAATAAGCAAGAA	3427	Db	4448	AGAAGAAATTTGACTAAGATCTTGGCTCAGTGGTTGAAGGAAAGCAATACGGAAGAG	4507
Qy	901	AGCCAGGTTCCCGAATTTCTGCTCTTGGAGAGAAACAAACACTCGGCTGAAAAAGTCA	960	Qy	1981	AGAGAGATTTTGGGAAATTTAGGTTCAGGCCCTAGACAGTCAAGGAACTCTGGGCAATAGGA	2040
Db	3428	AGCCAGGTTCCCGAATTTCTGCTCTTGGAGAGAAACAAACACTCGGCTGAAAAAGTCA	3487	Db	4508	AGAGAGATTTTGGGAAATTTAGGTTCAGGCCCTAGACAGTCAAGGAACTCTGGGCAATAGGA	4567
Qy	961	AGCCCTCTCTCATATCTACCCCGAGATTGAGGAGCCACCGGCTTGGCCGAAACCCCAAT	1020	Qy	2041	CCCCACTCGCAAGGACCAATGTGTCATTTGTAAAGAAAGAGACACTGGGCAAGGAACT	2100
Db	3488	AGCCCTCTCTCATATCTACCCCGAGATTGAGGAGCCACCGGCTTGGCCGAAACCCCAAT	3547	Db	4568	CCCCACTCGCAAGGACCAATGTGTCATTTGTAAAGAAAGAGACACTGGGCAAGGAACT	4627
Qy	1021	CTGTTTCCCGACCCCTTATCTGGCAGAGGTTGCGGAGGGGACCCCTTGGCCCTCTG	1080	Qy	2101	CCCCCAAGAGGGGAAACAAAGGACCAAGGATCCTAGCTCTAGAGAGAGATAAAGATTAGG	2160
Db	3548	CTGTTTCCCGACCCCTTATCTGGCAGAGGTTGCGGAGGGGACCCCTTGGCCCTCTG	3607	Db	4628	CCCCCAAGAGGGGAAACAAAGGACCAAGGATCCTAGCTCTAGAGAGAGATAAAGATTAGG	4687
Qy	1081	GAGCTCCGGGTGAGGAGACTGTGTGAGGAGACTCGGAGCGGAGGGGCGCCACCCCGG	1140	Qy	2161	GGAGAGCGGGTTCCGAGCCCTCCCGAGCCCGAGGTAATTTTGAAGGTGGAGGGGCAAC	2220
Db	3608	GAGCTCCGGGTGAGGAGACTGTGTGAGGAGACTCGGAGCGGAGGGGCGCCACCCCGG	3667	Db	4688	GGAGAGCGGGTTCCGAGCCCTCCCGAGCCCGAGGTAATTTTGAAGGTGGAGGGGCAAC	4747
Qy	1141	AGCGGACAGACGAGATCCGACATTTACCGCTGCGACGTCAGGCTCCCAACACGGGGG	1200	Qy	2221	CAGTTGAGTTCTCTGTTGATACCGGAGCGGAAACATTCAGTGTCTACTACAGCAATTAGGAA	2280
Db	3668	AGCGGACAGACGAGATCCGACATTTACCGCTGCGACGTCAGGCTCCCAACACGGGGG	3727	Db	4748	CAGTTGAGTTCTCTGTTGATACCGGAGCGGAAACATTCAGTGTCTACTACAGCAATTAGGAA	4807
Qy	1201	GCCAAATTCAGCCCTCAGTATTGGCCCTTTTCTTCTGCAGATCTCTATTAATTGGAAA	1260	Qy	2281	AACATAAGAGATAAAAAATTCCTGGGTGATGGGTGCCACAGGCGCAACAGTATCCATGGA	2340
Db				Db	4808	AACATAAGAGATAAAAAATTCCTGGGTGATGGGTG- CACAGGGCAACACAGTATCCATGGA	4866

QY	2341	CTACCCGAAGAACAGTTGACTTGGGAGTGGGACGGGTAAACCACTCGTTCTTGCTCATAC	2400	TTTTGGGGACAGCTGGATTTTGCAGACTGTGTGATCCCGGGGTTTGGCAGCTTAGCAGCCC	3480
Db	4867	CTACCCGAAG-A-CAGTTGACTTGGGAGTGGGACGGGTAAACCACTCGTTCTTGCTCATAC	4925	TTTTGGGGACAGCTGGATTTTGCAGACTGTGTGATCCCGGGGTTTGGCAGCTTAGCAGCCC	6005
QY	2401	CTGAGTGCCAGCACCCCTCTTAGGTAGAGACTTATTGACCAAGATGGGAGCACAATTT	2460	CACTCTACCCGCTAAACCAAGAAAAGGGGAAATTCCTCTGGGCTCTGAGCACCAGAAGG	3540
Db	4926	CTGAGTGCCAGCACCCCTCTTAGGTAGAGACTTATTGACCAAGATGGGAGCACAATTT	4985	CACTCTACCCGCTAAACCAAGAAAAGGGGAAATTCCTCTGGGCTCTGAGCACCAGAAGG	6065
QY	2461	CTTTTGAACAAGGGAAACAGAAAGTCTCTGCAAAATAACAAACCTATCACTGTGTGACCC	2520	CAATTGATCTATCAAAAAGGCCCTGCTGAGGCGACCTGCTCTGGGCCCTCCCTGACGTAA	3600
Db	4986	CTTTTGAACAAGGGAAACAGAAAGTCTCTGCAAAATAACAAACCTATCACTGTGTGACCC	5045	CAATTGATCTATCAAAAAGGCCCTGCTGAGGCGACCTGCTCTGGGCCCTCCCTGACGTAA	6125
QY	2521	TCCAAATTAGATGACGAATATCGACTATCTCTCCCTAGTAAAGCCGTGATCAAAATATAC	2580	CTAAACCCCTTTACCTTTATGTGGATGAGCGTAAGGGAGTAGCCCGGGAGTTTAAACCC	3660
Db	5046	TCCAAATTAGATGACGAATATCGACTATCTCTCCCTAGTAAAGCCGTGATCAAAATATAC	5105	CTAAACCCCTTTACCTTTATGTGGATGAGCGTAAGGGAGTAGCCCGGGAGTTTAAACCC	6185
QY	2581	AATTTCTGGTTGGAACAGTTTCCCAAGCCTGGGCAGAAACCGGAGGGATGGTTTGGCAA	2640	AAACCCCTAGGACCATGAGGAGACCTGTGCGCTACCTGTCAAAGAGCTCGATCCTGTAG	3720
Db	5106	AATTTCTGGTTGGAACAGTTTCCCAAGCCTGGGCAGAAACCGGAGGGATGGTTTGGCAA	5165	AAACCCCTAGGACCATGAGGAGACCTGTGCGCTACCTGTCAAAGAGCTCGATCCTGTAG	6245
QY	2641	AGCAAGTCCCCACAAAGTTATTCAACTGAAGCCAGTGCACACCAAGTGTCACTCAGAC	2700	CCAGTGGTTGGGCCCATATGCTGAAAGGCTATCGCAGCTGTGGCCCATATCTGGTCAAGGACG	3780
Db	5166	AGCAAGTCCCCACAAAGTTATTCAACTGAAGCCAGTGCACACCAAGTGTCACTCAGAC	5225	CCAGTGGTTGGGCCCATATGCTGAAAGGCTATCGCAGCTGTGGCCCATATCTGGTCAAGGACG	6305
QY	2701	AGTACCCCTTGAGTAAAGAGCTCAAGAAAGGAATTCGGCCGCAATGTCCAAGATTAAATCC	2760	CTGACAAATTTGACTTTTGGGAC--AGAAATAAATCTGTAATAAGCCCCCATGCAATTGGAGAAC	3839
Db	5226	AGTACCCCTTGAGTAAAGAGCTCAAGAAAGGAATTCGGCCGCAATGTCCAAGATTAAATCC	5285	CTGACAAATTTGACTTTTGGGACAAAGATAAATCTGTAATAAGCCCCCATGCAATTGGAGAAC	6365
QY	2761	AACAGGGATCTTAGTTCTGTCCTCAATCTCCCTGGAAATCTCCCTGCTACCGTTAGAA	2820	ATCGTTTCGACAGCCAGCCGATGATGACCAACCGCCGATGACCACTATCAAGC	3899
Db	5286	AACAGGGATCTTAGTTCTGTCCTCAATCTCCCTGGAAATCTCCCTGCTACCGTTAGAA	5345	ATCGTTTCGACAGCCGATGATGACCAACCGCCGATGACCACTATCAAGC	6425
QY	2821	AGCCTGGGACTAATGACTATCGACCAAGTACAGACTTGGAGAGGTCAATAACGGGTGC	2880	CTGCTTCTCACAGAGGGGTCAAGTTGCTCCACCAACCGCTCTCAACCTGCGCACTTT	3959
Db	5346	AGCCTGGGACTAATGACTATCGACCAAGTACAGACTTGGAGAGGTCAATAACGGGTGC	5405	CTGCTTCTCACAGAGGGGTCAAGTTGCTCCACCAACCGCTCTCAACCTGCGCACTTT	6485
QY	2881	AGGATATACACCCAAACAGTCCCGAACCTTTATAACCTCTTGTTGCTCTCCACCCCAAC	2940	CTGCTTCTCACAGAGGGGTCAAGTTGCTCCACCAACCGCTCTCAACCTGCGCACTTT	6485
Db	5406	AGGATATACACCCAAACAGTCCCGAACCTTTATAACCTCTTGTTGCTCTCCACCCCAAC	5465	CTGCTTCTCACAGAGGGGTCAAGTTGCTCCACCAACCGCTCTCAACCTGCGCACTTT	6485
QY	2941	GGAGCTGGTATACAGTATTGGACTTAAGAGTATGCTTCTTGCTGCTGAGATTACACCCCA	3000	CTGCTTCTCACAGAGGGGTCAAGTTGCTCCACCAACCGCTCTCAACCTGCGCACTTT	6485
Db	5466	GGAGCTGGTATACAGTATTGGACTTAAGAGTATGCTTCTTGCTGCTGAGATTACACCCCA	5525	CTGCTTCTCACAGAGGGGTCAAGTTGCTCCACCAACCGCTCTCAACCTGCGCACTTT	6485
QY	3001	CTAGCCAAACCACTTTTGGCTTCGAATGGAGAGTCCAGGTACGGGAAGAACCGGGCAGC	3060	CTGCTTCTCACAGAGGGGTCAAGTTGCTCCACCAACCGCTCTCAACCTGCGCACTTT	6485
Db	5526	CTAGCCAAACCACTTTTGGCTTCGAATGGAGAGTCCAGGTACGGGAAGAACCGGGCAGC	5585	CTGCTTCTCACAGAGGGGTCAAGTTGCTCCACCAACCGCTCTCAACCTGCGCACTTT	6485
QY	3061	TCACCTGGACCCGACTGCCCCAAGGGTTCAAGAACTCCCGACCATCTTTTGACGAAGCCC	3120	GGGACCCGCAAGTCTGGGCCAGCAGCTTGGCCGAAGGAACTTTTCAGCACAAAAAGGCTGAG	6725
Db	5586	TCACCTGGACCCGACTGCCCCAAGGGTTCAAGAACTCCCGACCATCTTTTGACGAAGCCC	5645	GGGACCCGCAAGTCTGGGCCAGCAGCTTGGCCGAAGGAACTTTTCAGCACAAAAAGGCTGAG	6725
QY	3121	TACACAGAGACCTGGCCAACTTCAGGATCCAAACACCTCAGGTGACCCCTCTCAGTACG	3180	CTCATGGCCCTCACGCAAGCTTTGCGGCTGGCCGAAGGGAAATTCATAAACATTTATACG	6785
Db	5646	TACACAGAGACCTGGCCAACTTCAGGATCCAAACACCTCAGGTGACCCCTCTCAGTACG	5705	CTCATGGCCCTCACGCAAGCTTTGCGGCTGGCCGAAGGGAAATTCATAAACATTTATACG	6785
QY	3181	TGGATCAGCTGCTTCTGGCGGAGCCAAACAGGACTGCTTTAGAGGACGACGAAGGCAC	3240	GAACGAGGTATGCGCTTTGCGACTGACACGTTACATGGGGCCATCTATAAACAAAGGGGG	6845
Db	5706	TGGATCAGCTGCTTCTGGCGGAGCCAAACAGGACTGCTTTAGAGGACGACGAAGGCAC	5765	GAACGAGGTATGCGCTTTGCGACTGACACGTTACATGGGGCCATCTATAAACAAAGGGGG	6845
QY	3241	TACTGCTGGAATTTGCTGACCTAGGCTTACAGAGCCTCTGCTAAGAGAGCCAGATTGCA	3300	TTGCTTAACTCTAGCGGGAGGGAATAAAGAAACAAAGAGGAATTTCTTAAGCCCTATTAGAA	6905
Db	5766	TACTGCTGGAATTTGCTGACCTAGGCTTACAGAGCCTCTGCTAAGAGAGCCAGATTGCA	5825	TTGCTTAACTCTAGCGGGAGGGAATAAAGAAACAAAGAGGAATTTCTTAAGCCCTATTAGAA	6905
QY	3301	GGAGAGAGGTAAATCTTTGGGGTACAGTTTGGGAGCGGGCAGCGATGGCTGACGGAGG	3360	GGCGTACATTTTACCAGGCTTAGCTATTATACCTGCTGGACATCAGAAAGCTAAA	4439
Db	5826	GGAGAGAGGTAAATCTTTGGGGTACAGTTTGGGAGCGGGCAGCGATGGCTGACGGAGG	5885	GGCGTACATTTTACCAGGCTTAGCTATTATACCTGCTGGACATCAGAAAGCTAAA	6965
QY	3361	CACGGAAGAAACTGTAGTCCAGATACCGGCCCAACCAAGCCCAACCAAGAGAGT	3420	GATCTCATATCCAGAGGAAACAGATGGCTGACCGGGTTGCCAAGCAGGCGAGCCAGGGT	4499
Db	5886	CACGGAAGAAACTGTAGTCCAGATACCGGCCCAACCAAGCCCAACCAAGAGAGT	5945	GATCTCATATCCAGAGGAAACAGATGGCTGACCGGGTTGCCAAGCAGGCGAGCCAGGGT	7025
				GTTAACTTCTGCTCTATATAAGAAATGCCCAAGCCCCAGAACCCAGACGAGTACACC	4559

Db	7026	GTAAACCTTCTGCTTAATAATAGAAATGCCCAAGCCCCAGAACCCAGACGACGTACACC	7085
Qy	4560	CTAGAGACTGGCAGAGATATAAAGATAGACAGTCTCTGAGACTCCGAGGAGACC	4619
Db	7086	CTAGAGACTGGCAGAGATATAAAGATAGACCA-TTCTCTGAGACTCCGAGGAGACC	7144
Qy	4620	TGCTATACCTCAGATGGGAAGAAATCCTGCCCCACAAAGAGGGTTAGAAATATGTCAA	4679
Db	7145	TGCTATACCTCAGATGGGAAGAAATCCTGCCCCACAAAGAGGGTTAGAAATATGTCAA	7204
Qy	4680	C-AGATACATGCTTAACCCACCTAGGAACCTAAACACCTGAGCAGTTGGTCAGAACATC	4738
Db	7205	CAAGATACATGCTTAACCCACCTAGGAACCTAAACACCTGAGCAGTTGGTCAGAACATC	7264
Qy	4739	CCCTTATCATGTTCTGAGGCTTACAGAGTGGCTGACTCGGTGGTCAAAATTTGTGGCC	4798
Db	7265	CCCTTATCATGTTCTGAGGCTTACAGAGTGGCTGACTCGGTGGTCAAAATTTGTGGCC	7324
Qy	4799	CTGCCAGCTGTTAATGCTAATCTCTCCAGAAATGCTTCCAGGGAAGAGACTAAGGGGAAG	4858
Db	7325	CTGCCAGCTGTTAATGCTAATCTCTCCAGAAATGCTTCCAGGGAAGAGACTAAGGGGAAG	7384
Qy	4859	CCACCCAGGCGCTCACTGGGAAGTGGACTTCACTGAGGTAAAGCCGCTAAATACGAAA	4918
Db	7385	CCACCCAGGCGCTCACTGGGAAGTGGACTTCACTGAGGTAAAGCCGCTAAATACGAAA	7444
Qy	4919	CAAAATCACTATGTTTTTTGTAGACACCTTTTCAAGATGGGTAGAGCTTATCTACTAA	4978
Db	7445	CAAAATCACTATGTTTTTTGTAGACACCTTTTCAAGATGGGTAGAGCTTATCTACTAA	7504
Qy	4979	GAAAGACATTCACCGTGGTGGCTTAAAGAAATCTGAAGAAATTTTCCAGATTTGG	5038
Db	7505	GAAAGACATTCACCGTGGTGGCTTAAAGAAATCTGAAGAAATTTTCCAGATTTGG	7564
Qy	5039	AATACCTAAGGTAATAGGGTCAGACAAATGGTCCAGCTTTTGTCCCGAGTAAGTCAGGG	5098
Db	7565	AATACCTAAGGTAATAGGGTCAGACAAATGGTCCAGCTTTTGTCCCGAGTAAGTCAGGG	7624
Qy	5099	ACTGGCCAAAGATATGGGGATTGATGGAAATCTGCATGCTGATACAGACCCCAAGCTC	5158
Db	7625	ACTGGCCAAAGATATGGGGATTGATGGAAATCTGCATGCTGATACAGACCCCAAGCTC	7684
Qy	5159	AGGACAGGTAGAGAGGATGATAGAACCATTAAGAGACCTTACTAAATTTGACCGCGGA	5218
Db	7685	AGGACAGGTAGAGAGGATGATAGAACCATTAAGAGACCTTACTAAATTTGACCGCGGA	7744
Qy	5219	GACTGGCGTTAATGATGGATAGCTCTCTGCCCTTTGTGCTTTTATAGGGTTAGGAACAC	5278
Db	7745	GACTGGCGTTAATGATGGATAGCTCTCTGCCCTTTGTGCTTTTATAGGGTTAGGAACAC	7804
Qy	5279	CCCTGGACAGTTTGGGCTGACCCCTATGAATTAATCTACGCGGGAACCCCCCAATGGT	5338
Db	7805	CCCTGGACAGTTTGGGCTGACCCCTATGAATTAATCTACGCGGGAACCCCCCAATGGT	7864
Qy	5339	AGAAATGCTTCTGTACATAGTGTGCTGCTGCTTCCAGCCTTTGTTCTCTAGCT	5398
Db	7865	AGAAATGCTTCTGTACATAGTGTGCTGCTTCCAGCCTTTGTTCTCTAGCT	7924
Qy	5399	CAAGGCACTTCAGTGGGTGAGACAACAGCGGTGGAGGCAACTCCGGGAGGCTTACTCAGG	5458
Db	7925	CAAGGCACTTCAGTGGGTGAGACAACAGCGGTGGAGGCAACTCCGGGAGGCTTACTCAGG	7984
Qy	5459	AGGAGGAGACTTGCAGATCCCAATCGTTTCCAAAGTGGGAGATTCAGTCTACGTTAGACG	5518
Db	7985	AGGAGGAGACTTGCAGATCCCAATCGTTTCCAAAGTGGGAGATTCAGTCTACGTTAGACG	8044
Qy	5519	CCACCGTCAGAGAAC	5534
Db	8045	CCACCGTCAGAGAAC	8060

RESULT 15

ADK43412

ID ADK43412 standard; cDNA; 8060 BP.

XX

AC ADK43412;

XX 20-MAY-2004 (first entry)

DT

XX Porcine retrovirus, Tsukuba-1, cDNA.

DE

XX swine retrovirus; gene; virus; transplantation;

KW miniature swine retrovirus; porcine retroviral infection;

KW porcine retrovirus; Tsukuba-1; ss.

XX

OS Porcine endogenous retrovirus; Tsukuba-1.

XX

PN US6699663-B1.

XX

PD 02-MAR-2004.

XX

PF 14-SEP-2000; 2000US-00661858.

XX

PR 14-DEC-1995; 95US-00572645.

PR 13-DEC-1996; 96US-00766528.

XX

PA (GEHO) GEN HOSPITAL CORP.

XX

PI Fishman JA;

XX

DR WPI; 2004-200897/19.

XX

PT New purified nucleic acid molecules that specifically hybridize with swine retroviral sequences, useful for detecting the presence of porcine retrovirus, e.g., for assessing the potential risk associated with the transplantation.

PT

XX Claim 2; SEQ ID NO 1; 82pp; English.

PS

XX

CC The invention relates to purified nucleic acid molecule that can specifically hybridise with the sequence of swine retroviruses. The nucleic acid is useful in methods for: determining the copy number or size of a porcine retrovirus from a human; screening a cell, tissue or a human being for the presence or expression of a porcine retrovirus or retroviral sequence; assessing the potential risk associated with the transplantation of a graft from a donor miniature swine or swine into a recipient animal or human; determining if an endogenous miniature swine or swine retrovirus or retroviral sequence genome includes a mutation that modulates its expression; providing a swine free of an endogenous retrovirus or retroviral sequence; evaluating a treatment for the ability to activate a retrovirus; localising the origin of a porcine retroviral infection; and inhibiting expression of an endogenous porcine retrovirus; and detecting a recombinant virus or other pathogens, e.g. protozoa or fungi. The present sequence represents porcine retrovirus, Tsukuba-1, cDNA.

CC

XX

SQ Sequence 8060 BP; 2233 A; 1959 C; 2012 G; 1856 T; 0 U; 0 Other;

Qy

Query Match 67.1%; Score 5460; DB 12; Length 8060;

Best Local Similarity 99.7%; Pred. No. 0;

Matches 5521; Conservative 0; Mismatches 10; Indels 5; Gaps 5;

Qy

1 GCGTGGTGTACGACTGTGGGCCCCAGCGCGCTTGGAAATAAAATCCTCTTCTGTTTGA 60

Db

2528 GCGTGGTGTACGACTGTGGGCCCCAGCGCGCTTGGAAATAAAATCCTCTTCTGTTTGA 2587

Qy

61 TCAAGACCGCTTCTCGTAGTGATTAAGGGAGTCGCTTTCCGAGCCTGAGGTTCTT 120

Db

2588 TCAAGACCGCTTCTCGTAGTGATTAAGGGAGTCGCTTTCCGAGCCTGAGGTTCTT 2647

Qy

121 TTTGCTGCTTACATTTGGGGCTCGTCCGGGATCTGTCCGGCCACCCCTAACACCCG 180

Db

2648 TTTGCTGCTTACATTTGGGGCTCGTCCGGGATCTGTCCGGCCACCCCTAACACCCG 2707

Qy

181 AGAACCGACTTGGAGGTAAAGGATCCTCTTTTAACTGTATGTCATGTACCGGCCGCG 240

Db	2708	AGAACCGACTGGAGGTAAAAAGGATCCTCTTTTAAACGTGTATGATGTACCGGCGGC	2767	Db	3788	CTAAACATCCCCCTTTCTCGAGAGGATCCCAAGCCTC	3847
Qy	241	GTCTCTGTTCTGAGTCTCTGTTTTTCAAGTGTGCGCGCTTTTCGTTTTGACAGTGTCTCTC	300	Qy	1321	TGTTCTCTCACCAGCCTACTTGGGATGATTGTCAACAGCTGTCTGACAGACACTCTTACAAA	1380
Db	2768	GTCTCTGTTCTGAGTGTCTGTTTTTCAAGTGTGCGCGCTTTTCGTTTTGACAGTGTCTCTC	2827	Db	3848	TGTTCTCTCACCAGCCTACTTGGGATGATTGTCAACAGCTGTCTGACAGACACTCTTACAAA	3907
Qy	301	AGGCCCTAAAGGGCTGGGGACCTGTGATCAGCAGACGTGCTAGGAGGATCACAGGCTGCTG	360	Qy	1381	CCGAGAGCGAGAGAAATTTCTATTAGAGGCTAGAAAAAATGTTCTCGGGCGGACGGGC	1440
Db	2828	AGGCCGTAAAGGGCTGGGGACCTGTGATCAGCAGACGTGCTAGGAGGATCACAGGCTGCTG	2887	Db	3908	CCGAGAGCGAGAGAAATTTCTATTAGAGGCTAGAAAAAATGTTCTCGGGCGGACGGGC	3967
Qy	361	CCCTGGGGACGCCCGGAGAGGTGAGAGAGCGCAGGAGCGCTGTGGTCTCTACTGTC	420	Qy	1441	GACCCACCGGTTGCAAAATGAGATTGACATCGGATTTCCCTTAACTCCGCCCGGTTGG	1500
Db	2888	CCCTGGGGACGCCCGGAGAGGTGAGAGAGCGCAGGAGCGCTGTGGTCTCTACTGTC	2947	Db	3968	GACCCACCGGTTGCAAAATGAGATTGACATCGGATTTCCCTTAACTCCGCCCGGTTGG	4027
Qy	421	GGTCAGAGACCGAAATCTGTTGCTGAAGCGAAGCTTCCCTCCGCGACCGTCCGACT	480	Qy	1501	ACTCAACACACGGCTGAAGGTAGGAGAGCTTGAATAATCTATCGCCAGGCTCTGGTGGCG	1560
Db	2948	GGTCAGAGACCGAAATCTGTTGCTGAAGCGAAGCTTCCCTCCGCGACCGTCCGACT	3007	Db	4028	ACTCAACACACGGCTGAAGGTAGGAGAGCTTGAATAATCTATCGCCAGGCTCTGGTGGCG	4087
Qy	481	CTTTTGCCTGCTTGTGGAAAGACGTGACCGGGTCACTGTGTCTGGATCTGTGGTTCTG	540	Qy	1561	GTCTCCGGGGCGCTCAAGACGGCCCACTAAATTTGGCTAAGGTAAAGAAAGTATGATCCAG	1620
Db	3008	CTTTTGCCTGCTTGTGGAAAGACGTGACCGGGTCACTGTGTCTGGATCTGTGGTTCTG	3067	Db	4088	GTCTCCGGGGCGCTCAAGACGGCCCACTAAATTTGGCTAAGGTAAAGAAAGTATGATCCAG	4147
Qy	541	TTTTTGTGTCTTGTGTGTGTCTTGTCTACAGTTTTTAATATGGACAGACGGTGA	600	Qy	1621	GACCGAATGAACCCCTCTGTTTTTCTTGAGAGGCTCTTGAAGCTTTCAGSCGTGACA	1680
Db	3068	TTTTTGTGTCTTGTGTGTGTCTTGTCTACAGTTTTTAATATGGACAGACGGTGA	3127	Db	4148	GACCGAATGAACCCCTCTGTTTTTCTTGAGAGGCTCTTGAAGCTTTCAGSCGTGACA	4207
Qy	601	CGACCCCTCTAGTTTGAATCTCGACCATTTGGACTGAAGTTAAATCCAGGGCTCAATAAT	660	Qy	1681	CCCCCTTTTGTATCCCACTCAGAGGGCCCAAAAAGCCCTCAGTGGCTTTGGCTTTTATAGGAC	1740
Db	3128	CGACCCCTCTAGTTTGAATCTCGACCATTTGGACTGAAGTTAAATCCAGGGCTCAATAAT	3187	Db	4208	CCCCCTTTTGTATCCCACTCAGAGGGCCCAAAAAGCCCTCAGTGGCTTTGGCTTTTATAGGAC	4267
Qy	661	TGTCAGTTTCAAGGAGGACCTTGGCAGACTTTTCTGTCTCTGATGCGCCGACAT	720	Qy	1741	AGTCAGCCTTGGATATTAGAAAGAGCTTTCAGAGACTGGAAGGTTTACAGAGGCTTGAGT	1800
Db	3188	TGTCAGTTTCAAGGAGGACCTTGGCAGACTTTTCTGTCTCTGATGCGCCGACAT	3247	Db	4268	AGTCAGCCTTGGATATTAGAAAGAGCTTTCAGAGACTGGAAGGTTTACAGAGGCTTGAGT	4327
Qy	721	TGATTTGGATGGCCATCAGAGGGGACCTTTAAATTTCTGAGATTATCTGGCTGTAAAG	780	Qy	1801	TACGTGATCTAGTGAAGGAGGAGAGAAAGTATATTACAAAAGGGAGACAGAGAGAGAAA	1860
Db	3248	TGATTTGGATGGCCATCAGAGGGGACCTTTAAATTTCTGAGATTATCTGGCTGTAAAG	3307	Db	4328	TACGTGATCTAGTGAAGGAGGAGAGAAAGTATATTACAAAAGGGAGACAGAGAGAGAAA	4387
Qy	781	CAGTTATTTTTCAGACTGGACCGGCTCTCATCCCGATCAGGAGCCCTATATCTTACCT	840	Qy	1861	GGGAAACAAAGAAAG	1920
Db	3308	CAATTAATTTTTCAGACTGGACCGGCTCTCATCCCGATCAGGAGCCCTATATCTTACCT	3367	Db	4388	GGGAAACAAAGAAAG	4447
Qy	841	GGCAAGATTGGCAGAGGATCTCTCGCCATGGGTTAAACCATGGCTGAATAAGCCAAAGAA	900	Qy	1921	AGAAAGATTGACTAAGATCTTGGCTGCACTGGTGTGAAGGAGAGAGAGAGAGAGAGAGAG	1980
Db	3368	GGCAAGATTGGCAGAGGATCTCTCGCCATGGGTTAAACCATGGCTGAATAAGCCAAAGAA	3427	Db	4448	AGAAAGATTGACTAAGATCTTGGCTGCACTGGTGTGAAGGAGAGAGAGAGAGAGAGAGAG	4507
Qy	901	AGCCAGTCCCGAATTTCTGGCTCTTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	960	Qy	1981	AGAGAGATTTTAGGAGAAATTTAGTTCAGGCCCTTAGACAGTCAGGAGACCTGGGCAATAGGA	2040
Db	3428	AGCCAGTCCCGAATTTCTGGCTCTTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	3487	Db	4508	AGAGAGATTTTAGGAGAAATTTAGTTCAGGCCCTTAGACAGTCAGGAGACCTGGGCAATAGGA	4567
Qy	961	AGCCCTCTCTCATATCTACCCGAGATTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	1020	Qy	2041	CCCCACTCGACAG	2100
Db	3488	AGCCCTCTCTCATATCTACCCGAGATTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	3547	Db	4568	CCCCACTCGACAG	4627
Qy	1021	CTGTTCCTCCACCCCTTATCTGGCAGAGGTCGCGAGGGAGCCCTTTTGGCCCTCTCTG	1080	Qy	2101	GCCCCAAG	2160
Db	3548	CTGTTCCTCCACCCCTTATCTGGCAGAGGTCGCGAGGGAGCCCTTTTGGCCCTCTCTG	3607	Db	4628	GCCCCAAG	4687
Qy	1081	GAGCTCCGCGGTGGAGGACCTGTCTGAGGGATCTCGAGAGAGAGAGAGAGAGAGAGAGAG	1140	Qy	2161	GGAGAGCGGGTTTGGAG	2220
Db	3608	GAGCTCCGCGGTGGAGGACCTTCTGAGGGATCTCGAGAGAGAGAGAGAGAGAGAGAGAG	3667	Db	4688	GGAGAGCGGGTTTGGAG	4747
Qy	1141	AGCGGACAGACGAGATCGGACATTAACCGTGGCAGAGTACGGCCCTCCACACCGGGGG	1200	Qy	2221	CAGTTGAGTCTCTGGTTGATACCGAGCGAAACATTTCACTGTCTACTACAGCCATTAGGAA	2280
Db	3668	AGCGGACAGACGAGATCGGACATTAACCGTGGCAGAGTACGGCCCTCCACACCGGGGG	3727	Db	4748	CAGTTGAGTCTCTGGTTGATACCGAGCGAAACATTTCACTGTCTACTACAGCCATTAGGAA	4807
Qy	1201	GCCAAATGACGCCCTCCAGTATTTGGCCCTTTTCTGACAGATCTCTAATTTGAAAAA	1260	Qy	2281	AATAAAGATAAAAATCCTGGGTGATGGGTGCCACAGGGCAACAAACATGATTCATGGA	2340
Db	3728	GCCAAATGACGCCCTCCAGTATTTGGCCCTTTTCTGACAGATCTCTAATTTGAAAAA	3787	Db	4808	AATAAAGATAAAAATCCTGGGTGATGGGTGCCACAGGGCAACAAACATGATTCATGGA	4866
Qy	1261	CTAACCATCCCCCTTTCTCGAGGATCCCAACCGCTCTACGGGGTTGGTGGATCCCTTA	1320	Qy	2341	CTACCCGAGACAGTTGAGTCTGGGAGTGGGAGCGGTACCCACTCGTTTCTGCTCATAC	2400
				Db	4867	CTACCCGAGAG-ACAGTTGACTTTGGGAGTGGGAGCGGTAAACCCACTCGTTTCTGCTCATAC	4925

Qy	2401	CTGAGTCCCGACACCCCTCTTAGGTAGAGACTTATTGACAAAGATGGGAGCACAAATTT	2460	3481	CACCTACCCGCTAAACAAAGAAAAAGGGGAATTTCTCTGGGCTCTCTGAGCACCAGAGG	3540
Db	4926	CTGAGTCCCGACACCCCTCTTAGGTAGAGACTTATTGACAAAGATGGGAGCACAAATTT	4985	6006	CACCTACCCGCTAAACAAAGAAAAAGGGGAATTTCTCTGGGCTCTCTGAGCACCAGAGG	6065
Qy	2461	CTTTTGAACAAAGGGAACCAAGAGTGTCTGCAATAACAAACCTATCACTGTGTGACCC	2520	3541	CATTTGATGCTATCAAAAGGCCCTGCTGAGCGCACCTGCTCTGGCCCTCCCTGACGTAA	3600
Db	4986	CTTTTGAACAAAGGGAACCAAGAGTGTCTGCAATAACAAACCTATCACTGTGTGACCC	5045	6066	CATTTGATGCTATCAAAAGGCCCTGCTGAGCGCACCTGCTCTGGCCCTCCCTGACGTAA	6125
Qy	2521	TCCAAATAGATGAGCAATATCGACTACTCTCCCTTAGTAAAGCCTGATCAAAATATAC	2580	3601	CTAAAACCCCTTTACCTTTTATGTGATGAGCGTAAAGGAGTAGCCCGGGAGTTTAAACCC	3660
Db	5046	TCCAAATAGATGAGCAATATCGACTACTCTCCCTTAGTAAAGCCTGATCAAAATATAC	5105	6126	CTAAAACCCCTTTACCTTTTATGTGATGAGCGTAAAGGAGTAGCCCGGGAGTTTAAACCC	6185
Qy	2581	AATTTCTGTTGGAAACAGTTTCCCAAGCTGGGAGCAAAACCGCAGGATGGGTTTGGCAA	2640	3661	AAACCCCTAGGACCATGAGAGAACCTGTGCGCTACCTGTCAAAGAGCTCGATCCTGTAG	3720
Db	5106	AATTTCTGTTGGAAACAGTTTCCCAAGCTGGGAGCAAAACCGCAGGATGGGTTTGGCAA	5165	6186	AAACCCCTAGGACCATGAGAGAACCTGTGCGCTACCTGTCAAAGAGCTCGATCCTGTAG	6245
Qy	2641	AGCAAGTTCGCCCAACAAGTTATTCAACTGAAGGCCAGTGCACACCAAGTGTGAGTCAGAC	2700	3721	CCAGTGGTGGGCCCATATGCTCGAAGCTATCGCAGCTGTGGCCTACTGTGTAAGGACG	3780
Db	5166	AGCAAGTTCGCCCAACAAGTTATTCAACTGAAGGCCAGTGCACACCAAGTGTGAGTCAGAC	5225	6246	CCAGTGGTGGGCCCATATGCTCGAAGCTATCGCAGCTGTGGCCTACTGTGTAAGGACG	6305
Qy	2701	AGTACCCCTTGAGTAAAGAGCTCAAGAGGAATTCGGCCGCATGTCCAAGATTATATCC	2760	3781	CTGACAAATTTGACTTTTGGGAC-AGAAATATACTGTATATAGCCCCCCTATGATGGAGAAC	3839
Db	5226	AGTACCCCTTGAGTAAAGAGCTCAAGAGGAATTCGGCCGCATGTCCAAGATTATATCC	5285	6306	CTGACAAATTTGACTTTTGGGACAGAAATATACTGTATATAGCCCCCCTATGATGGAGAAC	6365
Qy	2761	AACAGGCACTCTAGTTCCCTGTCCAATCTCCCTGGAATACTCCCTCTGACCGGTTAGAA	2820	3840	ATCGTTGGCAGCCCCCAGACCCGATGATGACAAACCCCGCATGACCCATATCAAAGC	3899
Db	5286	AACAGGCACTCTAGTTCCCTGTCCAATCTCCCTGGAATACTCCCTCTGACCGGTTAGAA	5345	6366	ATCGTTGGCAGCCCCCAGACCCGATGATGACAAACCCCGCATGACCCATATCAAAGC	6425
Qy	2821	AGCCTGGGACTAATGACTATCGACAGTACAGGACTTGGAGAGGTCATAAACCGGTGC	2880	3900	CTGCTTCTCAGAGAGGGTCACTGTCGCTCCACAGCGCTCTCAACCCCTGCCACTCTT	3959
Db	5346	AGCCTGGGACTAATGACTATCGACAGTACAGGACTTGGAGAGGTCATAAACCGGTGC	5405	6426	CTGCTTCTCAGAGAGGGTCACTGTCGCTCCACCAACCGCTCTCAACCCCTGCCACTCTT	6485
Qy	2881	AGGATATACACCAACAGTCCGAAACCTTATAACCTTGTGTGCTCTCCACCCCAAC	2940	3960	CTGCTGAAGAGACTGATGAACCAAGTCACTCATGATGGCCATCAATATTGATTTAGGAGAG	4019
Db	5406	AGGATATACACCAACAGTCCGAAACCTTATAACCTTGTGTGCTCTCCACCCCAAC	5465	6486	CTGCTGAAGAGACTGATGAACCAAGTCACTCATGATGGCCATCAATATTGATTTAGGAGAG	6545
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GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

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Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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1: gb_ba.*
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15: gb_pl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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5	8039.8	98.9	8132 4 AF038599 Sus scrofa
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7	7263.8	89.3	8305 13 AY953542 Porcine e
8	6931.2	85.2	8918 6 AX546207 Sequence
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11	6822.2	83.9	8918 13 PEN279056 Porcine e
12	6746.2	83.0	8849 13 PEN133817 Porcine e
13	6727	82.7	8714 13 AY093323 Porcine e
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15	6502.8	80.0	8911 13 AF435967 Porcine e
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ALIGNMENTS

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DEFINITION Sequence 3 from patent US 6190861.
ACCESSION AR130475
VERSION AR130475.1 GI:14118800
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 8132)
AUTHORS Fishman,J.A.
TITLE Molecular sequences of swine retroviruses method of using
JOURNAL Patent: US 6190861-A 3 20-FEB-2001; ✓
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source location/Qualifiers
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/organism="unknown"
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ORIGIN			
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Db	61	TCAAGACCGCTTCTCGTAGTGATTAAGGGGAGTCGCTTTTCCGAGCGCTGAGGTTCTT	120
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Db	121	TTTCTGCTCTTACATTTGGGGGCTCGTCCGGGATCTGTCGGGCGCACCCCTAACACCG	180
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THE GENERAL HOSPITAL CORPORATION (US)

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ORIGIN

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VERSION AR478286.1 GI:47236938
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SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 8132)
AUTHORS Fishman,J.A.
TITLE Molecular sequence of swine retrovirus
JOURNAL Patent: US 6699663-AV3 02-MAR-2004;
The General Hospital Corporation; Boston, MA
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DB 2761 AACAGGGCATCTAGTTCCTGCTCCCAATCTCCCTGGAAATCTCCCTGCTACCGGTTAGAA 2820
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Qy	4081	CT	GACGGAGCAGCTATGTGGTGGAAAGTAAAGAGATGCTGGGGCGGGTGGTGGACG	4140
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Db	4621	GC	TATACCTCAGATGGGAAGAAATCTGCGCCACAAAGAGGGTTAGATATGTCCAAC	4680
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Qy	4981	AA	GAGACTTCAACCGTGGCTGCTAAAAAATACTGGAAGAAAAATTTTTTCCAAGATTTGGA	5040
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RESULT 4	AF038600	Sus scrofa porcine endogenous retrovirus PERV-MSL mRNA, complete	
LOCUS	AF038600	8132 bp mRNA linear MAM 21-MAY-1998	
DEFINITION	AF038600	sequence.	
ACCESSION	AF038600		
VERSION	AF038600.1	Gr:3133301	
KEYWORDS			
SOURCE	Sus scrofa (pig)		
ORGANISM	Sus scrofa		

REFERENCE	1 (bases 1 to 8132)	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae; Sus.
AUTHORS	Akiyoshi,D.E., Denaro,M., Zhu,H., Greenstein,J.L., Banerjee,P. and Fishman,J.A.	
TITLE	Identification of a full-length cDNA for an endogenous retrovirus of miniature swine	
JOURNAL	J. Virol. 72 (5): 4503-4507 (1998)	
PUBMED	9557749	
REFERENCE	2 (bases 1 to 8132)	
AUTHORS	Fishman,J.A.	
TITLE	Direct Submission	
JOURNAL	Submitted (16-DEC-1997) Infectious Disease Unit, Massachusetts General Hospital, 55 Fruit Street, Boston, MA 02114, USA	
REFERENCE	3 (bases 1 to 8132)	
AUTHORS	Fishman,J.A.	
TITLE	Direct Submission	
JOURNAL	Submitted (15-MAY-1998) Infectious Disease Unit, Massachusetts General Hospital, 55 Fruit Street, Boston, MA 02114, USA	
REMARK	Sequence update by submitter	
COMMENT	On May 16, 1998 this sequence version replaced gi:3116441.	
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Dd	4327	TTGCTTACTCAGCAGGAGGGAATAAAGAACAAAGAGGAAATTTCTAAGCCTATTAGAA	4386			
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Dd	4507	GTTAACTTCTGCTCTATA	TAGAAATGCCAAAGCCCCAGAACCCAGACGACAGTACACC	4566		
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Dd	4746	CCCTTATCATGTTCTCAGGCT	ACCAGAGTGGCTGACTCGGTGGTCAAAATTTGTGTGCC	4805		
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RESULT 6	
AY570980	8188 bp DNA linear VRL 26-NOV-2004
LOCUS	Porcine endogenous retrovirus C/A gag protein gene, complete cds;
DEFINITION	pol protein gene, partial cds, and env protein gene, complete cds.
ACCESSION	AY570980
VERSION	AY570980.1 GI:50429161
KEYWORDS	
SOURCE	Porcine endogenous retrovirus C/A
ORGANISM	Porcine endogenous retrovirus C/A
REFERENCE	Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae; Gammaretrovirus; 1-Mammalian type C virus group. 1 (bases 1 to 8188)
AUTHORS	Bartosch,B., Stefanidis,D., Myers,R., Weiss,R., Patience,C. and Takeuchi,Y.
TITLE	Evidence and Consequence of Porcine Endogenous Retrovirus Recombination
JOURNAL	J. Virol. 78 (24), 13880-13890 (2004)
PUBMED	15564496
REFERENCE	2 (bases 1 to 8188)
AUTHORS	Bartosch,B., Patience,C., Weiss,R. and Takeuchi,Y.
TITLE	Direct Submission
JOURNAL	Submitted (11-MAR-2004) Wohl Virion Centre, Windeyer Institute, UCL, 46 Cleveland Str, London W1R4JF, UK
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Dd	500	TCTTTTGCCTGCTGTAAGACGTGGACGGGTCAAGTGTCTGATCTCTGTTGTTCT	559	Dd	1580	GGTCTCCGGGGCGCTCAAGACGCCCACTAATTTGGCTAAGTAAAGAGAGTATGATGAG	1639
Qy	540	GTTTTGTGCTGTTTGTCTGTGCTCTGTCTACAGTTTTAAATATGGGACAGACGGTG	599	Qy	1620	GGACCGAATGAACCCCTCTGTTTTTCTTGAGAGGCTCTTGGAGGCTTCAAGGGGTAC	1679
Dd	560	GTTTTGTGCTGTTTGTCTGTGCTCTGTCTACAGTTTTAAATATGGGACAGACGGTG	619	Dd	1640	GGACCGAATGAACCCCTCTGTTTTTCTTGAGAGGCTCTTGGAGGCTTCAAGGGGTAC	1699
Qy	600	ACGACCCCTTTAGTGTGACTCTGACCAATTGGAAGTGAAGTTAAATCCAGGCTCATAT	659	Qy	1680	ACCCCTTTTGATCCACCTCAGAGGCCCAAAAGCCTCAGTGGCTTTGGCCCTTTATAGGA	1739
Dd	620	ACGACCCCTTTAGTGTGACTCTGACCAATTGGAAGTGAAGTTAAATCCAGGCTCATAT	679	Dd	1700	ACCCCTTTTGATCCACCTCAGAGGCCCAAAAGCCTCAGTGGCTTTGGCCCTTTATAGGA	1759
Qy	660	TGTGAGTTCAGTTAAAGAGGACCTTGGCAGACTTCTGTCTCTGATCTGATGAGGAGCA	719	Qy	1740	CAGTCAGCCTTTGGATATTAGAAAAGAGCTTCAGAGACTTGAAGGGTTTACAGAGGCTGAG	1799
Dd	680	TGTGAGTTCAGTTAAAGAGGACCTTGGCAGACTTCTGTCTCTGATCTGATGAGGAGCA	739	Dd	1760	CAGTCAGCCTTTGGATATTAGAAAAGAGCTTCAGAGACTTGAAGGGTTTACAGAGGCTGAG	1819
Qy	720	TTCGATGTTGGATGCCATCAGAGGGACCTTTAATCTGAGATTATCTGGCTGTTAAA	779	Qy	1800	TTAGCTGATCTAGTGAAGGAGAGAAAGTATATTACAAAAGGGAGACAGAGAAGAA	1859
Dd	740	TTCGATGTTGGATGCCATCAGAGGGACCTTTAATCTGAGATTATCTGGCTGTTAAA	799	Dd	1820	TTAGCTGATCTAGTGAAGGAGAGAAAGTATATTACAAAAGGGAGACAGAGAAGAA	1879
Qy	780	GCAGTTATTTTTCAGATGGAACCGGCTCTCATCCGATCAGGAGCCCTATATCCTTACG	839	Qy	1860	AGGAAACAAAGAAAG	1919
Dd	800	GCAATTTATTTTTCAGATGGAACCGGCTCTCATCCGATCAGGAGCCCTATATCCTTACG	859	Dd	1880	AGGAAACAAAGAAAG	1939
Qy	840	TGGGAAGATTTGGCAGAGATCTCTCGCATGGGTAAACCATGGCTGAATTAAGCAAGA	899	Qy	1920	GAGAAATTTTGAATTAAGATCTTGGCTGCACTGTTGAAGGGAAAAGCAATACGGAAGA	1979
Dd	860	TGGCAAGATTTGGCAGAGATCTCTCGCATGGGTAAACCATGGCTGAATTAAGCAAGA	919	Dd	1940	GAGAAATTTTGAATTAAGATCTTGGCTGCACTGTTGAAGGGAAAAGCAATACGGAAGA	1999
Qy	900	AAGCCAGTCCCGGAATTTGCTCTTGGAGAGAAAAACAACACTCGGCTGMAAAGTC	959	Qy	1980	GAGAGATTTTGAAGAAATTTAGTTCAGGCCCTAGACAGTCAAGGAACTCTGGGCAATAGG	2039
Dd	920	AAGCCAGTCCCGGAATTTGCTCTTGGAGAGAAAAACAACACTCGGCTGMAAAGTC	979	Dd	2000	GAGAGATTTTGAAGAAATTTAGTTCAGGCCCTAGACAGTCAAGGAACTCTGGGCAATAGG	2059
Qy	960	AAGCCCTCTCTCATATCTACCCCGAGATTGAGGAGCCACCGGCTTGGCCGGAACCCCAA	1019	Qy	2040	ACCCCTCTCGACAGGACCAATGTCTAATTTGAAGAAAGAGGACACTTGGGCAAGGAC	2099
Dd	980	AAGCCCTCTCTCATATCTACCCCGAGATTGAGGAGCCACCGGCTTGGCCGGAACCCCAA	1039	Dd	2060	ACCCCTCTCGACAGGACCAATGTCTAATTTGAAGAAAGAGGACACTTGGGCAAGGAC	2119
Qy	1020	TCTGTTCCGCCACCCCTTATCTGGACAGGGTGGCGAGGGACCCCTTTGGCCCTCTCT	1079	Qy	2100	TGCCCAAGAGGGAAAACAAAGGACCAAGGATCTTAGCTCTAGAGAAAGATTAAGATTAG	2159
Dd	1040	TCTGTTCCGCCACCCCTTATCTGGACAGGGTGGCGAGGGACCCCTTTGGCCCTCTCT	1099	Dd	2120	TGCCCAAGAGGGAAAACAAAGGACCAAGGATCTTAGCTCTAGAGAAAGATTAAGATTAG	2179
Qy	1080	GGAGTCCGGCGGTGGAGGACCTGTCAGGAGCTCGGAGCGGAGGGGCGCACCCCG	1139	Qy	2160	GGGAGACGGGGTTCCGACCCCTCTCCGAGCCAGGGTAACTTTGAAGGTTGAGGGGCA	2219
Dd	1100	GGAGTCCGGCGGTGGAGGACCTGTCAGGAGCTCGGAGCGGAGGGGCGCACCCCG	1159	Dd	2180	GGGAGACGGGGTTCCGACCCCTCTCCGAGCCAGGGTAACTTTGAAGGTTGAGGGGCA	2239
Qy	1140	GAGCGGACAGAGAGATTCGACATTTACCGCTGCGCAGTACGGCCCTCCACACCGGGG	1199	Qy	2220	CGAGTTGAGTTCTGTTGATACCGGAGCGAAACATTCAGTGTCTACTACAGCCATTAGGA	2279
Dd	1160	GAGCGGACAGAGAGATTCGACATTTACCGCTGCGCAGTACGGCCCTCCACACCGGGG	1219	Dd	2240	CGAGTTGAGTTCTGTTGATACCGGAGCGAAACATTCAGTGTCTACTACAGCCATTAGGA	2299
				Qy	2280	AAACTAAAAGATAAAAAATCCTGGGTGATGGTGCCACAGGGCAACACAGTATCCATGG	2339

Db	2300	AAACTAAAGATTAATAAAATCTCTGGGTGATGGGTGCCACAGGGCAAACAACAGTATTATATG 2359	Db	3380	GCACGGAAGAAAACCTGTAGTCCAGATACCGGGCCCCAACCAACAGCCAAAACAAATGAGAGAG 3439
Qy	2340	ACTACCGAAGAAACAGTGTGACTTTGGGAGTGGGACGGGTAAACCCATCGTGTTCGTGTCATA 2399	Qy	3420	TTTTTGGGACAGCTGGATTTTTTGCAGACTGTGTATCCCGGGGTTTTCGACCTTTAGCAGCC 3479
Db	2360	ACTACCGAAGAAACAGTGTGACTTTGGGAGTGGGACGGGTAAACCCATCGTGTTCGTGTCATA 2419	Db	3440	TTTTTGGGACAGCTGGATTTTTTGCAGACTGTGTATCCCGGGGTTTTCGACCTTTAGCAGCC 3499
Qy	2400	CTGTAGTCCGACGACCCCTCTTAGTGTAGAGACTTATTGACCAAGATGGGAGCACAAAT 2459	Qy	3480	CCACTCTACCCGCTAACCAAGAAAAGGGGAATTTCTCTGGGCTCTCTGAGCACCAAGAG 3539
Db	2420	CCTGAGTGGCCACGACCCCTCTTAGTGTAGAGACTTATTGACCAAGATGGGAGCACAAAT 2479	Db	3500	CCACTCTACCCGCTAACCAAGAAAAGGGGAATTTCTCTGGGCTCTCTGAGCACCAAGAG 3559
Qy	2460	TCCTTTTGAACAAGGAAACAGAAAGTGTCTGCAAAATAACAAACCTATCACTGTGTGACC 2519	Qy	3540	GCATTTGATGCTATCAAAAAGGCCCTGTCTGAGGACCTGTCTCTGGCCCTCCCTGACGTA 3599
Db	2480	TCCTTTTGAACAAGGAAACAGAAAGTGTCTGCAAAATAACAAACCTATCACTGTGTGACC 2539	Db	3560	GCATTTGATGCTATCAAAAAGGCCCTGTCTGAGGACCTGTCTCTGGCCCTCCCTGACGTA 3619
Qy	2520	CTCAATTTAGATGACGAATATCGACTATATCTCTCCCTAGTAAAGCTGATCAAAATATA 2579	Qy	3600	ACTAAACCTTTTACCCCTTTATGTGGATGAGCGTAAAGGAGTAGCCCGGGAGTTTTAAACC 3659
Db	2540	CTCAATTTAGATGACGAATATCGACTATATCTCTCCCTAGTAAAGCTGATCAAAATATA 2599	Db	3620	ACTAAACCTTTTACCCCTTTATGTGGATGAGCGTAAAGGAGTAGCCCGGGAGTTTTAAACC 3679
Qy	2580	CAATTTCTGGTTGGAAACAGTTTTCCCAAGCCTGGGCGAGAAACCGGAGGGATGGTTGGCA 2639	Qy	3660	CAAAACCTTAGGACCAATGGAAGACCTGTCTGCCCTACTCTCTCAAAAGAGCTCGATCCTGTA 3719
Db	2600	CAATTTCTGGTTGGAAACAGTTTTCCCAAGCCTGGGCGAGAAACCGGAGGGATGGTTGGCA 2659	Db	3680	CAAAACCTTAGGACCAATGGAAGACCTGTCTGCCCTACTCTCTCAAAAGAGCTCGATCCTGTA 3739
Qy	2640	AAGCAAGTTCCTCCACACAGTTATTCAACTGAAGCCAGTGCACACACAGTGTCAAGTCAGA 2699	Qy	3720	GCAGTGGTTGGCCCATATATGCTTGAAGGCTATGCGAGCTGTGGCCCATATCTGTCAAGGAC 3779
Db	2660	AAGCAAGTTCCTCCACACAGTTATTCAACTGAAGCCAGTGCACACACAGTGTCAAGTCAGA 2719	Db	3740	GCAGTGGTTGGCCCATATATGCTTGAAGGCTATGCGAGCTGTGGCCCATATCTGTCAAGGAC 3799
Qy	2700	CAGTACCCCTTGTAGTAAAGAGCTCAAGAAGGAATTCGGCGCGATGTCCTCAAGATTAATC 2759	Qy	3780	GCTGACAAATTTGACTTTTGGGACAGAAATATACTGTATAGCCCCCATGTCATTTGGAGAAC 3839
Db	2720	CAGTACCCCTTGTAGTAAAGAGCTCAAGAAGGAATTCGGCGCGATGTCCTCAAGATTAATC 2779	Db	3800	GCTGACAAATTTGACTTTTGGGACAGAAATATACTGTATAGCCCCCATGTCATTTGGAGAAC 3859
Qy	2760	CAACAGGGCATCTCTAGTCTCTGTCCTCAATCTCCCTGGAATATCTCCCTGTCTACCGTTAGA 2819	Qy	3840	ATCGTTTCGGCAGCCCGACAGACCGATGGATGACCAACGCGCGCATGACCCACTATCAAGC 3899
Db	2780	CAACAGGGCATCTCTAGTCTCTGTCCTCAATCTCCCTGGAATATCTCCCTGTCTACCGTTAGA 2839	Db	3860	ATCGTTTCGGCAGCCCGACAGACCGATGGATGACCAACGCGCGCATGACCCACTATCAAGC 3919
Qy	2820	AAGCCTGGGACTAATGACTATCGACAGTACAGGACTTGAGAGGTCATTAACGGGTG 2879	Qy	3900	CTGCTTCTCACAGAGGGTTCAGTTCGTTCCACAGCGCTCTCAACCTCGCCACTCTT 3959
Db	2840	AAGCCTGGGACTAATGACTATCGACAGTACAGGACTTGAGAGGTCATTAACGGGTG 2899	Db	3920	CTGCTTCTCACAGAGGGTTCAGTTCGTTCCACAGCGCTCTCAACCTCGCCACTCTT 3979
Qy	2880	CAGGATATACCCCAACAGTCCCGAACCTTTATACCTCTTTGTGTCTCTCCACCCCAA 2939	Qy	3960	CTGCTTGAAGAGACTGATGAACCAAGTACTCATGATGTCATCACTCACTATTGATTGAGGAG 4019
Db	2900	CAGGATATACCCCAACAGTCCCGAACCTTTATACCTCTTTGTGTCTCTCCACCCCAA 2959	Db	3980	CTGCTTGAAGAGACTGATGAACCAAGTACTCATGATGTCATCACTCACTATTGATTGAGGAG 4039
Qy	2940	CGGAGCTGGTATACAGTATTGGAACTTAAAGATGCTTCTCTGCTGAGATTAACCC 2999	Qy	4020	ACTGGGCTCGCAAGGACCTTACAGACATACCGCTGACTGCGAGAGTGCTTAAACCTGTTTC 4079
Db	2960	CGGAGCTGGTATACAGTATTGGAACTTAAAGATGCTTCTCTGCTGAGATTAACCC 3019	Db	4040	ACTGGGCTCGCAAGGACCTTACAGACATACCGCTGACTGCGAGAGTGCTTAAACCTGTTTC 4099
Qy	3000	ACTAGCCAAACACTTTTTCGCTTTCGAATGGAGATCCAGTACGGGAGAACCGGGCAG 3059	Qy	4080	ACTGACGGAAGCAGCTATGTGTGGAGGTAAAGAGATGCTGGGGCGGGTGGTGAC 4139
Db	3020	ACTAGCCAAACACTTTTTCGCTTTCGAATGGAGATCCAGTACGGGAGAACCGGGCAG 3079	Db	4100	ACTGACGGAAGCAGCTATGTGTGGAGGTAAAGAGATGCTGGGGCGGGTGGTGAC 4159
Qy	3060	CTACCTGGACCGGACTGCCCAAGGGTTCAAGAACTCCCGACCATCTTTGACGAAGCC 3119	Qy	4140	GGGACCCGACGATCTGGGCCAGCAGCTCGCGGAGGAATCTTTCAGACAAAAGGCTGAG 4199
Db	3080	CTACCTGGACCGGACTGCCCAAGGGTTCAAGAACTCCCGACCATCTTTGACGAAGCC 3139	Db	4160	GGGACCCGACGATCTGGGCCAGCAGCTCGCGGAGGAATCTTTCAGACAAAAGGCTGAG 4219
Qy	3120	CTACACAGAGACCTGGCCAACTTTCAGGATCCAAACCCCTCAGGTGACCTCTCCAGTAC 3179	Qy	4200	CTCATGGCCCTCAGCAAGCTTTTGGGCTCGCGCGAGGGAATCCATAAATATTATACG 4259
Db	3140	CTACACAGAGACCTGGCCAACTTTCAGGATCCAAACCCCTCAGGTGACCTCTCCAGTAC 3199	Db	4220	CTCATGGCCCTCAGCAAGCTTTTGGGCTCGCGCGAGGGAATCCATAAATATTATACG 4279
Qy	3180	GTGATGACCTGCTTCTGGCGGAGCCACCAAAACAGGACTGCTTAGAAGGACCAAGGCA 3239	Qy	4260	GACAGCAGGTATGCTTTTGGGATGACACGATACATGGGGCCATCTATAACAAAGGGGG 4319
Db	3200	GTGATGACCTGCTTCTGGCGGAGCCACCAAAACAGGACTGCTTAGAAGGACCAAGGCA 3259	Db	4280	GACAGCAGGTATGCTTTTGGGATGACACGATACATGGGGCCATCTATAACAAAGGGGG 4339
Qy	3240	CTACTGCTGGAATTTGCTGACTAGGCTACAGAGCTCTGCTAAGAGGCCAGATTTCG 3299	Qy	4320	TTGCTTACCTCAGCAGGGAGGGAATAAAGAAACAAAGAGGAATTTCTAAGCCTATTAGAA 4379
Db	3260	CTACTGCTGGAATTTGCTGACTAGGCTACAGAGCTCTGCTAAGAGGCCAGATTTCG 3319	Db	4340	TTGCTTACCTCAGCAGGGAGGGAATAAAGAAACAAAGAGGAATTTCTAAGCCTATTAGAA 4399
Qy	3300	AGGAGAGAGGTAAACATCTTGGGGTACAGTTTGGGGACGGGACCGATGCTGACGGAG 3359	Qy	4380	GCCGTATATTACCAAAAGGCTAGCTATTATACACTGTCTGACATCAGAAAGCTAAA 4439
Db	3320	AGGAGAGAGGTAAACATCTTGGGGTACAGTTTGGGGACGGGACCGATGCTGACGGAG 3379	Db	4400	GCCGTATATTACCAAAAGGCTAGCTATTATACACTGTCTGACATCAGAAAGCTAAA 4459
Qy	3360	GCACGGAAGAAAACCTGTAGTCCAGATACCGGGCCCCAACCAACAGCCAAAACAAATGAGAGAG 3419	Qy	4440	GATCTCATATCCAGAGGAAACAGATGGCTGACCGGGTTGCCAAGCAGGACCCAGGGT 4499
			Db	4460	GATCTCATATCCAGAGGAAACAGATGGCTGACCGGGTTGCCAAGCAGGACCCAGGGT 4519

QY	4500	GTAAACCTTCTGCTTATATAGAAATGCCAAAGCCCGAGAACCCAGACGACGAGTACACC	4559	5580	CCAAACGGCTGTGAAGTCCGAAGGAATCTCCACCTGGATCCATGCATCCACGTTTAAACCG	5639
Db	4520	GTTAACCTTCTGCTTATATAGAAATGCCAAAGCCCGAGAACCCAGACGACGAGTACACC	4579	5597	CCAAACGGCTGTGAAGTCCGAAGGAATCCCAACCTGGATCCATGCATCCACGTTTAAACCG	5656
QY	4560	CTAGAAGACTGCGCAAGAGATAGAAAGATAGACCAAGTCTCTGAGACTCCGGAAGGACC	4619	5640	GCGCACCTCCGATTCGGGGTGGAAAGCGGAAAGAGCTGAAATCCCTTAAAGCTTCGC	5699
Db	4580	CTAGAAGACTGCGCAAGAGATAGAAAGATAGACCAAGTCTCTGAGACTCCGGAAGGACC	4639	5657	GCGCACCTCCGATTCGGGGTGGAAAGCGGAAAGAGCTGAAATCCCTTAAAGCTTCGC	5716
QY	4620	TGCTATACCTCAGATGGGAAGGAATCTGCCCCCAAGAGAGGGTTAGATATATGCCAA	4679	5700	CTCCATCCGCTGGTTCCTTACTCTGTCTCAATAACCTCTCAGACTAATGTGTATGCGCATAGG	5759
Db	4640	TGCTATACCTCAGATGGGAAGGAATCTGCCCCCAAGAGAGGGTTAGATATATGCCAA	4699	5717	CTCCATCCGCTGGTTCCTTACTCTGTCTCAATAACCTCTCAAGTAAAGTAAAGCCTTGT	5776
QY	4680	CAGATACATCGTCTAACCCACTAGCAACTAAACCTGCAGCAGTGTGTCAGAACATCC	4739	5760	AGACAGCTGAACTCCCATAAACCTTATCTCTCACTCGGTTTAAATTAATGATCCGCGCAC	5819
Db	4700	CAGATACATCGTCTAACCCACTAGCAACTAAACCTGCAGCAGTGTGTCAGAACATCC	4759	5777	GAAACAGTCCGAACCTCCCATAAACCTTATCTCTCACTGGTTACTTACTGATCCGCGTAC	5836
QY	4740	CCTTATCATGTCTCAGGCTACACGAGTGGCTGACTCGGTGGTCAAACTTGTGTGCC	4799	5820	AGGTATTAATTAACAACACTCAAGGGGAGGCTCTTTAGAACCTGGTGGCTGTATCT	5879
Db	4760	CCTTATCATGTCTCAGGCTACACGAGTGGCTGACTCGGTGGTCAAACTTGTGTGCC	4819	5837	AGGTATTAATTAACAACACTCAAGGGGAGGCTCTTTAGAACCTGGTGGCTGTATCT	5896
QY	4800	TGCCAGCTGGTAAATGCTTAATCTTCCAGATGCTCCAGGGAAGAGACTAAGGGAAGC	4859	5880	ATACGTTTGCCTCAGATCAGTTATTTCTTAGTCTCTCTCTCACTCCCTCAGATAT	5930
Db	4820	TGCCAGCTGGTAAATGCTTAATCTTCCAGATGCTCCAGGGAAGAGACTAAGGGAAGC	4879	5897	ATATGTCTGCTTCCATTCAGTCAATCCCTGGTCTCAATGACAGGCCACACCTCCGATGT	5956
QY	4860	CACCCAGCGCTCACTGGGAAGTGGACTTCACTGAGGTAAAGCCGGCTAAATACGGAAC	4919	5931	CCTCCATGCTCAGCGATTTTATGTTCGCCAGGACCAAAATAATGAAAAACATTCGGG	5990
Db	4880	CACCCAGCGCTCACTGGGAAGTGGACTTCACTGAGGTAAAGCCGGCTAAATACGGAAC	4939	5957	ACTCGTCTTACGGGTTTTACGTTTTGCCAGGACCCCAATAATGAAGAATAATTGTGG	6016
QY	4920	AAATACCTATTTGTTTGTAGACACCTTTTTCAGGATGGGTAGAGGCTTATCTACTAAG	4979	5991	AAATCCAGAGATTTCTTTTGTAAACATGAACTGTGTAACTCTTAATGATGGATATG	6050
Db	4940	AAATACCTATTTGTTTGTAGACACCTTTTTCAGGATGGGTAGAGGCTTATCTACTAAG	4999	6017	AAATCTCAGGATTTCTTTTGTCAAGCAATGGAGCTGCGTAACCTTCAATGATGGAAATG	6076
QY	4980	AAAGAGACTTCAACCGTGTGCTAAATAAATACTGGAAGAAATTTTCCAGATTTTGA	5039	6051	GAAATGGCCAACTCTCAGCAGGATAGGTAAGTTTTTCTTATGTCAACACCTATACCAAG	6110
Db	5000	AAAGAGACTTCAACCGTGTGCTAAATAAATACTGGAAGAAATTTTCCAGATTTTGA	5059	6077	GAAATGGCCAGTCTCTCAGCAAGACAGAGTAAGTTACTCTTTTGTGTAAACATCTACCAG	6136
QY	5040	ATACCTAAGGTAAATAGGCTCAGACAAATGCTCCAGCTTTTGTGCCAGGTAAGTCAGGA	5099	6111	CTCTGGACAATTTAATTAATACCTGACCTGGATTAGAACTGGAAGCCCCAAG-----	6159
Db	5060	ATACCTAAGGTAAATAGGCTCAGACAAATGCTCCAGCTTTTGTGCCAGGTAAGTCAGGA	5119	6137	TTATAATCAATTTAATTTATGCGCATGGGAGATGGAAGATTTGGCAACAGCGGTTACAAA	6196
QY	5100	CTGGCAAGATATTGGGATTTGATTTGGAACTGCAATTTGTGCATACAGACCCCAAGCTCA	5159	6160	-----TGCTCTCTTTCAGACCTAGATTACCTTAAATAAAG	6194
Db	5120	CTGGCAAGATATTGGGATTTGATTTGGAACTGCAATTTGTGCATACAGACCCCAAGCTCA	5179	6197	AGATGTACGAATAAGCAATAAAGCTGTCTTCTGTAGACCTAGATTACTTAAATAAAG	6256
QY	5160	GGAACAGGTAGAGAGATGAATAGAACCAATTAAGAGACCTTACTTAAATTTGACCGCGAG	5219	6195	TTTCACTCAGAAAGGAAACCAAGAAATACTCTAAATGGGTAAATGGTATCTCTTGGG	6254
Db	5180	GGAACAGGTAGAGAGATGAATAGAACCAATTAAGAGACCTTACTTAAATTTGACCGCGAG	5239	6257	TTTCACTGAAAGGAAACCAAGAAATACTCTAAATGGGTAAATGGTATCTCTTGGG	6316
QY	5220	ACTGGGTTTATGATTTGGATAGCTCTCTGCTTGTGCTTTTGGGTTTGGGTTAGGAACACC	5279	6255	AATGTTATTTATGAGGCTCGGGTAAACCAACAGGCTCCCAATTTAACTATTTCGCTCAA	6314
Db	5240	ACTGGGTTTATGATTTGGATAGCTCTCTGCTTGTGCTTTTGGGTTTGGGTTAGGAACACC	5299	6317	AATGTTATTTATGAGGCTCGGGTAAACCAACAGGCTCCCAATTTAACTATTTCGCTCAA	6376
QY	5280	CCTGACAGCTTTGGGCTGACCCCTTATGAATTTACTCTACGGGGGACCCCGGCTTGGTA	5339	6315	AATAAACAGCTGGAGCTCCAAATGGCTATAGGACCAATAACGGCTTGTGACGGGTCAAAG	6374
Db	5300	CCTGACAGCTTTGGGCTGACCCCTTATGAATTTACTCTACGGGGGACCCCGGCTTGGTA	5359	6377	AATAAACAGCTGGAGCTCCAAATGGCTATAGGACCAATAACGGCTTGTGACGGGTCAAAG	6436
QY	5340	GAAATTTGCTTTGATACATAGTCTGACGTGCTTTTCCAGCTTTGTTCTTCTAGGCTC	5399	6375	ACCCCAACCCCAAGACAGGACCAATCTCTTAAACATAAATCTTGTGATCAGACCCCACTGA	6434
Db	5360	GAAATTTGCTTTGATACATAGTCTGACGTGCTTTTCCAGCTTTGTTCTTCTAGGCTC	5419	6437	ACCCCAACCCCAAGACAGGACCAATCTCTTAAACATAAATCTTGTGATCAGACCCCACTGA	6496
QY	5400	AGGCACCTTGAAGTGGGTGAGACCAAGCGGTGGAGGCACTCCGGGAGGCTTACTCAGGA	5459	6435	GTCTAAACAGCAGCACTAAATAGGGGGCAAACTTTTATAGCCTCATCCAGGGAGCTTTTCA	6494
Db	5420	AGGCACCTTGAAGTGGGTGAGACCAAGCGGTGGAGGCACTCCGGGAGGCTTACTCAGGA	5476	6497	GTCTAAACAGCAGCACTAAATAGGGGGCAAACTTTTATAGCCTCATCCAGGGAGCTTTTCA	6556
QY	5460	GGAGGAGACTTGCAGATCCCATCGTTTCCAAAGTGGGAGATTTCACTTACGTTTGAAGCC	5519	6495	AGCTTTAACTTCCAGACTCCAGAGGCTACCTCTTTCTTGTGCTTATGCTTACGTTTCGGG	6554
Db	5477	GGAGGAGACTTGCAGATCCCATCGTTTCCAAAGTGGGAGATTTCACTTACGTTTGAAGCC	5536	6557	AGCTTTAACTTCCAGACTCCAGAGGCTACCTCTTTCTTGTGCTTATGCTTACGTTTCGGG	6616
QY	5520	CAACCGTGCAGGAACCTCGAGACTCGGTGGAAGGGCCCTTATCTCGTACTTTTGAACCA	5579	6555	CCCACTTACTATGAGGAATGGCTTAGAAGGGGAAATTAATGTGCAAAAAGACATAG	6614
Db	5537	CAACCGTGCAGGAACCTCGAGACTCGGTGGAAGGGCCCTTATCTCGTACTTTTGAACCA	5596	6617	CCCACTTACTATGAGGAATGGCTTAGAAGGGGAAATTAATGTGCAAAAAGACATAG	6676
				6615	AGACCAATGCATGGGGATCCCAAAATAAGCTTACTAGGTTTCTGAGGTTTCTGGAAGAAGG	6674

Db	6677	AGACCAATGCACATGGGATCCCAAAATAAGCTTACCCTTACTGAGGTTCTGGAAAAGG	6736	Db	7757	GCGGAAGTAAATAGGCCCTGAGTACATGTCTCTAGGCATGAAACTTCTTGAACATATTT	7816
Qy	6675	CACCTCATAGGAAAGGTTCCCCCATCCCAACACACCTTTGTAAACACACACTGAAGCCTT	6734	Qy	7755	GAGATAACAAGAAAAGGAGTTTCTAACTGCTTTTGTAGCTTCTGTAAACTGGTTGCGC	7814
Db	6737	CACCTGCATAGGAAAGGTTCCCCCATCCCAACACACCTTTGTAAACACACTGAAGCCTT	6796	Db	7817	GAGATAACAAGAAAAGGAGTTTCTAACTGCTTTTGTAGCTTCTGTAAACTGGTTGCGC	7876
Qy	6735	TAATCAAACTCTGAGAGCAATATCTGTGTACCTGGTTATGACAGGTGGTGGCATGTAA	6794	Qy	7815	CATAAGATGTTGAAATGTTGATACACATATCTGGTGACAACATGTCTCCCCACCCCG	7874
Db	6797	TAATCAAACTCTGAGAGCAATATCTGTGTACCTGGTTATGACAGGTGGTGGCATGTAA	6856	Db	7877	CATAAGATGTTGAAATGTTGATACACATATCTGGTGACAACATGTCTCCCCACCCCG	7936
Qy	6795	TACTGATTAACCCCTTGTGTTCCACCTTGGTTTAAACCAACTAAAGATTTTGGCAT	6854	Qy	7875	AAACATGCCAAATGTGAATCTTAAACAAATTTAAATTAATTTGGTCCACGAAGCGCGG	7934
Db	6857	TACTGATTAACCCCTTGTGTTTCCACTTTGGTTTAAACCAACTAAAGATTTTGGCAT	6916	Db	7937	AAACATGCCAAATGTGAATCTTAAACAAATTTAAATTAATTTGGTCCACGAAGCGCGG	7996
Qy	6855	TATGGTCCAAATGTTCCCGAGTGATTAATCTCCGAAAGCAATCTTCATGAATA	6914	Qy	7935	CTCTCGAAGTTTAAATGACCTGGTTTGTGATATTTTGAATGATTTGTTGTAAGCGC	7994
Db	6917	TATGGTCCAAATGTTCCCGAGTGATTAATCTCCGAAAGCAATCTTCATGAATA	6976	Db	7997	CTCTCGAAGTTTAAATGACCTGGTTTGTGATATTTTGAATGATTTGTTGTAAGCGC	8056
Qy	6915	TGACTACAGAAATCATCGACAAAGAGAGAACCCATATCTCTGACACTTGTCTGTGATCT	6974	Qy	7995	GGGCTTTGTTGAAACCCCATAAAGCTGTCCCGACTCCACACTCGGGCGCGAGTCCTC	8054
Db	6977	TGACTACAGAAATCATCGACAAAGAGAGAACCCATATCTCTGACACTTGTCTGTGATCT	7036	Db	8057	GGGCTTTGTTGAAACCCCATAAAGCTGTCCCGACTCCACACTCGGGCGCGAGTCCTC	8116
Qy	6975	CGGACTTGGAGTGGCAGAGGTGTAGGAAACAGGACAGCTGCCCTGGTCAAGGGACACA	7034	Qy	8055	TACCCCTGCGTGTACGACTGTGGGCCCC-AGCGCGCTTGGAAATAAAATCTCTTGC	8113
Db	7037	CGGACTTGGAGTGGCAGAGGTGTAGGAAACAGGACAGCTGCCCTGGTCAAGGGACACA	7096	Db	8117	TACCCCTGCGTGTACGACTGTGGGCCCCAGCGCGCTTGGAAATAAAATCTCTTGC	8176
Qy	7035	GCAGCTAGAACAGGACTTGTAGTAACTTACATCGAATTTGTAAACAGAGATCTCCAAGCCCT	7094	Qy	8114	TGTTTGCATCAA 8125	
Db	7097	GCAGCTAGAACAGGACTTGTAGTAACTTACATCGAATTTGTAAACAGAGATCTCCAAGCCCT	7156	Db	8177	TGATTGCATCAA 8188	
Qy	7095	AGAAAATCTGTCTAGTAACTTGGAGGAATCCCTAAACCTCTTATCTGAAGTAGTCTCTACA	7154	RESULT 7			
Db	7157	AGAAAATCTGTCTAGTAACTTGGAGGAATCCCTAAACCTCTTATCTGAAGTAGTCTCTACA	7216	AY953542			
Qy	7155	GAATAGAAAGGGTGTAGTATTTATTTCTAAAGAAAGAGGATTTATGTAGACCTTGAA	7214	LOCUS			
Db	7217	GAATAGAAAGGGTGTAGTATTTATTTCTTAAAGAAAGAGGAGTATGTGTAGCCCTGAA	7276	DEFINITION			
Qy	7215	GGAGGATCTGTTTATCTGATCACTTCCAGGGCCATCAGAGACTCCATGAACAGCT	7274	AY953542	8305 bp	DNA	linear VRL 01-JUN-2005
Db	7277	GGAGGATCTGTTTATGTGGAATCACTCAGGGGCCATCAGAGACTCCATGAGCAGCT	7336	Porcine endogenous retrovirus C/A isolate C/A 4 gag protein (gag),			
Qy	7275	TAGAAAGGTTGGAGAGCGTCAAGGGAAAGGAACTACTCAAGGGTGGTTTGAGGG	7334	pol protein (pol), and envelope glycoprotein (env) genes, complete			
Db	7337	TAGAAAGGTTGGAGAGCGTCAAGGGAAAGGAACTACTCAAGGGTGGTTTGAGGG	7396	cds.			
Qy	7335	ATGTTCAACAGGCTCTTTGGTTGGCTACCTACTTCTGCTTTAAGAGACCTTTAAT	7394	AY953542			
Db	7397	ATGTTCAACAGGCTCTCTTGGTTGGCTACCTACTTCTGCTTTAAGAGACCTTTAAT	7456	AY953542.1	GI:63054320		
Qy	7395	AGTCTCTCTGTTACTCAGTTGGCCATGTTATTATTAACAGTTAATTCGCTTCAT	7454	Porcine endogenous retrovirus C/A			
Db	7457	AGTCTCTCTGTTACTCAGTTGGCCATGTTATTATTAACAGTTAATTCGCTTCAT	7516	Porcine endogenous retrovirus C/A			
Qy	7455	TAGAAACGAATAAGTCAGTCCAGATCATGTTACTTTAGACAACAGTACCAGCCCGCTC	7514	Viruses; Retro-transcribing viruses; Retroviridae;			
Db	7517	TAGAAACGAATAAGTCAGTCCAGATCATGTTACTTTAGACAACAGTACCAGCCCGCTC	7576	Orthoretrovirinae; Gammaretrovirus; 1-Mammalian type C virus group.			
Qy	7515	TAGAGGGAAGCTGGCGCTAGCTCTACAGTCTTAAGATTAGAACTATTAAACAGAGAA	7574	1 (bases 1 to 8305)			
Db	7577	TAGAGGGAAGCTGGCGCTAGCTCTACAGTCTTAAGATTAGAACTATTAAACAGAGAA	7636	Denner, J., Karlas, A. and Votteler, Jr.			
Qy	7575	GAAGTGGGATGAAGGATGAATAACAACCTAAGCTTAATGAGAAGCTTAAATTTGTC	7634	Nucleotide sequence and extended characterization of a high passage			
Db	7637	GAAGTGGGATGAAGGATGAATAACAACCTAAGCTTAATGAGAAGCTTAAATTTGTC	7696	human cell-adapted recombinant PERV-C/A			
Qy	7635	TGAATTCAGAGTTTGTTCCTTATAGGTAAGATTTAGGTTTTTGTCTGTTTTTAAATAT	7694	Unpublished			
Db	7697	TGAATTCAGAGTTTGTTCCTTATAGGTAAGATTTAGGTTTTTGTCTGTTTTTAAATAT	7756	2 (bases 1 to 8305)			
Qy	7695	GCGAAGTAAATAGGCCCTGAGTACATGTCTCTAGGCATGAACCTCTTGAACATATTT	7754	Denner, J., Karlas, A. and Votteler, Jr.			
				Direct Submission			
				Submitted (04-MAR-2005)			
				Robert Koch Institute, Nordufer 20, Berlin			
				D-13353, Germany			
				Location/Qualifiers			
				1. 8305			
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				PERV-C/A isolate from C. Wilson, FDA"			
				/specific host="Homo sapiens"			
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				/db_xref="GI:63054321"			

Db	1201	GCCAAATTGACGCCCTCCAGTATTGGCCCTTTTCTCTCGAGATCTCTATAATTGGAAAA	1260
Qy	1261	CTAAACCATCCCTTTCTCGAGGATCCCAACGCCTCAGCGGTTGGTGGAGTCCCTTTA	1320
Db	1261	CTAAACCATCCCTTTCTCGAGGATCCCAACGCCTCAGCGGTTGGTGGAGTCCCTTTA	1320
Qy	1321	TGTTCTCTCACACGCTACTTGGGATGATGTGTCAACAGCTGTGTGACAGACTCTTTCACAA	1380
Db	1321	TGTTCTCTCACACGCTACTTGGGATGATGTGTCAACAGCTGTGTGACAGACTCTTTCACAA	1380
Qy	1381	CCGAGGAGGAGAGAAATCTATTAGAGCTAGAAAATCTTCTGGGGCGACGGGC	1440
Db	1381	CCGAGGAGGAGAGAAATCTATTAGAGCTAGAAAATCTTCTGGGGCGACGGGC	1440
Qy	1441	GACCCACGGGTTGCAAAATGACATTCACATGGGATTTCCCTTAACTCGCCCCGGTTGGG	1500
Db	1441	GACCCACGGGTTGCAAAATGACATTCACATGGGATTTCCCTTAACTCGCCCCGGTTGGG	1500
Qy	1501	ACTAACACGGCTGAAGGTAGGAGAGCTTGAAAATCTATCGCCAGGCTCTGGTGGCGG	1560
Db	1501	ACTAACACGGCTGAAGGTAGGAGAGCTTGAAAATCTATCGCCAGGCTCTGGTGGCGG	1560
Qy	1561	GTCTCGGGGGCTCTAAGCGGCCACTAAATTTGGCTAAGGTAAAGAGTGAATGCAGG	1620
Db	1561	GTCTCGGGGGCTCTAAGCGGCCACTAAATTTGGCTAAGGTAAAGAGTGAATGCAGG	1620
Qy	1621	GACCGAATGAACCCCTCTGTGTTTCTTGAGAGGCTCTTGGAGGCTTCAGGCGGTACA	1680
Db	1621	GACCGAATGAACCCCTCTGTGTTTCTTGAGAGGCTCTTGGAGGCTTCAGGCGGTACA	1680
Qy	1681	CCCTTTTGATCCACCTCAGAGGCCCAAAAGCCTCAGTGGCTTTGGCCTTTATAGGAC	1740
Db	1681	CCCTTTTGATCCACCTCAGAGGCCCAAAAGCCTCAGTGGCTTTGGCCTTTATAGGAC	1740
Qy	1741	AGTCAGCCTTTGGATATTAGAAAGAGCTTCAGAGACTGGAAAGGTTTACAGGAGCTGAGT	1800
Db	1741	AGTCAGCCTTTGGATATTAGAAAGAGCTTCAGAGACTGGAAAGGTTTACAGGAGCTGAGT	1800
Qy	1801	TAGTGATCTAGTGAAGGAGCAGAGAAAGTATTATCAAAAGGGAGACAGAAAGAAAA	1860
Db	1801	TAGTGATCTAGTGAAGGAGCAGAGAAAGTATTATCAAAAGGGAGACAGAAAGAAAA	1860
Qy	1861	GGGAACAAAGAAAGAGAGAAAGAGAGAAAGGAGGAGAAAGCGTAATAACCGGCAAG	1920
Db	1861	GGGAACAAAGAAAGAGAGAAAGAGAGAAAGGAGGAGAAAGCGTAATAACCGGCAAG	1920
Qy	1921	AGAAAGATTTGACTAAGATCTTGGCTCAGTGGTTGAAGGGAAAGCAATACCGAAAGAG	1980
Db	1921	AGAAAGATTTGACTAAGATCTTGGCTCAGTGGTTGAAGGGAAAGCAATACCGAAAGAG	1980
Qy	1981	AGAGAGATTTTAGGAAATTTAGGTACGGCCCTAGACAGTACGGGAACCTGGGCAATAGGA	2040
Db	1981	AGAGAGATTTTAGGAAATTTAGGTACGGCCCTAGACAGTACGGGAACCTGGGCAATAGGA	2040
Qy	2041	CCCCACTCGACAAGGACCAATGTGCATTTGTAAAGAAAGGACACTGGGCAAGGAAC	2100
Db	2041	CCCCACTCGACAAGGACCAATGTGCATTTGTAAAGAAAGGACACTGGGCAAGGAAC	2100
Qy	2101	GCCCCAAGAGGGAAAAAAGGACCAAGGATCTTAGCTCTAGAGAGAGATAAGATTAGG	2160
Db	2101	GCCCCAAGAGGGAAAAAAGGACCAAGGATCTTAGCTCTAGAGAGAGATAAGATTAGG	2160
Qy	2161	GGAGACGGGTTCCGACCCCTCCCGAGCCAGGGTAACTTTTCAAGTGGAGGGGCAAC	2220
Db	2161	GGAGACGGGTTCCGACCCCTCCCGAGCCAGGGTAACTTTTCAAGTGGAGGGGCAAC	2220
Qy	2221	CAGTTGAGTTCTGTTGATACCGGAGCGAAACATTCAGTGTCTACTACAGCCATTAGGAA	2280
Db	2221	CAGTTGAGTTCTGTTGATACCGGAGCGAAACATTCAGTGTCTACTACAGCCATTAGGAA	2280
Qy	2281	AACATAAAGATAAAAAATCCTGGGTGATGGGTGCCACAGGGCAACAGTATCCATGGA	2340
Db	2281	AACATAAAGATAAAAAATCCTGGGTGATGGGTGCCACAGGGCAACAGTATCCATGGA	2340
Qy	2341	CTACCCGAAGAACAGTTGACTTGGAGTGGGACGGGTAAACCACTCGTTTCTTGGTCATAC	2400
Db	2341	CTACCCGAAGAACAGTTGACTTGGAGTGGGACGGGTAAACCACTCGTTTCTTGGTCATAC	2400
Qy	2401	CTGAGTGGCCAGACACCCCTCTTAGGTAGAGACTTATTGACCAAGATGGGAGACAAATTT	2460
Db	2401	CTGAGTGGCCAGACACCCCTCTTAGGTAGAGACTTATTGACCAAGATGGGAGACAAATTT	2460
Qy	2461	CTTTTGAACAAGGGAAAAACAGAAAGTGTCTGCAAAATAAACAACCTATCATCTGTGTGACCC	2520
Db	2461	CTTTTGAACAAGGGAAAAACAGAAAGTGTCTGCAAAATAAACAACCTATCATCTGTGTGACCC	2520
Qy	2521	TCCAATTAGATACGAATATCGACTACTCTCCCTAGTAAAGCCTGATCAAAATATAC	2580
Db	2521	TCCAATTAGATACGAATATCGACTACTCTCCCTAGTAAAGCCTGATCAAAATATAC	2580
Qy	2581	NATTCTGGTTGGAACAAGTTTCCCAAGCCTGGGCAGAAAACCGCAGGGATGGGTTTGGCAA	2640
Db	2581	NATTCTGGTTGGAACAAGTTTCCCAAGCCTGGGCAGAAAACCGCAGGGATGGGTTTGGCAA	2640
Qy	2641	AGCAAGTTTCCCCACAAAGTTATTCAACTGAAGCCAGTGCACACCACTGTCTAGTCAGAC	2700
Db	2641	AGCAAGTTTCCCCACAAAGTTATTCAACTGAAGCCAGTGCACACCACTGTCTAGTCAGAC	2700
Qy	2701	AGTACCCCTTGAGTAAAGAGCTCAAGAGGAATTCGGCGGATGTCCAAAGATTAAATCC	2760
Db	2701	AGTACCCCTTGAGTAAAGAGCTCAAGAGGAATTCGGCGGATGTCCAAAGATTAAATCC	2760
Qy	2761	AAACAGGGCATCTAGTTCTGTCTCCCTGGAATACTCTCCCTGTCTACCGGTTAGAA	2820
Db	2761	AAACAGGGCATCTAGTTCTGTCTCCCTGGAATACTCTCCCTGTCTACCGGTTAGAA	2820
Qy	2821	AGCCTGGGACTAATGACTATCGACCAAGTACAGGACTTGAGAGAGGTCAATAAACGGGTGC	2880
Db	2821	AGCCTGGGACTAATGACTATCGACCAAGTACAGGACTTGAGAGAGGTCAATAAACGGGTGC	2880
Qy	2881	AGGATATACACCAACAGTCCCGAACCTTATAACCTCTGTGTGTCTCTCCACCCCAAC	2940
Db	2881	AGGATATACACCAACAGTCCCGAACCTTATAACCTCTGTGTGTCTCTCCACCCCAAC	2940
Qy	2941	GGAGCTGGTATACAGTATTGGACTTAAAGGATGCTTCTTCTGCTGAGATTACACCCCA	3000
Db	2941	GGAGCTGGTATACAGTATTGGACTTAAAGGATGCTTCTTCTGCTGAGATTACACCCCA	3000
Qy	3001	CTAGCCAAACCACTTTTGGCTTCCAAATGGAGAGATCCAGGTACGGGAAGAACCGGGCAGC	3060
Db	3001	CTAGCCAAACCACTTTTGGCTTCCAAATGGAGAGATCCAGGTACGGGAAGAACCGGGCAGC	3060
Qy	3061	TCACCTGGACCCGACTGCCCCCAAGGGTTCAAGAACTCCCGGACCATCTTTGACGAAGCCC	3120
Db	3061	TCACCTGGACCCGACTGCCCCCAAGGGTTCAAGAACTCCCGGACCATCTTTGACGAAGCCC	3120
Qy	3121	TACACAGAGACCTGGCCAACTTCAGGATCCAAACACCTCAGGTGACCCCTCTCCAGTACG	3180
Db	3121	TACACAGAGACCTGGCCAACTTCAGGATCCAAACACCTCAGGTGACCCCTCTCCAGTACG	3180
Qy	3181	TGATGACCTGCTTCTGGCGGAGGCCAACAAACAGGACTCTCTTAGAAGGACGAAGGCAC	3240
Db	3181	TGATGACCTGCTTCTGGCGGAGGCCAACAAACAGGACTCTCTTAGAAGGACGAAGGCAC	3240
Qy	3241	TACTGTGGAAATGTCTGACCTAGGCTTACAGAGCCTCTGTAGAGAGCCAGATTGGA	3300
Db	3241	TACTGTGGAAATGTCTGACCTAGGCTTACAGAGCCTCTGTAGAGAGCCAGATTGGA	3300
Qy	3301	GGAGAGAGTAAACATCTTGGGGTACAGTTTGGGGACGGGACGGATGGCTGACGGAGG	3360
Db	3301	GGAGAGAGTAAACATCTTGGGGTACAGTTTGGGGACGGGACGGATGGCTGACGGAGG	3360
Qy	3361	CACGGAGAGAAACTGTAGTCCAGATCCGGCCCCCAACCAAGCCCAACAAATGAGAGAT	3420
Db	3361	CACGGAGAGAAACTGTAGTCCAGATCCGGCCCCCAACCAAGCCCAACAAATGAGAGAT	3420

Qy 3421 TTTTGGGACAGCTGGATTTTGCAGACTGTGGATCCCGGGTTTGGACCTTAGCAGCCC 3480
Db TTTTGGGACAGCTGGATTTTGCAGACTGTGGATCCCGGGTTTGGACCTTAGCAGCCC 3480
Qy 3481 CACTCTACCGCTTAACCAAGAAAGGGGAAATCTCTGGGCTCCTGAGCACCAGAGG 3540
Db CACTCTACCGCTTAACCAAGAAAGGGGAAATCTCTGGGCTCCTGAGCACCAGAGG 3540
Qy 3541 CATTGTGATGTATCAAAAAGGCCCTGTGAGCGCACTGTCTGGCCCTCCCTGACGTAA 3600
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Qy 3601 CTRAAACCTTTACCTTTATGTGATGAGCGTAAGGGAGTAGCCCGGGAGTTTAAACCC 3660
Db CTRAAACCTTTACCTTTATGTGATGAGCGTAAGGGAGTAGCCCGGGAGTTTAAACCC 3660
Qy 3661 AAACCTTAGGACATGAGAAAGACCTGTGGCTACCTGTCAAGAAAGCTCGATCCTGTAG 3720
Db AAACCTTAGGACATGAGAAAGACCTGTGGCTACCTGTCAAGAAAGCTCGATCCTGTAG 3720
Qy 3721 CCAGTGGTTGGCCCATATGCTGAAGGCTATCGCAGCTGTGGCCCATACTGGTCAAGGACG 3780
Db CCAGTGGTTGGCCCGTATGCTGAAGGCTATCGCAGCTGTGGCCCATACTGGTCAAGGACG 3780
Qy 3781 CTGCAAAATTGACTTTGGGACAGAAATAAATGTAATAGCCCCCATGCAATGGAGAA 3840
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Qy 3841 TCGTTCCGAGCCCCCAGACCGATGATGATGACCAACGCGCGGATGACCCACTATCAAGCC 3900
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Qy 3901 TGCTTCTCAGAGAGGGTCACTGCTCCAGCAGCGCTCTCAACCTGCCACTCTC 3960
Db TGCTTCTCAGAGAGGGTCACTGCTCCAGCAGCGCTCTCAACCTGCCACTCTC 3960
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Qy 4021 CTGGGGTCCGCAAGGACTTACAGACATACCGCTGACTGGAGAGTGTAACTGGTTCA 4080
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Db CTGACGAGCAGCTATGTGTGGAAGTGAAGAGATGGCTGGGGCGCGGTGGGACG 4140
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Qy 4441 ATCTCATATCCAGAGGAACACAGATGGCTGACCGGGTTGCCAAGCAGCAGCCAGGGT 4500
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Qy 4501 TTAACCTTCTGCCTTATAAAGTATGCAAAAGCCCCAGAAACCCAGACGACGATACACCC 4560

Db 4501 TTAACCTTCTGCCTTATGATAGAAACACCCAAAGCCCCAGAAACCCGAGCAGTACACCC 4560
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Db TAGAAGACTCGCAAGAGATAAAAAGATAGACAGATTCTCTGAGACTCCCGAAGGACCT 4620
Qy 4621 GCTATACCTCAGATGGGAAGAAATCTGCCCCCAAAAAGAGGTTTGAATATATCTCAAC 4680
Db GCTATACCTCAGATGGGAAGAAATCTGCCCCCAAAAAGAGGTTTGAATATATCTCAAC 4680
Qy 4681 AGATACATCTGTCTAAACCCACTAGGAATAAACCTGACAGCAGTTCGTCAGAACATCCC 4740
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Qy 4741 CTTTATCATGTTCTGAGGCTACACAGGAGTGCTGACTCGGTGGTCAAAACATTTGTGTGCC 4800
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Qy 4861 ACCAGCGCTCACTGGGAAGTGGACTTCACTGAGGTAAAGCCGGCTAAATACGGAACA 4920
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Qy 4921 AATACCTATTGTTTGTGTAGACACCTTTTTCAGATGGGTAGAGGCTTATCTCTACTAAGA 4980
Db AATATCTATTGTTTGTGTAGACACCTTTTTCAGATGGGTAGAGGCTTATCTCTACTAAGA 4980
Qy 4981 AAGAGACTTCAACCGTGGTGGCTAAAAAATACTGGAAGAAATTTTTTCCAGATTGTGAA 5040
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Qy 5041 TACCTAAGTAAATAGGTCAGACAAATGGTCCAGCTTTTGTTCACAGTAAAGTCAGGAC 5100
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Qy 5221 CTGGCGTTAATGATGATAGCTCTCTGCGCTTTGTGCTTTTGTAGGGTTAGGAACACCC 5280
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Db AGGCATTTGATGGGTGAGCAACAGCGGTGGAGGCAACTCCCGGGAGGCTTACTCAGGAG 5460
Qy 5461 GAGGAGACTTGCAGATCCCATCGTTTCCAGGTGGGAGATTCACTAGCTTACGTTAGACGCC 5520
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Qy 5521 ACCGTGAGGAAACCTCGAGACTCGGTGGAGGGCCCTTATCTCGTACTTTTGTAGCCAC 5580
Db ACCGTGAGGAAACCTCGAGACTCGGTGGAGGGCCCTTATCAGTACTTTTGTAGCCAC 5580
Qy 5581 CAACGGCTGTGAAAGTCAAGGAATCTCCACCTGGATCCATGCAATCCACGTTAAACGG 5640

D	b	5581	CAACGGCTGTGAAGTCGAAGGAATCTCCACCTGGATCATGCAATCCCACTGTAAGCCGG	5640	Q	y	6658	GAGGTTTCTGGAAAAGGCACCTGCGATAGGAAGGTTCCCCCATCCCAACCAACACCTTTCT	6717
Q	y	5641	CGCCACTCCGATTCGGGGTGAAGCCGAAAGAGCTGAAATCCCTTAAGCTTTGGCC	5700	D	b	6721	GAGGTTTCTGGAAAAGGCACCTGCGATAGGAAGGTTCCCCCATCCCAACCAACCTTTCT	6780
D	b	5641	CGCCACTCCGATTCGGGGTGAAGCCGAAAGAGCTGAAATCCCTTAAGCTTTGGCC	5700	Q	y	6718	RACACACTGAAGCCCTTAAATCAAACTCTGAGAGTCAATATCTGGTACTCTGGTATGATGAC	6777
Q	y	5701	TCCATCGCTGGTTCCTTACTCTGTCAATAAACCCTCTCAGACTAAATGGTATGCGATAGGA	5760	D	b	6781	AACCACTGAAGCCCTTAAATCGAACTCTGAGAGTCAGTATCTGGTACTCTGGTATGATGAC	6840
D	b	5701	TCCATCGCTGGTTCCTTACTCTGTCAATAAACCCTCTCAGACTAAATGGTATGCGATAGGA	5760	Q	y	6778	AGGTGGTGGGCATGTAATACTGGATTAAACCCCTTGCTGTTTCCACTTGGTATTAACCAA	6837
Q	y	5761	GACAGCTGAATCCCATAAACCCCTTATCTCACCTGGTAAATTAATCTGACTCCGGCACA	5820	D	b	6841	GGGTGGTGGGCATGTAATACTGGATTAAACCCCTTGCTGTTTCCACTTGGTATTAACCAA	6900
D	b	5761	GACAGCTGAATCCCATAAACCCCTTATCTCACCTGGTAAATTAATTAATGACTCCGGTACA	5820	Q	y	6838	ACTAAGATTTTGGCATTAATGCTCAAAATGTTCCCGAGTGTATTAATTAATTAATTAATTA	6897
Q	y	5821	GGTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA	5880	D	b	6901	ACTAAGAGCTTTTGGGTTATGGTCCAAATTTGTCCTGGGTGCTACTATATCCGAAAAA	6960
D	b	5821	GGTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA	5880	Q	y	6898	GCAATCCTTGATGAATATGACTACAGAAATCATCGAATAAGAGAGAACCCATATCTCTG	6957
Q	y	5881	TAGCTTTGGCTCAGATCAGTTATTCCTAGTCT-----GACCTCACCCCCAGATATC	5931	D	b	6961	GCAGTCTTGATGAATATGACTATAGATATAATTCGCCAAAGAGAGCCCATATCCCTG	7020
D	b	5881	TATGCTGCTTCGATCAGTAAATCCCTGCTCAATGACCCAGGCCACACCCCCGATGTA	5940	Q	y	6958	ACACTTGTCTGTGATGCTCGGACTTGGAGTGGCAGCAGGTGTAGGAAACAGGAAACAGTGCC	7017
Q	y	5932	CTCCATGCTCAGGATTTATGTTTGGCCAGGACCAACCAATTAATGGAACATTCGGGA	5991	D	b	7021	ACACTAGCTGTAATGCTCGGATTGGAGTGGCTGCAGGCGTGGGAACAGGAAACGGCTGCC	7080
D	b	5941	CTCCGTGCTTACGGGTTTACGTTTGGCCAGGACCCCAATTAATGAAGATTAATTTGGA	6000	Q	y	7018	CTGTGTCGCGGACCAAGCAGAGCTAGAAACAGGACTTAGTAACTACATCGAATTTGTAACA	7077
Q	y	5992	AATCCCGAGATTTCTTTGTAACAATGGAATCTGTGTAACCTCTAATGATGATATTTGG	6051	D	b	7081	CTAATCACAGGACCGCAACAGCTGGAGAAAGGACTTAGTAACCTACATCGAATTTGTAACG	7140
D	b	6001	AATCCTCAGGATTTCTTTGCAAGCAATGAGCTGGTAACCTCTTAATGATGATGATTTGG	6060	Q	y	7078	GAGATCTCCAAGCCCTAGAAAACTCTGCAGTAACCTCGAGGAATCCCTAACCTCTCTTA	7137
Q	y	6052	AAATGGCCAACTCTCAGCAGGATAGGGTAAGTTTCTTATGTCACACCTATACAGC	6111	D	b	7141	GAGATCTCTCAAGCCCTAGAAAACTCTGCAGTAACCTCGAGGAATCCCTAACCTCTCTTA	7200
D	b	6061	AAATGGCCAGTCTCTCAGCAAGACAGAGTAACTTCTTTGTTAACAATCTACCACT	6120	Q	y	7138	TCTGAAGTAGTCTCTCAGAAATAGAGAGGTTAGATTTATTTCTTAAAGAGGAGGA	7197
Q	y	6112	CTGTGCAATTTAATTAACCTGACCTGGATTAGAACTTGAAGTGGAGCCCGAAG-----	6159	D	b	7201	TCTGAAGTGGTCTCAGAAACAGAGAGGCTTAGATCTGTATTCTTAAAGAGGAGGA	7260
D	b	6121	TATAATCAATTTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT	6180	Q	y	7198	TTATGTGTAGCTTGAAGAGGAAATGCTGTTTATGTGGATCATTCAGGGGCCATCAGA	7257
Q	y	6160	-----TGCTCTCTTTCAGACCTAGATTACCTTAAATAAAGT	6195	D	b	7261	TTATGTGTAGCTTGAAGAGGAAATGCTGTTTATGTGGATCATTCAGGGGCCATCAGA	7320
D	b	6181	GATGTAGCAATTAAGCAATAAGCTGTCTTCGTAGACCTAGATTACTTAAATAAAGT	6240	Q	y	7258	GACTCCATGAACAAAGCTTAGAGAAAGGTTGGAGAGCGTCTGAAGGAAAGGAAACTACT	7317
Q	y	6196	TTCACTGAGAAAGGAAACAAAGAAATATCTTAAATGGTAAATGGTATGTCTTGGGGA	6255	D	b	7321	GACTCCATGAACAAAGCTTAGAGAAAGGTTGGAGAGCGTCTGAAGGAAAGGAAACTACT	7380
D	b	6241	TTCACTGAAAGAGAAACAAAGAAATATTTCAAAGTGGGTAAATGGTATGTCTTGGGGA	6300	Q	y	7318	CAAGGCTGGTTTGGAGGATGGTTCAACAGGCTCTTTTGGTTGGCTACCCCTACTCTGCT	7377
Q	y	6256	ATGGTATTAATGAGGCTCGGTAAACACAGGCTCCATTTCTAATTAATTCGCTCAAA	6315	D	b	7381	CAAGGCTGGTTTGGAGGATGGTTCAACAGGCTCTCTTGGTTGGCTACCCCTACTCTGCT	7440
D	b	6301	ATAGTGTACTATGAGGCTCTGGGAGAAAGAAAGGATCTGTTCTGACTATTTCGCTCAGA	6360	Q	y	7378	TTAAACAGGACCCCTTAATAGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT	7437
Q	y	6316	AT---AAACAGCTGGAGCTCCAAATGGCTATAGGACCAATACGGTCTTTGACGGGTCAA	6372	D	b	7441	TTAAACAGGACCCCTTAATAGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT	7500
D	b	6361	ATAGAAATCAGATGGAACTTCGGTTGCTATAGGACCAATAGGTTTGGCGCAACAA	6420	Q	y	7438	AGCTTAATTTGCTTCAATAGAGAACGAATAGTGAGTCCAGATCATGGTACTTAGACAA	7497
Q	y	6373	AGACCCCAACCCAGGACGAGGACCATCTCTAAC-----ATACTTCT	6417	D	b	7501	AGCTTAATTTGCTTCAATAGAGAACGAATAGTGAGTCCAGATCATGGTACTTAGACAA	7560
D	b	6421	GGACTCCAAATCCAAGAACAGAGGCCATCTCTAACCCCTCTGATTACAATAACAACCTCT	6480	Q	y	7498	CAGTACCAAGCCGCTCTACAGGAGAGCTGGCGCTAGCTCTACCAAGTTCTAAGATTAG	7557
Q	y	6418	GGATCAGACCCCACTGATGCTTAACAGCAGCATTAATTTGGGGCAAACTTTTAGGCTC	6477	D	b	7561	CAGTACCAAGCCGCTCTACAGGAGAGCTGGCGCTAGCTCTACCAAGTTCTAAGATTAG	7620
D	b	6481	AGATCAGTCCCACTGAGCCCTAAATCACTATTATTAACAGGGCGCAAACTTTTAACCTC	6540	Q	y	7558	AATATTAAACAGAGAAAGAGTGGGAAATGAAGGATGAAGGATGAAGGATGAAGGATGAAG	7607
Q	y	6478	ATCCAGGAGCTTTTCAAGCTTTAACTCCACGACTCCAGAGGCTACTCTCTTTGTTGG	6537	D	b	7621	AATATTAAACAGAGAAAGTGGGAAATGAAGGATGAAGGATGAAGGATGAAGGATGAAG	7680
D	b	6541	ATCCAGGAGCTTTTCAAGCTTTAACTCCACGACTCCAGAGGCTACTCTCTTTGTTGG	6600	Q	y	7608	-----AAGCTTAATGAGAAGCTTAAATTTGTTGAAATTCAGAGTTTGTTCCTTAT	7658
Q	y	6538	CTATGCTTAGCTTCGGGCCCACTTACTATGAAGGAATGGCTAGAAGGGAATTCAT	6597	D	b	7681	GAACCCAGGAGTTAATTAAGAGCTCTAATGCGCTCGAATTCAGAGCCCTGTTCCCTAT	7740
D	b	6601	CTTTGCTTAGCTTCGGGCCCACTTACTATGAGGGAATGGCTAGAGGAGGGAATTCAT	6660	Q	y	7659	AGGTAAAGATTTAGTTTTTGTGTTTTTAAATAATGC-----	7696
Q	y	6598	GTGCAAAAGAACATAGAGCAATGCAATGGGAGTCCCAAAATAGCTTACCCTTACT	6657	D	b	7741	AGGTAAAGATCATACTTTTTTGTGTTTTTAGGGCTTCTTTTCTGCTCTGTACAAACATTT	7800
D	b	6661	GTGCAAAAGGAACATAGAGCAATGCAATGGGAGTCCCAAAATAGCTTACCCTTACT	6720					

[illegible]

Qy	1190	CACACGGGGGCAATTCAGACCCCTCCAGTATTGGCCCTTTTCTTCTGCGATCTCTA	1249	Qy	2270	GCCATTAGGAAACTAAAGATAAAAAATCCTGGGTGATGGTGCCACAGGGCAACAACA	2329
Db	1758	CATACGGGGGCAATTCAGACCCCTCCAGTATTGGCCCTTTTCTTCTGCGATCTCTA	1817	Db	2838	GCCATTAGGAAACTAAAGATAAAAAATCCTGGGTGATGGTGCCACAGGGCAACAACA	2897
Qy	1250	TAAATTGGAAACTTAACCATCCCTTTCTCGGAGGATCCCAACGCTCACGGGGTTGTT	1309	Qy	2330	GTATCCATGGACTACCCGAAGAACAGTTGACTTTGGAGTGGGACGGGTAAACCCTCGTT	2389
Db	1818	TAAATTGGAAACTTAACCATCCCTTTCTCGGAGGATCCCAACGCTCACGGGGTTGTT	1877	Db	2898	ATATCCATGGACTACCCGAAGAACAGTTGACTTTGGAGTGGGACGGGTAAACCCTCGTT	2957
Qy	1310	CGAGTCCCTTATGTTCTCTCACAGCCTACTTGGGATGATTTGTCAACAGCTGTCGAGAC	1369	Qy	2390	TCGTGTCATACCTGAGTGCCAGCACCCCTCTTAGTGAGACTTATTGACCAAGATGGG	2449
Db	1878	GGAGTCCCTTATGTTCTCTCACAGCCTACTTGGGATGATTTGTCAACAGCTGTCGAGAC	1937	Db	2958	TCGTGTCATACCTGAGTGCCAGCACCCCTCTTAGTGAGACTTATTGACCAAGATGGG	3017
Qy	1370	ACTTTTCAACACGAGGAGCGAGAGAAATTTCTATTAGAGGCTAGAAAAATTTCTCTGG	1429	Qy	2450	AGCACAAATTTCTTTTGAACAGGAAACCAAGAGTGTCTGCAAAATAACAAACCTATCAC	2509
Db	1938	ACTTTTCAACACGAGGAGCGAAAGAAATTTCTTTAGAGGCTAGAAAAATTTCTCTGG	1997	Db	3018	AGCACAAATTTCTTTTGAACAGGAAACCAAGAGTGTCTGCAAAATAACAAACCTATCAC	3077
Qy	1430	GGCCGACGGCGNACCCACCGGTTGCAAAATGAGATTGACATGGGATTTCCCTTAACCTG	1489	Qy	2510	TGTGTTGACCCCTCCAATTAGATGACGAATATCGACTATCTCTCCCTTAGTAAAGCTGA	2569
Db	1998	GGCCGACGGCGNACCCACCGAGTTGCAAAATGAGATTGACATGGGATTTCCCTTAACCTG	2057	Db	3078	TGTGTTGACCCCTCCAATTAGATGACGAATATCGACTATCTCTCCCTTAGTAAAGCTGA	3137
Qy	1490	CCCCGGTTGGGACTACAACACGCTGAAGGTAGGGAGAGCTTGAAATCTATCGCCAGGC	1549	Qy	2570	TCAAAATATACAATTTCTGGTTGGAAACAGTTTCCCAAGCCTGGGAGAAACCGCGGGAT	2629
Db	2058	CCCCGGTTGGGACTACAACACGCTGAAGGTAGGGAGAGCTTGAAATCTATCGCCAGGC	2117	Db	3138	TCAAAATATACAATTTCTGGTTGGAAACAGTTTCCCAAGCCTGGGAGAAACCGCGGGAT	3197
Qy	1550	TTCTGTTGGGGTCTCCGGGGCCCTCAAGA CGGCCCACTAATTTGGCTAAGTAAGAGA	1609	Qy	2630	GGGTTTGGCAAGCAAGTTCCCCCAAGTTTCAACTGAAGGCCAGTGCCACACAGT	2689
Db	2118	TTCTGTTGGGGTCTCCGGGGCCCTCAAGACGGGCCACTAATCTTGGCTAAGTAAGAGA	2177	Db	3198	GGGTTTGGCAAGCAAGTTTCCCCCAAGTTTCAACTGAAGGCCAGTGCTGCACAGT	3257
Qy	1610	AGTGATGCGAGGACCGAATGAACCCCTCTGTTTCTTGAGAGGCTCTTGAAGCCCTT	1669	Qy	2690	GTCACTCAGACAGTACCCCTTGAGTAAAGAACTCAAGAAAGAAATTCGGCGCGGATGTCCA	2749
Db	2178	GGTGATGCGAGGACCGAATGAACCCCTCTGTTTCTTGAGAGGCTCTTGAAGCCCTT	2237	Db	3258	GTCACTCAGACAGTACCCCTTGAGTAAAGAACTCAAGAAAGAAATTCGGCGCGGATGTCCA	3317
Qy	1670	CAGCGGTAACACCCCTTTTGATCCCACTCAGAGGCCCAAAAAGCTCTAGTGCTTTGGC	1729	Qy	2750	AAAGTTAATCCAAACAGGGCATCTCTAGTTCTCTGCTCAATCTCTCTGAAATCTCCCTGCT	2809
Db	2238	CAGCGGTTACCCCTTTTGATCTACTCTCGAGGCTCAGAAAGCTCAATGCTGCTGGC	2297	Db	3318	AAAGTTAATCCAAACAGGGCATCTCTAGTTCTCTGCTCAATCTCTCTGAAATCTCCCTGCT	3377
Qy	1730	CTTTATAGGACAGTCAAGCTTGATATTAGAAAGAAAGCTTTCAGAGCTGGAAGGGTTACA	1789	Qy	2810	ACCGGTTAGAAAGCTGGGACTAATGACTATCGACAGTACAGGACTTCAGAGAGGTCAA	2869
Db	2298	CTTTATAGGACAGTCAAGCTTGATATTAGAAAGAAAGCTTTCAGAGCTGGAAGGGTTACA	2357	Db	3378	ACCGGTTAGAAAGCTGGGACTAATGACTATCGACAGTACAGGACTTCAGAGAGGTCAA	3437
Qy	1790	GGAGGCTGATTCAGTATCTAGTGAGGAGGAGAGAAAGTATTATACAAAGGGAGAC	1849	Qy	2870	TAAACGGGTGCGAGATATACCCCAACAGTCCCGAAACCCCTTATAACCTCTGTGTGCTCT	2929
Db	2358	GGAGGCTGATTCAGTATCTAGTGAGGAGGAGAGAAAGTATTATACAAAGGGAGAC	2417	Db	3438	TAAACGGGTGCGAGATATACCCCAACAGTCCCGAAACCCCTTATAACCTCTGTGTGCTCT	3497
Qy	1850	AGAAGAAAGAGGAAACAAAGAAAGAGAGAGAAAGAGAGGAGGAGAAAGACGTAA	1909	Qy	2930	CCCAACCCCAACGGAGCTGTATACAGTATTGAGACTTAAAGGATGCTCTCTCTGCTGAG	2989
Db	2418	AGAAGAAAGAGGAAACAAAGAAAGAGAGAGAAAGAGAGGAGGAGAAAGACGTAA	2477	Db	3498	CCCAACCCCAACGGAGCTGTATACAGTATTGAGACTTAAAGGATGCTCTCTCTGCTGAG	3557
Qy	1910	TAAACGGCAAGAGAAATTTGACTAAGATCTTGGCTGAGTGGTTGAAGGGAAAGCAA	1969	Qy	2990	ATTACACCCCACTAGGCAACCACTTTTTCCTTCGAATGGAGAGATCCAGGTACGGGAAG	3049
Db	2478	TAAACGGCAAGAGAAATTTGACTAAGATCTTGGCTGAGTGGTTGAAGGGAAAGCAA	2537	Db	3558	ACTACATCCCACTAGGCAACCACTTTTTCCTTCGAATGGAGAGATCCAGGTACGGGAAG	3617
Qy	1970	TACGGAAGAGAGAGATTTTAGGAAATTTAGTTCAGGCCCTAGACAGTACGGGAACCT	2029	Qy	3050	AACCGGGCAGCTCACCTGGAACCGACTGCCCCAAGGGTTCAAGAACTCCCGGACCATCTT	3109
Db	2538	TACGGAAGAGAGAGATTTTAGGAAATTTAGTTCAGGCCCTAGACAGTACGGGAACCT	2597	Db	3618	AACCGGGCAGCTCACCTGGAACCGACTGCCCCAAGGGTTCAAGAACTCCCGGACCATCTT	3677
Qy	2030	GGGCAATAGGACCCCACTCGACAAAGGACCAATGTGCATATTGTAAAGAAAGAGACACTG	2089	Qy	3110	TGACGAAGCCCTACACAGAGACCTGGCCAACTTCAGGATCCAAACCCCTCAGGTGACCTT	3169
Db	2598	GGGCAATAGGACCCCACTCGACAAAGGACCAATGTGCATATTGTAAAGAAAGAGACACTG	2657	Db	3678	TGACGAAGCCCTACACAGAGACCTGGCCAACTTCAGGATCCAAACCCCTCAGGTGACCTT	3737
Qy	2090	GGCAAGAACTGCCCCAAGAGGAAACAAAGGACCAAGGATCTAGCTTAGAAGAGA	2149	Qy	3170	CTTCCAGTACGTGGATGACCTGCTTCTGGCGGAGGCCAACAAACAGGACTGCTTAGAAGG	3229
Db	2658	GGCAAGGACTGCCCCAAGAGGAAACAAAGGACTGAAGTCTTAGCTCTGGAAGAGA	2717	Db	3738	CTTCCAGTACGTGGATGACCTGCTTCTGGCGGAGGCCAACAAACAGGACTGCTTAGAAGG	3797
Qy	2150	TAAAGATTAGGGAGACGGGTTCCGACCCCTCCCGAGCCCGAGGTAACTTTGAAGGT	2209	Qy	3230	CACGAAGGCACTACTGCTGGAATTTGTCTGACCTAGGCTACAGAGCTCTCTTAAGAAAGGC	3289
Db	2718	TAAAGATTAGGGAGACGGGTTCCGACCCCTCCCGAGCCCGAGGTAACTTTGAAGGT	2777	Db	3798	TACGAAGGCACTACTGCTGGAAATTTCTGACCTAGGCTACAGAGCTCTCCCTTAAGAAAGC	3857
Qy	2210	GGAGGCAACACGATTGAGTTCTCTGTTGATACCGGAGCGGAAACATTCAGTGTCTACTACA	2269	Qy	3290	CCAGATTTCAGAGAGAGAGTAACTACTTTGGGTTACAGTTTCGGGACCGGCGAGCCGATG	3349
Db	2778	GGAGGCGCAACCGATTGAGTTCTCTGTTGATACCGGAGCGGAAACATTCAGTGTCTACTACA	2837	Db	3858	CCAGATTTCAGAGAGAGAGTAACTACTTTGGGTTACAGTTTCGGGCGGCGGAGCCGATG	3917
				Qy	3350	GCTGACGGGCGCACGGAAGAAAACTGTAGTCCAGATACCGGCGGCCCAACCAACGACGCAAAACA	3409

3918	Db		GCTGACGAGCGCACGGAAGAACTGTAGTCCAGATACCGCGCCCAACCAACGACCCAAACA	3977
3410	QY		AATGAGAGAGT TTTTGGGGACAGCTGGATTTTGACAGACTGTGATCCCGGGGTTTCGGAC	3469
3978	Db		AGTGAGAGAGT TTTTGGGGACAGCTGGATTTTGACAGACTGTGATCCCGGGGTTTCGGAC	4037
3470	QY		CTTAGCAGCCCCACTCTACCGCTTAACCAAGAA AAAGGGAAATTCCTCTGGGCTCTCTGA	3529
4038	Db		CTTAGCAGCCCCACTCTACCGCTTAACCAAGAA AAAGGGAAATTCCTCTGGGCTCTCTGA	4097
3530	QY		GCACCAGAGGCATTTGATGCTATCAAAAAGGCGCTGCTGAGCGCACCTGCTCTGGCCCT	3589
4098	Db		GCACCAGAGGCATTTGATGCTATCAAAAAGGCGCTGCTGAGCGCACCTGCTCTGGCCCT	4157
3590	QY		CCCTGAGCTAACTAAACCCCTTTATGTGGATGAGCGTAAGGGAGTAGCCCGGG	3649
4158	Db		CCCTGAGCTAACTAAACCCCTTTATGTGGATGAGCGTAAGGGAGTAGCCCGGG	4217
3650	QY		AGTTTTAACCCAAACCCCTAGGACCATGGAGAAGACCTGTGCCCTACCTGTCAAGAAGCT	3709
4218	Db		AGTTTTAACCCAAACCCCTAGGACCATGGAGAGACCTGTTGCCCTACCTGTCAAGAAGCT	4277
3710	QY		CGATCTGTAGCCAGTGGTGGCCCATATGCTGTGAAGGCTATGCGAGCTGTGGCCATACT	3769
4278	Db		CGATCTGTAGCCAGTGGTGGCCCATATGCTGTGAAGGCTATGCGAGCTGTGGCCATACT	4337
3770	QY		GGTCAAGGACGCTGACAAATTTGATTTGGGACAGATATTAAC TGTATATGCCCCCATGTC	3829
4338	Db		GGTCAAGGACGCTGACAAATTTGATTTGGGACAGATATTAAC TGTATATGCCCCCATGTC	4397
3830	QY		ATTGGAGAACATCGTTCCGAGCGCCCCAGACCGATGATGACCAACCGCCCGCATGACCCA	3889
4398	Db		GTTTGGAGAACATCGTTCCGAGCGCCCCAGACCGATGATGACCAACCGCCCGCATGACCCA	4457
3890	QY		CTATCAAAGCGCTGTTCTCAGAGAGGGTCA CGTTGCTGTCACACGCGCTCTCAACCC	3949
4458	Db		CTATCAAAGCGCTGTTCTCAGAGAGGGTCA CGTTGCTGTCACACGCGCTCTCAACCC	4517
3950	QY		TGCCACTCTTCTGCTCAAGAGACTGATGAACAGTCACTCATGATTTGCCATCAACTATT	4009
4518	Db		TGCCACTCTTCTGCTCAAGAGACTGATGAACAGTCACTCATGATTTGCCATCAACTATT	4577
4010	QY		GATTGAGGAGACTGGGCTCCGCAAGGACCTTTACAGACATACCGCTGACTGGAGAAGTGCT	4069
4578	Db		GATTGAGGAGACTGGGCTCCGCAAGGACCTTTACAGACATACCGCTGACTGGAGAAGTGTT	4637
4070	QY		AACCTGTTTCACTGACGGAGACGCTATGTTGGTGGAAAGGTAAGAGGATGCTGGGGCGGC	4129
4638	Db		AACCTGTTTCACTGACGGAGACGCTATGTTGGTGGAAAGGTAAGAGGATGCTGGGGCGGC	4697
4130	QY		GGTGGTGGACGGGACCGCACGATCTGGGCGCAGCAGCTCCGGAGGAAGTCTCAGCACA	4189
4698	Db		GGTGGTGGACGGGACCGCACGATCTGGGCGCAGCAGCTCCGGAGGAAGTCTCAGCACA	4757
4190	QY		AAAGGCTGAGCTCATGTGCGCTTCAGCAAGCTTTTGGCGTGGCCAGCAGCTCCGGAAGGAAATCCATAAA	4249
4758	Db		AAAGGCTGAGCTCATGTGCGCTTCAGCAAGCTTTTGGCGTGGCCAGGAGGAAATCCATAAA	4817
4250	QY		CATTTATACGACAGCAGGATGCTTTTGGGACTGCA CGTACATGGGGCCCATCTATAA	4309
4818	Db		CATTTATACGACAGCAGGATGCTTTTGGGACTGCA CGTACATGGGGCCCATCTATAA	4877
4310	QY		ACAAAGGGGGTGTCTTACTCAGAGGGAGGGAATTAAGAA CAAGAGGAATTTCTAAG	4369
4878	Db		GCAAAGGGGGTGTCTTACTCAGAGGGAGGGAATTAAGAA CAAGAGGAATTTCTAAG	4937
4370	QY		CCTATTAGAGCGCTGACATTTTACAAAGAGCTAGCTATTATAC TGTCTCTGAGCATCA	4429
4938	Db		CCTATTAGAGCGCTTACATTTTGGCCAAAGAGGCTAGCTATTATAC TGTCTCTGAGCATCA	4997
4430	QY		GAAGAGCTAAAGATCTCATATATCCAGAGGAAAC CAGATGGCTGACCGGGTGTGCCAAGCAGGC	4489
4490	QY		AGCCACAGGGTGTAAACCTTCTGCTATATAATAGAAATGCCCCAAGGCCCCAGAACCCACAGACG	4549
5058	Db		AGCCACAGGGTGTAAACCTTCTGCTATGATAGAAACACCA AAGGCCCCAGAACCCCGGACG	5117
4550	QY		ACAGTACACCCCTTAGAGACTGGC AAGAGATTA AAGATAGACCACTCTCTGAGACTCC	4609
5118	Db		ACAGTACACCCCTTAGAGACTGGC AAGAGATTA AAGATAGACCACTCTCTGAGACTCC	5177
4610	QY		GAAGGGGACTGCTATACCTCAGATGGGAAAGGAAATTCCTGCCCCCA AAGAGAGGGTTAGA	4669
5178	Db		GAAGGGGACTGCTGCTATACCTCAGATGGGAAAGGAAATTCCTGCCCCCA AAGAGAGGGTTAGA	5237
4670	QY		ATATGTC CAACAGATACATCGTCTAA CCACCTAGGAACTAAACACCTCGAGCAGTTGGT	4729
5238	Db		ATATGTC CAACAGATACATCGTCTAA CCACCTAGGAACTAAACACCTCGAGCAGTTGGT	5297
4730	QY		CAGAACATCCCTTATCATGTTCTGAGGCTAC CAGGAGTGGCTGACTCCGTTGTTCAAAACA	4789
5298	Db		CAGAACATCCCTTATCATGTTCTGAGGCTAC CAGGAGTGGCTGACTCCGTTGTTCAAAACA	5357
4790	QY		TTGTGTGCCCTCCAGCTGTTTAA TGTCTAACTCTTCCAGAA TGCCCTCCAGGGAAGAGACT	4849
5358	Db		TTGTGTGCCCTCCAGCTGTTTAA TGTCTAACTCTTCCAGAA TGCCCTCCAGGGAAGAGACT	5417
4850	QY		AAGGGGAAGCCACCCAGGCGCTCACTGGGAAGTGGA CTTCACTAGGTTAAAGCCGCTAA	4909
5418	Db		AAGGGGAAGCCACCCAGGCGCTCACTGGGAAGTGGA CTTCACTAGGTTAAAGCCGCTAA	5477
4910	QY		ATACGGAAACAAATATCTATGTTTGTAGACACCTTTT CAGGATGGGTAGAGGCTTA	4969
5478	Db		ATACGGAAACAAATATCTATGTTTGTAGACACCTTTT CAGGATGGGTAGAGGCTTA	5537
4970	QY		TCTACTTAGAAGAGACTTCAACCGTGGTCTAAAAAATA CTCGAAAGAAATTTTTC	5029
5538	Db		TCTACTTAGAAGAGACTTCAACCGTGGTCTAAAAAATA CTCGAAAGAAATTTTTC	5597
5030	QY		AAGATTGGGAATACCTAAGGTAA TAGGGT CAGACAA TGGTCCAGCTTTTGTGCCCAGGT	5089
5598	Db		AAGATTGGGAATACCTAAGGTAA TAGGGT CAGACAA TGGTCCAGCTTTTGTGCCCAGGT	5657
5090	QY		AGTCAAGGACTGGCCAAAGATATTTGGGGATTGATTTGGAAACTGTCATTTGTCATACAGACC	5149
5658	Db		AGTCAAGGACTGGCCAAAGATATTTGGGGATTGATTTGGAAACTGTCATTTGTCATACAGACC	5717
5150	QY		CCAAAGCTCAGGACAGTAGAGAGGATGAATAGAACCATTTAAAGAGACCCCTTACTAAAT	5209
5718	Db		CCAAAGCTCAGGACAGTAGAGAGGATGAATAGAACCATTTAAAGAGACCCCTTACTAAAT	5777
5210	QY		GACCGCGGAGACTGGCGTTTAAATGATTTGATAGTCTCTCTGCCCTTTGTGCTTTTAGGGT	5269
5778	Db		GACCAAGAGACTGGCGTTTAAATGATTTGGATGGCTCTCTCTGCCCTTTGTGCTTTTAGGGT	5837
5270	QY		TAGGAACA CCCCTGGA CAGTTTGGGCTGAC CCCCCTATAGAA TTACTCTA CGGGGGAC CCCC	5329
5838	Db		GAGGAACA CCCCTGGA CAGTTTGGGCTGAC CCCCCTATAGAA TTACTCTA CGGGGGAC CCCC	5897
5330	QY		CCCATTTGGTAGAAA TTGCTTCTGTACATAGTGTGCTGAGCTGCTTTTCCACGCTTTTGT	5389
5898	Db		CCCGTTTGGCAGAAA TTGCTTCTGTGCAATAGTGTGATGTGCTGCTTTTCCACGCTTTGTT	5957
5390	QY		CTCTAGGCTCAAGGCACTTTGAGTGGGTGAGACAA CAGAGCGTGGAGGCAACTCCGGGAGGC	5449
5958	Db		CTCTAGGCTCAAGGCGCTCGAGTGGGTGAGGCGAGCGGTGGAAGCAGCTCCGGGAGGC	6017
5450	QY		CTTACTCAGGAGGAGAGACTTGCAGATCCCA CATGTTTCCAA AGTGGGAGATTCAGTCTTA	5509
6018	Db		CTTACTC ---AGGAGGAGACTTTGCAAGT TCCACATCGCTTCCAA AGTGGGAGATTCAGTCTTA	6074
5510	QY		CGTTAGACGCCACCGTGTGAGAAAACCTCGAGACTCCGTTGGAAGGGCCCTTATCTCGTACT	5569
6075	Db		TGTTAGACGCCACCGTGTGAGAAAACCTCGAGACTCCGTTGGAAGGGACCTTATCTCGTACT	6134

Qy	5570	TTTGGACCAACAACGGCTGTGAAGTTCGAAGAAATCTCCACTGGATCCATGCATCCCA	5629	Qy	6587	GGAAATTCATGTGACAAAAGGACATAGAGACCAATGACATGGGGATCCCAAAATAAGC	6646
Dd	6135	TTTGGACCAACAACGGCTGTGAAGTTCGAAGAAATCTCCACTGGATCCATGCATCCCA	6194	Dd	7215	GGAAATTCATGTGACAAAAGGACATAGAGACCAATGACATGGGGATCCCAAAATAAGC	7274
Qy	5630	CGTTAAACGGCGCCACCTCCCGATTCGGGTGGAAAGCCGAAAGACTGAAATCCCT	5689	Qy	6647	TTACCCCTTACTGAGGTTTCTGGAAAGGCACTGTCATAGGAAGGTTCCCCCATCCAC	6706
Dd	6195	CGTTAAAGCGCGCCACCTCCCGATTCGGGTGGAAAGCCGAAAGACTGAAATCCCT	6254	Dd	7275	TTACCCCTTACTGAGGTTTCTGGAAAGGCACTGTCATAGGAAGGTTCCCCCATCCAC	7334
Qy	5690	TAAAGCTTCGCTCCATCGGCTGGTTCCTTACTCTGTCAATAACCTCTCAGACTAATGGTA	5749	Qy	6707	AACACCTTTGTAAACACACTGAGGCTTTAATCAACCTCTGAGAGTCAATATCTGGTAC	6766
Dd	6255	TAAAGCTTCGCTCCATCGGCTGGTTCCTTACTCTGTCAATAACCTCTCAGACTAATGGTA	6314	Dd	7335	AACACCTTTGTAAACACACTGAGGCTTTAATCAACCTCTGAGAGTCAATATCTGGTAC	7394
Qy	5750	TGCGCATAGGAGACAGCTGAACTCCCATAAACCTTATCTCTCACCCTGGTTAAATCTG	5809	Qy	6767	CTGGTTATGACAGAGTGGGTCATGTAATCTGGAATTAACCTCTGTTTCCACCTTGG	6826
Dd	6315	AAGCGCTTGTGGACAGCCGAACTCCCATAAACCTTATCTCTCACCCTGGTTAAATCTG	6374	Dd	7395	CTGGTTATGACAGAGTGGGTCATGTAATCTGGAATTAACCTCTGTTTCCACCTTGG	7454
Qy	5810	ACTCGGACAGGTATTAATATCAACAACACTCAAGGGAGGCTCTTTAGGACCTGGT	5869	Qy	6827	TTTTTAAACCAACTAAGATTTTTTGCATTAATGGTCCAAATTTGTTCCCGAGTGTATCT	6886
Dd	6375	ACTCGGATACAGGTATTAATATCAACAACACTCAAGGGAGGCTCTTTAGGACCTGGT	6434	Dd	7455	TTTTTCAACCAACTAAGATTTTTTGCATTAATGGTCCAAATTTGTTCCCGAGTGTATCT	7514
Qy	5870	GCCTCATCTATACGTTTCCTCAGATCAGTTATCTTAGTCT- - - - -GACCTCAC	5920	Qy	6887	ATCCCGAAAAAGCAATCTTGTATGATGACTACAGAAATCATCGACAAAAGAGAGAC	6946
Dd	6435	GGCTGAAATTAATGTCCTCCTCGATCAGTAATCCTCGTCTCAATGACCGCCACAC	6494	Dd	7515	ATCCCGAAAAAGCAATCTTGTATGATGACTACAGTAATTAATCGGCCAAAAAGAGAGC	7574
Qy	5921	CCCCAGATATCCTCCATGCTCAGGATTTTATGTTTGGCCAGGACCAACAAATAATGGAA	5980	Qy	6947	CCATATCTCTGACACTTGTCTGTGCTCGGACTTGGAGTGGCAGAGGTAGGAACAG	7006
Dd	6495	CCCCCGATGCTACCGTCTTACGGGTTTTACGTTTGGCCAGGACCCCCCAATTAATGAAG	6554	Dd	7575	CCATATCCTTGACACTAGCTGTAAATGCTCGGATTTGGAGTGGCTGCGAGGAGNACAG	7634
Qy	5981	AACATTTGGGAAATCCAGAGATTTCTTTTGTAAACAATGGAACTGTAACTCTAATG	6040	Qy	7007	GAACTGTTAAACAGAGATCTCAGGACCAACAGCTAGAAACAGGACTTAGTAACCTACATC	7066
Dd	6555	AATATTTGGGAAATCCCTCAGGATTTCTTTTGAAGCAATGGAGCTGCATTAATCTAATG	6614	Dd	7635	GAACTGTTAAACAGAGATCTCAGGACCAACAGCTAGAAACAGGACTTAGTAACCTACATC	7694
Qy	6041	ATGGATATTGGAATGSCCAACTCTCAGCAGGATAGGTTAAGTTTCTTATGTCAACA	6100	Qy	7067	GAACTGTTAAACAGAGATCTCAGGACCAACAGCTAGAAACAGGACTTAGTAACCTACATC	7126
Dd	6615	ATGGAAATTTGGAATGSCCAACTCTCAGCAGGATAGGTTAAGTTTCTTATGTAAACA	6674	Dd	7695	GAACTGTTAAACAGAGATCTCAGGACCAACAGCTAGAAACAGGACTTAGTAACCTACATC	7754
Qy	6101	CTTATACCACTCTGGACAAATTTAATTAACCTGACCTGGATTAAGAACTGGAAGCCCCAAG-	6159	Qy	7127	TAACTCTCTTATCTGAAGTGTCTTACAGAAATAGAGAGGTTAGATTTATTTATTTCTAA	7186
Dd	6675	ATCCTACCACTTATTAATCAATTTAATTTATGGCCATGGGAGATGGAAGATTTGCAACAGC	6734	Dd	7755	TAACTCTCTTATCTGAAGTGTCTTACAGAAATAGAGAGGTTAGATTTATTTATTTCTAA	7814
Qy	6160	- - - - -TGCTCTCTTCCAGACCTAGATTACC	6184	Qy	7187	AAGAAGGAGGATTTATGTGTAGCCTTTGAAGGAGGAAATGCTTTTATGTGGATCATTCAG	7246
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VERSION	AJ293656	env gene; envelope; gag gene; group specific antigen; pol gene;	
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SOURCE	AJ293656	Porcine endogenous type C retrovirus	
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AUTHORS	AJ293656	Krach, U., Fischer, N., Czaderna, F. and Tonjes, R.R.	
TITLE	AJ293656	Comparison of replication-competent molecular clones of porcine endogenous retrovirus class A and class B derived from pig and human cells	
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DB 6375 ACTCCGGTACAGGTATTAAATTAACAGCACTCAAGGGGAGGCTCCTTTGGGACCTGGT 6434
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DB 6435 GGCTGATTAATATATGCTGCTTCGATCAGTAATCCCTGCTCAATGACCGGCGCACAC 6494
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QY 6160 -----TGCTCTCTCTTCAGACCTAGATTACC 6184

Db	6735	GGGTACAAAAGATGTACGAAATTAAGCAATAAGCTGTCAATTCGTTAGACCTAGATTACT	6794	Db	7815	AAGAGGAGGGTTATGTGTAGCCTTAAAGAGGAATGCTGCTTTTATGTGGATCATTCAG	7874
Qy	6185	TAAATAATAGTTTCACTGAGAAGGAAACAGAAATATCTCTAAATCGGGTAAATGGTA	6244	Qy	7247	GGGCATCAGAGACTCCATGAACAAAGCTTTAGAGAAAGGTTGGAGAGCGTCCGAGGGAAA	7306
Db	6795	TAAATAATAGTTTCACTGAAAAGGAAACAAAGAAATATTCAAAAGTGGGTAATGGTA	6854	Db	7875	GAGCTATCAGGGACTCCATGAGCAAGCTCAGAGAAAGGTTAGAAAACGTCACAAAGAAA	7934
Qy	6245	TGCTTGGGCAATGGTATATTATGAGGCTCGGGTAAACAAACAGAGCTCCATTCTAACTA	6304	Qy	7307	AGGAAACTACTCAAGGGTGGTTGAGGGATGGTTCAACAGGTCTCTTTGGTTGGCTACCC	7366
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Qy	6305	TTGCGCTCAAAAT---AAACACAGCTGGAGCCTTCAATGCTATAGGACCAAAATAGCGTCT	6361	Qy	7367	TACTTCTGCTTTTAACAGGACCTTAAATAGTCTCTCTCTGTTACTCACAGTTGGGCCAT	7426
Db	6915	TTGCGCTCAGATAGAAACTCAGATGGAACCTCGGTTGCTATAGGACCAAAATAGGGTT	6974	Db	7995	TGCTTCTGCTCTAACAGGACCCCTAGTAATACTGCTCTGTTGTTTACAGTTGGGCTT	8054
Qy	6362	TGACGGGTCAAGAGACCCCAACCAAGGACGAGGACCATCTCTTAAC-----6408	6408	Qy	7427	GTATTATTAAACAAGTTAATTGCTTTCATTAGAGAAAGCAATAGTGCAGTCCAGATCATGG	7486
Db	6975	TGGCCGAACAAGGACCTCCAATCCAAGAACAGAGGCCATCTCTTAACCCCTCTGATTACA	7034	Db	8055	GCTTAATTAAATCGGTTTGTTCCTTTGTTAGAGAACAGTGTAGTGCAGTTCGGATCATGG	8114
Qy	6409	--ATAACTTCTGATCAGACCCCACTAGTCTAAACAGCACGACTAAATGGGGCAAAAC	6466	Qy	7487	TACTTAGACAACAGTACCAAGCCGCTTAGC---AGGAAAGCTGGCCGCTAGCTTACC	7543
Db	7035	ATAACAACCTCTGATCAGTCCCACTGAGCCTTAACATCACTATTAAACAGGGGCGAAAC	7094	Db	8115	TACTTAGACAAGTACCAAGCCCTTCAAGCTTCAAGCTAAGAGGAACTGACCTTTAGCCTTCT	8174
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Db	7095	TTTTTAGCCTCATCCAGGGAGCTTTTCAAGCTCTTAACTCCACGACTCCAGAGGCTACT	7154	Db	8175	AGTTCTAAGATTAGAACTATTAAACAGAGAGAGTGGGGAATGAAAGATGAAATGCA	8234
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Db	7155	CTTCTTGTGGCTTGTCTTAGCTTGGGGCCACCTTTACTATGAGGGAATGGCTAGAGGAG	7214	Db	8235	ACCTGACTCTCCAGAACCCAGGAAGTTAAATGAAGCTCTAAATGCCCTCGAATTCAG	8294
Qy	6587	GGAAATTCATGTGACAAAGAACATAGAGACCAATGACATGGGGATCCCAAAATAAGC	6646	Qy	7645	AGTTTGTCTCTTATAGGTAAAGATTTAGGTTTTTGTGTTTTTAAATAATGC-----	7696
Db	7215	GGAAATTCATGTGACAAAGAACATAGAGACCAATGACATGGGGATCCCAAAATAAGC	7274	Db	8295	ACCTGTTTCCCTTATAGTAAAGATCATACTTTTGTGTTTTTGTAGGGCTTGTCTTCTGCT	8354
Qy	6647	TTACCCCTTACTGAGGTTTCTGAAAAGGACCTGCAATAGGAAGGTTTCCCCATCCACC	6706	Qy	7697	-----GGAAATGAAATAGGCGCTGAGTACATGTCTCTAGGCATGA	7736
Db	7275	TTACCCCTTACTGAGGTTTCTGAAAAGGACCTGCAATAGGAAGGTTTCCCCATCCACC	7334	Db	8355	CTGTACAAAACCTTTGTGGAGGGGAAAAACAGGCCCTGAGTATGTGCTCTATGCTGA	8414
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Db	7335	AACACCTTTGTAAACCACTGAAGAGCTTTAATCGAACCTCTGAGAGTCAATATCTGGTAC	7394	Db	8415	AACTTCTTTGAAACTGCTCCTAACTGCTTGTGTTGGCTTCTGTAAACCTGCTTGCATAAGAT	8474
Qy	6767	CTGGTTATGACAGGTGGTGGCATGTAATCTGGAATTAACCCCTGTTTCCACCTCG	6826	Qy	7764	AGAAAGGGAGTTTCTTAACCTGCTTGTGTTTGTAGTTTCTGTAAAACTGGTTGCGCCATAAAGAT	7823
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Qy	6827	TTTTTAAACCAACTAAAGATTTTTGCAATATGCTTCAAAATTTGTTCCCGAGTGTATTACT	6886	Qy	7824	GTGAAAATGTTGATACATATCTTGGTGACAAATATGCTCTCCCAACCCAGAGACAGGCA	7883
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Qy	6887	ATCCCGAAAAGCAATCCTTGATGAATATGACTACAGAAATCATCGACAAAAGAGAGAAC	6946	Qy	7884	CAAAATGTGTAACCTTAAACAAATTTAAATTTAAATTTAAATTTAAATTTAAATTTAAATTT	7943
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Qy	6947	CMATATCTTGACACTTGTGTGATGCTCGGACTTGGAGTGGGACAGGAGTGAAGACAG	7006	Qy	7944	TTTTTAAATTTGACTGGTTTGTGATATTTT---GAAATGATTTGTTTGT---AAAGCGGGCTTT	8001
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Db	7635	GAACGGTCCCTTAAATCAGAGGACCGCAACAGCTGAGAAAGGACTTAGTAACCTTACATC	7694	Db	8715	GTGTGAAACCCCAATAAAGCTGTCCGACTCCACACTCGGGGCGGAGTCTCTACCCCT	8774
Qy	7067	GAATTTGTAACAGAGATCTCAAGCCCTAGAAAATCTGTGAGTAACTCTGGAGGAATCCC	7126	Qy	8062	GGTGTGTACGACTGTGGGCGCCAGCGCTTGGAAATAAATCTCTTGTCTGTTTGA	8121
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Qy	7127	TAACTCTTATCTGAAGTGTCTTACAGAAATAGAGGGGTTAGATTATTTATTCTAA	7186	Qy	8122	TCAAAA 8127	
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Qy	7187	AAGAAGGAGATTATGTAGTACCTTGAAGGAGGAATGCTGTTTTTATGTGATCATTCAG	7246				

LOCUS AX546209 8918 bp DNA linear PAT 26-NOV-2002
DEFINITION Sequence 3 from Patent WO02072836.
ACCESSION AX546209
VERSION AX546209.1 GI:25811408
KEYWORDS
SOURCE Pig endogenous retrovirus
ORGANISM Pig endogenous retrovirus
VIRUSES; Retro-transcribing viruses; Retroviridae;
Orthoretrovirinae; Gammaretrovirus.
1
REFERENCE Toenjes, R. and Krach, U.
AUTHORS Replication-competent molecular clones of porcine endogenous
TITLE retrovirus class a and class b derived from pig and human cells
JOURNAL Patent: WO 02072836-A 3 19-SEP-2002;
Paul-Ehrlich-Instituts, Prof Dr Johannes Loewer (DE)
FEATURES
Location/Qualifiers
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/mol_type="unassigned DNA"
/db_xref="taxon:184752"
/note="porcine primary fibroblasts
Replication-competent PERV-A clone PERV-A(Bac-130A12)"
ORIGIN
Query Match 84.0%; Score 6832.4; DB 6; Length 8918;
Best Local Similarity 91.0%; Pred. No. 0;
Matches 7542; Conservative 1; Mismatches 573; Indels 176; Gaps 19;
QY 1 GGGTGGTGTACGACTGTGGGCCCGCCAGCGCTTGGAAATAAAATCCTCTGCTGTTCGA 60
DB 560 GGGTGGCGTACGACTGTGGGCCCGCCAGCGCTTCGGNATAAAATCCTCTGCTGTTCGA 619
QY 61 TCAAGACCGCTTCTCGTGTGATTAAGGGAGTGCCTTTTCCGAGCTGTGAGG- ---- 115
DB 620 TCAAGACCGCTTCTCGTGTGATTT- TGGGGTGTGCGCTCTCCGAGTCAGGACGAGAGG 678
QY 116 ----TTCCTTTTGTGCTTACATTTGGGGGCTCGTCCGGGATCTGTGCGGCCACCC 171
DB 679 GATTTTAACTCGACTGGCGCTTTCAGTTTGTGTGCTGGCCGGAAACCCGGGACTACCCC 738
QY 172 TAACACCGAGAACCGACTTGGAGTAAAGGATCCTCTTTTAAACGTGT- -ATGCATG 229
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QY 230 TACCGCCGGCGCTCTCTGTCTGTAGTGTCTGTTTTTCAGTGTGCGCGCTTTTCGGTTTGA 289
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QY 290 GCTGTCTCTCAGGCCGTAAAGGCTGGGGGACTGTGATCAGCAGACGTGTAGGAGGATC 349
DB 858 GCTGTCTCTAAGACCGTAAGACTTGGGGGA- ----ATCAGCAGACGTGTCTAGGAGGATC 912
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DB 913 ACAGAGCTGCCACCTGGGGGACGCCCGCTGTGGAGGTGGGGAGCAGGAGCGCTG 972
QY 405 GTGGTCTCTACTGTCCGTTCAGAGACCGAAATTCGTTGCTCAAGCGAAAGCTTCCCCCT 464
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QY 465 CGCGACCGGTCCGACTCTTTTGGCTGTGTGTGGAAAGACGTGGAACGGGTCACTGTGTCTG 524
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DB 2053 ACTCGCCCGGTTGGGACTACAAACGCGCTGAAAGGTAGGAGAGCTTGAAATCTATGCG 2112
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Db	2353	TTACAGGAGCTGAGTTAGT	GTGATCTAGTGAAGGAGAGAGTATATTACAAAAG	2412
Qy	1845	GAGACAGAAAGAAAGGAA	CAAAAGAAAGAGAGAGAAAGGAGGAAAGAA	1904
Db	2413	GAGACAGAAAGAAAGGAA	CAAAAGAAAGAGAGAGAAAGGAGGAAAGAA	2472
Qy	1905	CGTAATAACCGCAAGAGAA	ATTTGACTTAAGATCTTCGGCTGAGTGGTTGAAGGAA	1964
Db	2473	CGTAATAACCGCAAGAGAA	ATTTGACTTAAGATCTTCGGCTGAGTGGTTGAAGGAA	2532
Qy	1965	AGCAATACCGAAGAGAGAA	TTTTAGGAAATTTAGTCAAGCCCTAGACAGTCAGG	2024
Db	2533	AGCAATACCGAAGAGAGAA	TTTTAGGAAATTTAGTCAAGCCCTAGACAGTCAGG	2592
Qy	2025	AACCTGGCAATAGGACCC	CACTCGACAAGGACCAATGTGCATATTTGTAAGAAAGAGAA	2084
Db	2593	AACCTGGCAATAGGACCC	CACTCGACAAGGACCAATGTGCATATTTGTAAGAAAGAGAA	2652
Qy	2085	CACTGGCAAGAACTGCCC	CAAGAAAGGAAACAAAGGACCAAGATCTTAGCTTAGAA	2144
Db	2653	CACTGGCAAGAACTGCCC	CAAGAAAGGAAACAAAGGACCTGAAGGTCTTAGCTCTGGAA	2712
Qy	2145	GAAGATAAGATTAGGGAG	AGGGGTTCCGACCCCTCCCGAGCCAGGGTAACTTTG	2204
Db	2713	GAAGATAAGATTAGGGAG	AGGGGTTCCGACCCCTCCCGAGCCAGGGTAACTTTA	2772
Qy	2205	AAAGTCAGGGGCAAC	CCAGTTGAGTTCTGTTGTATACCGGAGCGAAACATTCAGTGTCTA	2264
Db	2773	AAAGTCAGGGGCAAC	CCAGTTGAGTTCTGTTGTATACCGGAGCGAAACATTCAGTGTCTA	2832
Qy	2265	CTACAGCCATTAGGAAAA	CTTAAAGATATAAAAACTCCTGGGTGATGGTGCACAGGGCAA	2324
Db	2833	CTACAGCCATTAGGAAAA	CTTAAAGATATAAAAACTCCTGGGTGATGGTGCACAGGGCAA	2892
Qy	2325	CAACAGTATCCATGGACT	ATCCGAGAACGATTTGACTTTGGGAGTGGAGCGGTAAACCCAC	2384
Db	2893	CAACAGTATCCATGGACT	ATCCGAGAACGATTTGACTTTGGGAGTGGAGCGGTAAACCCAA	2952
Qy	2385	TGCTTTCTGTCATACCT	GATGCCAGCACCCCTCTTAGTGTAGACTTATTGACCAAG	2444
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Qy	2445	ATGGGAGCAAAATTTCT	TTTGAACAAAGGAAACCAAGAGTGTCTGCAATAACAAACCT	2504
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Qy	2565	CTGTATCAAAATATACA	ATTTCTGTTGGAACAGTTTCCCAAGCCTGGGAGAAACCGCA	2624
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Qy	3165	ACCTCTCTCCAGTAC	GTGATGACCTGCTTCTGGGGAGCCACCAACAGGACTCTTA	3224
Db	3733	ACCTCTCTCCAGTAC	GTGATGACCTGCTTCTGGGGAGCCACCAACAGGACTCTTA	3792
Qy	3225	GAAGCAACGAAGGCACT	ACTGCTGGAATTTGTCTGACCTTAGGCTACAGAGCTCTGTAAG	3284
Db	3793	GAAGCAACGAAGGCACT	ACTGCTGGAATTTGTCTGACCTTAGGCTACAGAGCTCTGTAAG	3852
Qy	3285	AAGGCCAGATTGACGAG	AGAGGTAACTATTCTGGGGTACAGTTTGGGGAGCGGGCAG	3344
Db	3853	AAGGCCAGATTGACGAG	AGAGGTAACTATTCTGGGGTACAGTTTGGGGAGCGGGCAG	3912
Qy	3345	CGATGGCTGACCGAG	CGACGGAAGAACTGTAGTCCAGTACCGGCCCCCAACACAGCC	3404
Db	3913	CGATGGCTGACCGAG	CGACGGAAGAACTGTAGTCCAGTACCGGCCCCCAACACAGCC	3972
Qy	3405	AAACAAATGAGAGAGT	TTTTTGGGACAGCTGGAATTTTGACAGCTGTGGATCCCGGGTTT	3464
Db	3973	AAACAAATGAGAGAGT	TTTTTGGGACAGCTGGAATTTTGACAGCTGTGGATCCCGGGTTT	4032
Qy	3465	GGGACCTTAGCAGCCCA	CTCTACCCGCTAAACAAAGAAAGGGGAAATTTCTCTGGGCT	3524
Db	4033	GGGACCTTAGCAGCCCA	CTCTACCCGCTAAACAAAGAAAGGGGAAATTTCTCTGGGCT	4092
Qy	3525	CCTGAGCACAGAGGCA	TTTGTATCAAAAAGCCCTCTGTAGCGCACCTGTCTG	3584
Db	4093	CCTGAGCACAGAGGCA	TTTGTATCAAAAAGCCCTCTGTAGCGCACCTGTCTG	4152
Qy	3585	GGCCTCCCTGACGTA	CTAAACCCCTTTTACCTTTATGTGGATGAGCGTAAAGGAGTAGCC	3644
Db	4153	GGCCTCCCTGACGTA	CTAAACCCCTTTTACCTTTATGTGGATGAGCGTAAAGGAGTAGCC	4212
Qy	3645	CGGGGAGTTTAAACCA	ACCCCTAGGACCAATGAGGAGACCTGTGCGCTACCTGTCTAAG	3704
Db	4213	CGGGGAGTTTAAACCA	ACCCCTAGGACCAATGAGGAGACCTGTGCGCTACCTGTCTAAG	4272
Qy	3705	AAGCTCATCTGTAGC	AGTGGTGGCCCATATGCTGAAGGCTATCGCAGCTGTGGCC	3764
Db	4273	AAGCTCATCTGTAGC	AGTGGTGGCCCATATGCTGAAGGCTATCGCAGCTGTGGCC	4332
Qy	3765	ATACTGCTCAAGGAG	CGCTGCAAAATTTGATTTTGGGACAGAAATATACTGTAATAGCCCC	3824
Db	4333	ATACTGCTCAAGGAG	CGCTGCAAAATTTGATTTTGGGACAGAAATATACTGTAATAGCCCC	4392
Qy	3825	CATGCAATGGAGAACT	TCGTCGGCAGCCCAACAGCCGATGGATGACCAACGCCCGCATG	3884
Db	4393	CATGCAATGGAGAACT	TCGTCGGCAGCCCAACAGCCGATGGATGACCAACGCCCGCATG	4452
Qy	3885	ACCCACTATCAAGCCT	GTCTTCTACAGAGAGGGTCACTGTCCTCCACAGCCGCTCTC	3944
Db	4453	ACCCACTATCAAGCCT	GTCTTCTACAGAGAGGGTCACTGTCCTCCACAGCCGCTCTC	4512

6670 TAAACATCCTACAGTTATAATCAATTTAATTATGGCCATGGAGATGGAAGATTGGCA 6729 Db
6156 CAAG-----TGCTCTCCTTCAGACCTAGA 6179 Qy
6730 ACAGCGGGTACAAAAAGATGTACGAATAAGCAAAATAAGCTGT/CATTCCTTTAGACCTAGA 6789 Db
6180 TTACCTAAAAATAAGTTTCACTGAGAAAGGAAAAAACAAGAAAAATATCCTAAAAATGGGTAAA 6239 Qy
6790 TTACTTAAAAATAAGTTTCACTGAAAGAAAGAAACCAAGAAATATTCANAAGTGGGTAAA 6849 Db
6240 TGTATGTCTTGGGGAATGGTATATTTATGAGGCTCGGGTAAACAAACAGAGGTCCATTCT 6299 Qy
6850 TGTATGTCTTGGGGAATAGTACTATGAGGCTCTGGAGAAAGAAAGGATCTCTTCT 6909 Db
6300 AACTATTCGCTCAAAAT---AAACCAGCTGGAGCCTCCAAATGGCTATAGGACCAATAC 6356 Qy
6910 GACTATTCGCTCAGAATAGAAACTCAGATGGAACTCCGGTTGCTATAGGACCAATAA 6969 Db
6357 GGTCTTGAGGGGTCAAAGACCCCAACCCAGGACGAGCACTCCTCTAAC-----6408 Qy
6970 GGGTTTGGCGGAACAAGGACCTCAATCCAGAACAGAGGCCATCTCCTAACCCCTCTGA 7029 Db
6409 -----ATAACTTCTGGATCAGACCCCACTGAGTCTAACAGACAAGCTAAAAATGGGGC 6461 Qy
7030 TTACAATACAACTCTGGATCAGTCCCACTGAGCCTTAACATCACTATTAAAAACAGGGGC 7089 Db
6462 AAACTTTTGTAGCTCATCAGGGAGCTTTTCAAGCTCTTAACCTCCAGCACTCCAGAGGC 6521 Qy
7090 GAAACTTTTAACTCATCCAGGGAGCTTTTCAAGCTCTTAACTCCAGCACTCCAGAGGC 7149 Db
6522 TACTCTCTTGTGTGGTATGCTTAGCTTCGGGCCCACTTACTATGAAAGGAATGGCTAG 6581 Qy
7150 TACTCTCTTGTGTGGCTTTGCTTAGCTTCGGGCCCACTTACTATGAGGGAATGGCTAG 7209 Db
6582 AAGAGGGAATTCAAATGTGACAAAGAAACATAGAGACCAATGACATGAGGGATCCCAAAA 6641 Qy
7210 AGGAGGGAATTCAAATGTGACAAAGGAACATAGAGACCAATGATACATGAGGGATCCCAAAA 7269 Db
6642 TAAGCTTACCTTACTGAGGTTTCTGGAAAGGCACTGATAGGAAGGTTCCCCCATC 6701 Qy
7270 TAAGCTTACCTTACTGAGGTTTCTGGAAAGGCACTGATAGGAAGGTTCCCCCATC 7329 Db
6702 CCACCAACCTTTGTAACCACTGAAGCCTTTAATCAAACTCTGAGAGTCAA-TATC 6760 Qy
7330 CCACCAACCTTTGTAACCACTGAAGCCTTTAATCGAACCTCTGAGAGTCAAATATC 7389 Db
6761 TGTACTCTGTTATGACAGTGTGGGCATGTAACTGGAATTAACCCCTTGTGTTCCA 6820 Qy
7390 TGTACTCTGTTATG-CAGTGTGGGCATGTAACTGGAATTAACCCCTTGTGTTCCA 7448 Db
6821 CTTTGGTTTAAACCAAACTAAAGATTTTGGCATTTATGGTCCAAATTTGTTCCCGAGTGT 6880 Qy
7449 CTTTGGTTTAAACCAAACTAAAGATTTTGGCATTTATGGTCCAAATTTGTTCCCGAGTGT 7508 Db
6881 ATTACTATCCGGAAGAAAGCAATCTTGAATATGACTACAGAAATCATCGCAAAAGA 6940 Qy
7509 ACTACTATCCGGAAGAAAGCAATCTTGAATATGACTACAGAAATCATCGCAAAAGA 7568 Db
6941 GAGAACCCATATCTCTGACACTTGTCTGATGCTCGGACTTGGAGTGGCAGCAGGTGTAG 7000 Qy
7569 GAGAGCCATATCCTCTGACACTAGTGTAACTGCTCGGTTGGGAGTGGCTGAGGCGTGG 7628 Db
7001 GAACAGGAAACAGTGCCTGGTCAACGGGACACAGCAGGTAGAAACAGGACTTAGTAACC 7060 Qy
7629 GAACAGGAAACAGTGCCTGGTCAACGGGACACAGCAGGTAGAAACAGGACTTAGTAACC 7688 Db
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7689 TACATCGAATTTGTAACAGAGATCTCCAGCCCTAGAAAATCTCTCAGTAACTCGGAGG 7748 Db
7121 AATCCCTAACCTCTTACTGAAGTGTCTTACAGAAATAGAGAGGTTAGATTTATTAT 7180 Qy
7749 AATCCCTAACCTCTTACTGAAGTGTCTTACAGAAACAGAGGGGTTAGATCTGTTAT 7808 Db

7181 TTCTAAAAGAGAGGATTTATGTAGCCTTGAAGAGGAATGCTGTTTTTTATGTGATC 7240 Qy
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7241 ATTCAAGGGCCATCAGAGACTCCATGAAACAAGCTTAGAGAAAGTTGGAGAACGTCGAA 7300 Qy
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7421 GGCATGTATTTAAACAAGTTAAATGCTCTTCAATAGAGAAACGAATAAGTGCAGTCCAGA 7480 Qy
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7481 TCATGCTACTTAGACAACAGTACCAAGCCGCTTAGC--AGGGAAGCTGGCGCTAGC 7537 Qy
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8169 CTTCTAGTTCTAAGATTAGAACTATTAAACAAGAGAAAGTGGGGAATGAAAGAGTAA 8228 Db
7598 AATAACAACCT-----AAGCTAATGAGAGCTTAAATTTGTTCTGAA 7638 Qy
8229 AATGCAACCTGACTCTCCAGAACCCAGGAAGTTAAAGAAAGCTTAAATGCCCTCGAA 8288 Db
7639 TTCCAGAGTTTGTCTCTTATAGTAAAGATTAGTTTGTGCTTTTAAATATATG-- 7696 Qy
8289 TTCCAGACCTGTTCTCCTATAGTAAAGATCATCTTTTGTGTTTTAGGGCTGCTT 8348 Db
7697 -----GGAAAGTAAAAATAGGCCCTGAGTCAATGCTCTGTAACCTGCTTGA 7730 Qy
8349 TCTGCTCTGTACAAAACCTTTGTGGAAGGGGAAAAACAGGCCCTGAGTATGCTCTAT 8408 Db
7731 GCATGAACTCTTGTAAA-----CTATTGTAG 7757 Qy
8409 GCTTGAACCTTCTTGAAACTGCTCTAACTGCTTTGCTTCTGTAACCTGCTTGA 8468 Db
7758 ATBACAAGAAAGGAGTTTCTAACTGCTTTGTTAGCTTCTGTAAACCTGTTGCGCAT 7817 Qy
8469 TAAGATAAAAAGAGGAGAGTCAATTGCTTAAACCGGACCCAGTAAGATCGGGGTGCGAC 8528 Db
7818 AAGAGTGTGAAATGTTGATACACATATCTTGTGACAAACATGCTCTCCCAACCCCGAAA 7877 Qy
8529 AAAATGTTGAAATCTGATTAATATATCTTGTGACAAATATGCTCTCCCAACCCAGAGA 8588 Db
7878 CATCGCAAAATGTAACTCTAAAAACAAATTAATTAATTTGGTCCAGAGCGGGGCTC 7937 Qy
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7938 TCAGAGTTTAAATTTGACTGTTTGTGATATTTT-GAAATGATTTGTTTCT-AAAGCGC 7995 Qy
8649 TCGAAGTTTGAATTTGACTGTTTGGATATTTTAAATAATGATTTGTAAGAGCGC 8708 Db
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8709 GGVTTTGTGAAACCCCAATAAAAGTGTCTCCGACTCCACACTCGGGGCGCAGTCTCT 8768 Db
8056 ACCCTCGCTGTGTACGACTGTGGGCCCCAGCGCGCTTCGGAATAAAAAATCTCTTGTG 8115 Qy
8769 ACCCTCGCTGTGTACGACTGTGGGCCCCAGCGCGCTTCGGAATAAAAAATCTCTTGTG 8828 Db
8116 TTTGCATCAAAA 8127 Qy
8829 TTTGCATCAAGA 8840 Db

QY	172	TAAACCCGAGAACCGACTTGGAGGTAAAGAGATCCTCTTTTAAACGTGT--ATGCATG	229	Db	1813	CTCTATAATTGAAAACTAAACCATCCCTTTCTCGAGGATCCCAACGCCTCACGGGG	1872
Db	739	TCACACCGAGAACCGACTTGGAGGT-AAAGGATCCCTTTGGAACGTTGAGTGTGTG	797	QY	1305	TTGGTGGAGTCCCTTATGTTCTCTACACGACCTACTTGGGATGATTTGTCAACAGCTGCTG	1364
QY	230	TACCGCGCGGCTCTCTGTTCTGAGTGTCTGTTTTTCAAGTGGTGGCGCTTTCGGTTTGA	289	Db	1873	TTGGTGGAGTCCCTTATGTTCTCTACACGACCTACTTGGGATGATTTGTCAACAGCTGCTG	1932
Db	798	TGTCGGCTGGCGTCTCTGTTCTGAGTGTCTGTTTTTTCGGTGTATCGCGCTTTCGGTTTGA	857	QY	1365	CAGACACTCTTCAACACCGAGGAGGAGAGAAATTTCTATTAGAGGCTAGAAAAATGTT	1424
QY	290	GCTGTCTCTCAAGCCGTAAAGGCTGGGGACTGTGATCAGCAGAGAGTGCTAGGAGGATC	349	Db	1933	CAGACACTCTTCAACACCGAGGAGGAGAGAAATTTCTGTTAGAGGCTAGAAAAATGTT	1992
Db	858	GCTGTCTCTCAAGCAGTAAAGACTGGGGA-----ATACAGCAGAGTGCTAGGAGGATC	912	QY	1425	CCTGGGCGCAGCGGGCGACCCACGCGTTGCAAAATGAGATTGACATGGGATTTCCCTTA	1484
QY	350	ACAGGCTGTCTCCCTCGGGGACGCCCC-----CGGAGGTGAGGAGGCCAGGCCCTG	404	Db	1993	CCTGGGCGCAGCGGGCGACCCACGCGATTGCAAAATGAGATTGACATGGGATTTCCCTG	2052
Db	913	ACAGGCTGCCACCTCGGGGACGCCCGCTGTGGGAGGTGGGAGAGCCAGGAGACGCTG	972	QY	1485	ACTCGGCCCGTTGGGACTACAAACGCGCTGAAGGTAGGGAGAGCTTTGAAAAATCTATCGC	1544
QY	405	GTGGTCTCTACGTGCGGTCAAGGACCGAAATTTCTGTTGCTGAAGCGAAAGCTTCCCCCT	464	Db	2053	ACTCGGCCCGTTGGGACTACAAACGCGCTGAAGGTAGGGAGAGCTTTGAAAAATCTATCGC	2112
Db	973	GTGGTCTCTCTGTCGGTCAAGGACCGAGTTCTGTTGTTGAAGCGAAAGCTTCCCCCT	1032	QY	1545	CAGGCTCTCGTGGCGGCTCTCGGGGCGCTCAAGAAGCGGCCCACTAAATTTGGCTAAGGTA	1604
QY	465	CCGCGACCGTCCGACTCTTTTGCTGCTGTGAAGACGTGGACGGGTCAAGTGTGCTG	524	Db	2113	CAGGCTCTCGTGGCGGCTCTCGGGGCGCTCAAGAAGCGGCCCACTAAATTTGGCTAAGGTA	2172
Db	1033	CCGCGCGGTCCGACTCTTTTGCTGCTGTGAAGACGGGAGCGGTGCGGTGTGCTG	1092	QY	1605	AGAGAAGTATGACAGGAGCGGATGAACCCCTCTGTTTCTTCTGAGAGGCTTTGGAA	1664
QY	525	GATCTGTGTTGTTCTGTTTGTGTCTTTGTCTGTTGTGCTCTGTTCTACAGTTTTAAT	584	Db	2173	AGAGAAGTATGACAGGAGCGGATGAACCCCTCTGTTTCTTCTGAGAGGCTTTGGAA	2232
Db	1093	GATCTGTGTTGTTCTGTTTGTGTCTTTGTCTGTTGCGTCTGTTCTACAGTTTTAAT	1152	QY	1665	GCCTTCAGCGGTTACACCCCTTTTGATCCACCTCAGAGGCCCAAAAGCCTCAGTGGCT	1724
QY	585	ATGGGACAGACGGTGACGACCCCTCTTAGTTTGTGCTCTCGACCATTTGGACTGAAGTTAA	644	Db	2233	GCCTTCAGCGGTTACACCCCTTTTGATCCACCTCAGAGGCCCTCAGAAAGCCTCAGTGGCT	2292
Db	1153	ATGGGACAGACGGTGACGACCCCTCTTAGTTTGTGCTCTCGACCATTTGGACTGAAGTTAA	1212	QY	1725	TTGGCTCTTATAGGACAGTCAGCCTTTGGATATTAGAAAGAGCTTCAGAGACTGGAAGG	1784
QY	645	TCCAGGCTCATAAATTTGTGAGTTTCAAGTTAAGAGGACCTTTGGCAGACTTTCTGTGTC	704	Db	2293	CTGGCTCTCATAGGACAGTCAGCCTTGGATATCAGAAAGAAAGCTTCAGAGACTGGAAGG	2352
Db	1213	TCCAGGCTCATAAATTTGTGAGTTTCAAGTTAAGAGGACCTTTGGCAGACTTTCTGTGTC	1272	QY	1785	TTACAGAGCTCAGTTTACGTGATCTAGTGAAGGAGCAGAGAGTATATTACAAAGG	1844
QY	705	TCTGAATGGCCGACATTCGATTTGGATGGCCATCAGAGGGGACCTTTAATTTGAGATT	764	Db	2353	TTACAGAGCTCAGTTTACGTGATCTAGTGAAGGAGCAGAGAGTATATTACAAAGG	2412
Db	1273	TCTGAATGGCCGACATTCGATTTGGATGGCCATCAGAGGGGACCTTTAATTTGAGATT	1332	QY	1845	GAGACAGAGAGAAAGGAGGAAACAAAGAAAGAGAGAGAAAGAGAGAAAGGAGGAGAAAGA	1904
QY	765	ATCCTGGCTTTAAAGCAGTTATTTTTCAGACTGGACCCCGGCTCTCATCCGATCAGGAG	824	Db	2413	GAGACAGAGAGAAAGGAGGACCAAGAAAGAGAGAGAAAGAGAGAAAGGAGGAGAAAGA	2472
Db	1333	ATCCTGGCTTTAAAGCAGTTATTTTTCAGACTGGACCCCGGCTCTCATCCGATCAGGAG	1392	QY	1905	CGTAATAAACCGCAAGAGAGAAATTTTACATAGATCTTGCTCAGTGGTTGAAGGAAA	1964
QY	825	CCCTATATCTTACGTGGCAAGATTTGGCAGAGGATCCTCCGCCATGGTTTAAACCATGG	884	Db	2473	CGTAATAAACCGCAAGAGAGAAATTTTACATAGATCTTGCTCAGTGGTTGAAGGAAA	2532
Db	1393	CCCTATATCTTACGTGGCAAGATTTGGCAGAGGATCCTCCGCCATGGTTTAAACCTTGG	1452	QY	1965	AGCAATACGAAAGAGAGAGAGATTTTATGSAATAATTAGTTCAGGCCCTAGACAGTCAAGG	2024
QY	885	CTGAATAAGCAAGAAAGCCAGGTCCCGGAATTTCTGGCTCTTGAGAGAGAAACAAACAC	944	Db	2533	AGCAATACGAAAGAGAGAGAGATTTTATGSAATAATTAGTTCAGGCCCTAGACAGTCAAGG	2592
Db	1453	CTGAATAAGCAAGAAAGCCAGGTCCCGGAATTTCTGGCTCTTGAGAGAGAAACAAACAC	1512	QY	2025	AACCTGGCAATAGGACCCACCTCGACAGGACCAATGTGCATATTGTAAAGAAAGAGGA	2084
QY	945	TCGGCTGAAAGGTCAAGCCCTCTCTCATATCTACCCCGAGATTGAGGAGCCACCGGCT	1004	Db	2593	AACCTGGCAATAGGACCCACCTCGACAGGACCAATGTGCATATTGTAAAGAAAGAGGA	2652
Db	1513	TCGGCTGAAAGGTCAAGCCCTCTCTCATATCTACCCCGAGATTGAGGAGCCCGGCT	1572	QY	2085	CACCTGGCAAGGAACTGCCCCCAAGAGGAGGAAACAAAGGACCAAGGATCTTAGCTCTAGAA	2144
QY	1005	TGGCGGAAACCCCAATCTGTTTCCCCACCCCTTATCTGSCACAGGCTCGCGAGGGGA	1064	Db	2653	CACCTGGCAAGGAACTGCCCCCAAGAGGAGGAAACAAAGGACTGAAGTCTTAGCTCTGAA	2712
Db	1573	TGGCGGAAACCCCAATCTGTTTCCCCACCCCTTATCTGSCACAGGCTCGCGAGGGGA	1632	QY	2145	GAAGATAAAGATTAGGGGAGACGGGTTTGGGAACCCCTCCCGAGCCCGAGGTAACCTTG	2204
QY	1065	CCCTTTCGCCCTCTGAGCTCGCGCGGTGGAGGACCTGCTGAGGAGACTCGAGAGCCGG	1124	Db	2713	GAAGATAAAGACTAGGGAGACGGGTTTGGGAACCCCTCCCGAGCCCGAGGTAACCTTTA	2772
Db	1633	CCCTTTCGCCCTCTGAGCTCGCGCGGTGGAGGACCTGTTGAGGAGACTCGAGAGCCGG	1692	QY	2205	AAGGTGGAGGGGCAACCAAGTTGATCTGTTGATACCCGAGCGAAACATTTCAGTGCTA	2264
QY	1125	AGGGCGCCACCCCGGAGCGGACAGACAGATTCGCAATTACCGCTGCGCAGTACGGC	1184	Db	2773	AAGGTGGAGGGGCAACCAAGTTGATCTGTTGATACCCGAGCGAAACATTTCAGTGCTA	2832
Db	1693	AGGGCGCCACCCCGGAGCGGACAGACAGATTCGCAATTACCGCTGCGCAGTACGGC	1752	QY	2265	CTACAGCATTAGGAAAACTTAAAGATATAAAATCTCTGGGTGATGGGTGCCACAGGGCAA	2324
QY	1185	CCTCCCAACACCGGGGGGCAATTCAGGCCCTTCAGTATTGGCCCTTTTCTTCTGAGAT	1244	Db	2833	CTACAGCATTAGGAAAACTTAAAGATATAAAATCTCTGGGTGATGGGTGCCACAGGGCAA	2892
Db	1753	CCTCCCAACACCGGGGGGCAATTCAGGCCCTTCAGTATTGGCCCTTTTCTTCTGAGAT	1812	QY	2325	CAAACAGTATCCATGGACTACCCGAGAAACAGTTGACTTTGGGAGTGGGACGGGTAAACCCAC	2384
QY	1245	CTCTATAATTGGAAAACTAACCATCCCTTTTCTCGGAGGATCCCAACGCTCACGGGG	1304				

Db 2893 CAAACAATATCCATGAGTACCCGAAGAAACAGTGTGACTTGGGAGTGGGACGGGTAAACCCAA 2952
Qy TCGTTTCTGGTCATACCTAGTATGCCAGACACCCCTCTTAGTGTAGAGACTTATGTACCAAG 2444
Db TCGTTCTGGGCATACCTAGTATGCCAGACACCCCTCTTAGTGTAGAGACTTACTGTAGCCACA 3012
Qy ATGGGAGCACAATTTCTTTGAAACAGGGGAAACAGAAAGTGTCTGCAAAATACAAACCT 2504
Db ATGGGAGCACAATTTCTTTGAAACAGGGGAAACAGAAAGTGTCTGCAAAATACAAACCT 3072
Qy ATCACTGTGTTCACCCCTCCAAATTTAGATGACGAATATCGACTATATCTCTCCCTAGTAAAG 2564
Db ATCACTGTGTGACCCCTCCAAATTTAGATGACGAATATCGACTATATCTCTCCCTAGTAAAG 3132
Qy CCTGATCAAAATATACAAATTTCTGGTTGGAAACAGTTTCCCAAGCCTGGGCGAGAAACCGCA 2624
Db CCTGATCAAAATATACAAATTTCTGGTTGGAAACAGTTTCCCAAGCCTGGGCGAGAAACCGCA 3192
Qy GGGATGGGTTGGCAAAAGCAAGTTCCGCCACAAGTTATTCACCTGAAGCCAGTGCACCA 2684
Db GGGATGGGTTGGCAAAAGCAAGTTCCGCCACAAGTTATTCACCTGAAGCCAGTGCACCA 3252
Qy CCAGTGTCTAGTCAGACAGTACCCCTTGAGTAAAGAGCTCAAGAAAGGAAATTCGGCCGCAT 2744
Db CCAGTGTCTAGTCAGACAGTACCCCTTGAGTAAAGAGCTCAAGAAAGGAAATTCGGCCGCAT 3312
Qy GTCCAAAGATTAATCCAAACAGGGCATCTTAGTCTCTGTCCTCAATCTCCCTGGAAATCTCCC 2804
Db GTCCAAAGATTAATCCAAACAGGGCATCTTAGTCTCTGTCCTCAATCTCCCTGGAAATCTCCC 3372
Qy CTGCTACCGGTTAGAAAGCCTGGGACTAATGACTATCGACCACTGACAGACTTGAGAGAG 2864
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Qy GCTCTCCCAACCCCAACGGAGCTGGTATACAGTATTTGGACTTAAAGGATGCTTCTTCTGC 2984
Db GCTCTCCCGCCCAACGGAGCTGGTATACAGTATTTGGACTTAAAGGATGCTTCTTCTGC 3552
Qy CTGAGATTAACCCCACTAGCCAAACCACTTTTGGCTTCGAATGGAGAGATCCAGGTGCG 3044
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Db GGAAGAACCGGGGAGCTCACTTGGACTCGACTGCCCCCAAGGGTTCAAAACCTCCCGACC 3672
Qy ATCTTTGACGAAGCCCTACACAGAGACCTGGCCAACTTCAGGATCCAAACACCTCAGGTG 3164
Db ATCTTTGACGAAGCCCTACACAGAGACCTGGCCAACTTCAGGATCCAAACACCTCAGGTG 3732
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Qy AAGGCCCCAGATTTGACGAGAGAGGTAAACATCTTGGGGTACAGTTTTGGGGGACGGGCAG 3344
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Qy CGATGCTACGAGGACCGAAGAAACTGTAGTCCAGATACCGGCCCCCAACACAGCC 3404
Db CGATGCTACGAGGACCGAAGAAACTGTAGTCCAGATACCGGCCCCCAACACAGCC 3972
Qy AACAATGAGAGATTTTGGGACAGCTGGATTTTGGAGACTGTGGATCCCGGGTTT 3464
Db AACAATGAGAGATTTTGGGACAGCTGGATTTTGGAGACTGTGGATCCCGGGTTT 4032

Qy GCGACCTTAGCAGCCCACTCTACCCGCTAACCAAGAAAGGGGAATTTCTCTGGGCT 3524
Db GCGACCTTAGCAGCCCACTCTACCCGCTAACCAAGAAAGGGGAATTTCTCTGGGCT 4092
Qy CCTGAGCACCAAGGCAATTTGATGCTATCAAAAGGCCCTGCTGAGCGCACCTGCTCTG 3584
Db CCTGAGCACCAAGGCAATTTGATGCTATCAAAAGGCCCTGCTGAGCGCACCTGCTCTG 4152
Qy GCGCTCCCTGACGTAACTAAACCCCTTTACCTTTATGTGGATGACGCTAAGGAGTAGCC 3644
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Qy CGGGAGGTTTAAACCAACCCCTAGGACCATGGAGAGACCTGTCCCTCACTGTCAAG 3704
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Qy AAGCTCGATCTGTAGCCAGTGGTGGCCCATATGSCCTGAAGGCTATCGCAGCTGTGGCC 3764
Db AAGCTCGATCTGTAGCCAGTGGTGGCCCATATGSCCTGAAGGCTATCGCAGCTGTGGCC 4332
Qy ATACTGTGTCAAGGACGCTGACAAAATTTGACTTTGGGACAGAAATATAAATGTAAATAGCC 3824
Db ATACTGTGTCAAGGACGCTGACAAAATTTGACTTTGGGACAGAAATATAAATGTAAATAGCC 4392
Qy CATGCAITGGAGAACATCGTTGGCAGCCGCCAGACCGATGGATGACCAACGCCCGCATG 3884
Db CATGCAITGGAGAACATCGTTGGCAGCCGCCAGACCGATGGATGACCAACGCCCGCATG 4452
Qy ACCCACTATCAAGCCTGCTTCTCACAGAGGGGTACGTTTCGCTCCACAGCCGCTCTC 3944
Db ACCCACTATCAAGCCTGCTTCTCACAGAGGGGTACGTTTCGCTCCACAGCCGCTCTC 4512
Qy AACCCTGCACTCTTCTGCTGAAGAGACTGATGAACCAAGTGAATCATGATTTGCCATCAA 4004
Db AACCCTGCACTCTTCTGCTGAAGAGACTGATGAACCAAGTGAATCATGATTTGCCATCAA 4572
Qy CTATTTGATTTGAGGAGACTGGGGTCCGAAAGGACCTTACAGACATACCCCTGACTGGAGAA 4064
Db CTATTTGATTTGAGGAGACTGGGGTCCGAAAGGACCTTACAGACATACCCCTGACTGGAGAA 4632
Qy GTGCTAACTCTGTTCACTGACGGAAGCAGCTATGTGTGGAGGTAAAGAGATGCTGGG 4124
Db GTGTTAACTCTGTTCACTGACGGAAGCAGCTATGTGTGGAGGTAAAGAGATGCTGGG 4692
Qy GCGGCGGTGTGGAGCGGACCCGACGATCTGGGCCAGCAGCTCCCGGAAGGAATTTCA 4184
Db GCGGCGGTGTGGAGCGGACCCGACGATCTGGGCCAGCAGCTCCCGGAAGGAATTTCA 4752
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Czauderna, F., Fischer, N., Boller, K., Krach, U., Kurth, R. and
Toenjes, R.R.
Molecular Characterization of Human-tropic and
Replication-competent Porcine Endogenous Retroviruses
Unpublished
2 (bases 1 to 8849)
Toenjes, R.R.
Direct Submission
Submitted (04-MAY-1999) Toenjes R.R., Medical Biotechnology,
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DB 1302 CTGTTAAAGCAGTTATTTTTCAGACTGGACCCCGCTCTCATCCCGATCAGAGGCCCTATA 1361
QY 832 TCCTTACGTGCGAAGATTTCGCGAGAGGATCTCCGCCATCGGCTGCTTAAACCATGGCTGAATA 891
DB 1362 TCCTTACGTGCGAAGATTTCGCGAGAGGATCTCCGCCATCGGCTGCTTAAACCATGGCTGAATA 1421
QY 892 AGCCAGAAAGCCAGGTCCCGAATTTCTGCTGCTTGGAGAGAAACAAACACTCGGCTG 951
```

[illegible]

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Db	3762	CGAAGGCACTACTGCTGGAAATGCTGACCTAGGCTACAGAGCCTCTGCTAAGAGGCC	3821	Db	4842	AAAGGGGTTGCTTACCTCAGCAGGAGGGAATAAAGAAACAAAGAGGAAATTTCTAAGCC	4901
Qy	3292	AGATTTGCGAGGAGAGGTAAACATCTTGGGTACAGTTTGGGACCGGCGGACGCGATGG	3351	Qy	4372	TATTAAGAGCCGTACATTTACAAAGAGCTAGCTATTATACACTGTCTCGACATCAGA	4431
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Db	3882	TGACGGAGGCA CGGAAGAAACTGTAGTCCAGATACCGGCCCAACACACAGCCAAACAA	3941	Db	4962	AAAGCCAAAGATCTCATATCTAGAGGAACAGATGGCTGACCGGTTGCCAAGCAGGACAG	5021
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Qy	3472	TAGCAGCCCACTCTACCCGCTAACCAAGAAAGAGGGAATTCCTCGGCTCTCTGAGC	3531	Qy	4552	AGTACACCCCTAGAGACTGGCAAGAGATAAAAGATAGACCAAGTTCTCTGAGACTCCGG	4611
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Qy	3532	ACCAGAGGCAATTGATGCTATCAAAAGGCCCTGCTGAGCGCACTGCTCTGCGCCCTCC	3591	Qy	4612	AAGGAGCCTGCTTATCTCAGATGGAGGAAATCTCTGCCCCACAAAGAGGTTAGAT	4671
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AUTHORS	Bartosch, B., Weiss, R.A. and Takeuchi, Y.
TITLE	Direct Submission
JOURNAL	Submitted (23-APR-2002) Wohl Virion Centre, Windeyer Institute, UCL, 46 Cleveland St, London W1T4JF, UK
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ORIGIN	
Query Match	82.7%; Score 6727; DB 13; Length 8714;
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QY	172	TAAACCCGAGAACCGACTTGGAGGTAAAGAGATCCTCTTTTAAAGTGATGCAATGTA	231
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QY	292	TGTCTCTCTCAGGCGCTAAGGGCTTGGGGGACTGTGTATCAGCAGACGTGTAGGAGATCAC	351
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QY	532	TGTTTTCTGT	591
Db	960	TGTTTTCTGT	1019
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QY	772	CTGTTAAAGCATTTATTTTTCAGACTGGACCGGGCTCTCATCCCGATCAGGACCCCTATA	831
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Db	2040	TGATCGAGGACCGAATGNAACCCCTCTGTCTTTTCTTGAGAGGCTCTTGAAGGCTTCA	2099
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Db	2100	GGCGGTACACCCCTTTTGTATCCACTCAGAGGGCCCAAAAGCCTCAGTGGCTTTGGCT	2159
QY	1732	TTATAGGACAGTCAGCCTTTGGATATTAAGAAAGCTTCAGAGACTGAGAGGTTACAGG	1791
Db	2160	TCATTTGGGCGTCCGCTCTCGGATATCAGGAAAGAACTTCAGAGACTGAGAGGTTACAGG	2219
QY	1792	AGGCTGAGTTAGCTGATCTAGTGAAGGAGGACAGAAAGTATTTACAAAAGGGAGACAG	1851
Db	2220	AGGCTGAGTTAGCTGATCTAGTGAAGGAGGACAGAAAGTATTTACAAAAGGGAGACAG	2279
QY	1852	AAAGAAAGGGGAAACAAAGAAAGAGAGAAAGAGAGAAAGGGAGAAAGACGCTTAATA	1911
Db	2280	AAAGAGAGAGAGAAACAGAGAAAGAAAGAGAGAGAGAGAAAGGGAGAAAGACGCTGATA	2339
QY	1912	AAACGCAAGAGAAAGAAATTTGACTAAGTCTTGGCTGAGTGTGAGAGGAAAGCAATA	1971
Db	2340	GACGCAAGAGAAAGAAATTTGACTAAGTCTTGGCGCGAGTGTGAGAGGAAAGACGCA	2399
QY	1972	CGGAAGAGAGAGAGATTTTAGGAAATTTAGTTCAGGCGCTAGACAGTCAAGGAACTCGG	2031
Db	2400	GAGAGAGAGAGAGATTTTAGGAAATTTAGTTCAGGCGCTAGACAGTCAAGGAACTCGG	2459
QY	2032	GCAATAGGACCCCACTCGACAAAGGACCAATGTGCAATTTGTAAAGAAAGAGGACACTGGG	2091
Db	2460	GCAATAGGACCCCACTCGACAAAGGACCAATGTGCAATTTGTAAAGAAAGGACACTGGG	2519
QY	2092	CAAGGAACTGCCCAAGAGAGGAAACAAAGGACCAAGGATCTAGTCTTAGAAGAGATA	2151
Db	2520	CAAGGAACTGCCCAAGAGAGGAAACAAAGGACCAAGGATCTAGTCTTAGAAGAGATA	2579
QY	2152	AAAGTTAGGGGAGACGGGGTTTCGGACCCCTTCCCGAGCCAGGGTTAACTTTTGAAGGTG	2211

[illegible]

QY 4372 TATTAGAACCGGTACATTTTACAAAAAGGCTAGCTATTATATACATGTCCTGGACATCAGA 4431
DB TATTAGAACGCTTTACATTTTGC AAAAAGGCTAGCTATTATATACATGTCCTGGACATCAGA 4859
QY 4432 AAGCTAAGATCTCATATCCAGAGGAAACACAGATGGCTGACCGGTTGCCAAGCAGGCAG 4491
DB AAGCCAAAGATCTCATATCTAGAGGAAACACAGATGGCTGACCGGTTGCCAAGCAGGCAG 4919
QY 4492 CCCAGGGTGTAAACCTTCTGCTTATATAGAAATGCCAAAGCCCCAGAACCCACAGACGAC 4551
DB CCCAGGCTGTAAACCTTCTGCTTATATAGAAACGCCCAAGCCCCAGAACCCACAGACGAC 4979
QY 4552 AGTACACCTTAGAAGACTGGCAAGAGATAAAAAGATAGACAGATTTCTCTGAGACTCCGG 4611
DB AGTACACCTTAGAAGACTGGCAAGAGATAAAAAGATAGACAGATTTCTCTGAGACTCCGG 5039
QY 4612 AAGGGACCTGTATACCTCAGATGGGAAGGAATCCTGCCACCAAGAGGGTTAGAAAT 4671
DB AAGGGACCTGTATACCTCATATGGGAAGGAATCCTGCCCAAGAAAGGGTTAGAAAT 5099
QY 4672 ATGTCCAAACAGATACATCGCTTAACCCACCTAGGAATAAACACCTTGACGAGTTGGTCA 4731
DB ATGTCCAAACAGATACATCGCTTAACCCACCTAGGAATAAACACCTTGACGAGTTGGTCA 5159
QY 4732 GAACATCCCTTATCATGTTCTGAGGCTACGAGGAGTGCCTGACTCGGTTGCTCAACATTT 4791
DB GAACATCCCTTATCATGTTCTGAGGCTACGAGGAGTGCCTGACTCGGTTGCTCAACATTT 5219
QY 4792 GTGTGCCCTGCCAGCTGGTTAAATGCTAATCCTTCCAGAAATGCTCCAGGGAAGAGACTAA 4851
DB GTGTGCCCTGCCAGCTGGTTAAATGCTAATCCTTCCAGAAATGCTCCAGGGAAGAGACTAA 5279
QY 4852 GGGGAAGCCACCCAGCGCTCACTGGGAAGTGGACTTCACTGAGGTAAAGCCGGCTAAAT 4911
DB GGGGAAGCCACCCAGCGCTCACTGGGAAGTGGACTTCACTGAGGTAAAGCCGGCTAAAT 5339
QY 4912 ACGGAAACAAATACCTATTGGTTTTTGTAGACACCTTTTTCAGATGGGTAGAGGCTTATC 4971
DB ACGGAAACAAATATCTATTGGTTTTTGTAGACACCTTTTTCAGATGGGTAGAGGCTTATC 5399
QY 4972 CTACTAAGAAAGAGACTTCAACCGTGGTCTTAAAGAAATACCTGGNAGAAATTTTCCAA 5031
DB CTACTAAGAAAGAGACTTCAACCGTGGTCTTAAAGAAATACCTGGNAGAAATTTTCCAA 5459
QY 5032 GATTTGGAATACCTAAGGTAAATAGGTCAGACAAATGGTCCAGCTTTTGTGCCCAGGTAA 5091
DB GATTTGGAATACCTAAGGTAAATAGGTCAGACAAATGGTCCAGCTTTTGTGCCCAGGTAA 5519
QY 5092 GTCAGGGAATGGCCAAAGATTTGGGATTTGATTTGGAATCTGATTTGTGATATGATACAGACCC 5151
DB GTCAGGGAATGGCCAAAGATTTGGGATTTGATTTGGAATCTGATTTGTGATATGATACAGACCC 5579
QY 5152 AAAGCTCAGGACAGGTAGAGAGATCAATAGAACCAATTAAGAGACCTTACTTAATTTGA 5211
DB AAAGCTCAGGACAGGTAGAGAGATCAATAGAACCAATTAAGAGAGACCTTACTTAATTTGA 5639
QY 5212 CCGCGGAGACTGGCGTTAATGATTTGATAGTCTCTCGTCCCTTTTGTGCTTTTGTAGGTTA 5271
DB CCAGAGAGACTGGCATTAATGATTTGATAGTCTCTCGTCCCTTTTGTGCTTTTGTAGGTTA 5699
QY 5272 GGAACACCCCTGAGACTTTGGGCTGACCCCTTATGAATTACTCTACGGGGACCCCCC 5331
DB GGAACACCCCTGAGACTTTGGGCTGACCCCTTATGAATTACTCTACGGGGACCCCCC 5759
QY 5332 CATTTGTAGAAATTTGCTTCTGTACATAGTGTGCTGCTGCTTTCCAGCCCTTTGTCT 5391
DB CATTTGTAGAAATTTGCTTCTGTACATAGTGTGCTGCTGCTTTCCAGCCCTTTGTCT 5819
QY 5392 CTAGGCTCAAGGCACTTGTAGTGGGTGAGACCAACGAGCTGGAGGCAACTCCGGGAGGCT 5451
DB CTAGGCTCAAGGCACTTGTAGTGGGTGAGACCAACGAGCTGGAGGCAACTCCGGGAGGCT 5879

QY 5452 ACTCAGGAGGAGGAGACTTGCAGATCCCAATCGTTTCCAAAGTGGAGATTCAAGTACG 5511
DB ACTC---AGGAGGAGACTTGCAGATCCCAATCGTTTCCAAAGTGGAGATTCAAGTACG 5936
QY 5512 TTAGACGCCACCGTGCAGGAAACCTTCGAGACTCGGTGGAAGGCCCTTATCTCGTACTTT 5571
DB TTAGACGCCACCGTGCAGGAAACCTTCGAGACTCGGTGGAAGGCCCTTATCTCGTACTTT 5996
QY 5572 TGACACACCAACCGCTGTGAAAGTCTGAAAGTCTCCACCTGGATCATGATCCCAAG 5631
DB TGACACACCAACCGCTGTGAAAGTCTGAAAGTCTCCACCTGGATCATGATCCCAAG 6056
QY 5632 TTAAACCGGCGCCACCTCCGATTCGGGTGGAAGCCGAAAGACTGAAATCCCTTAA 5691
DB TTAAACCGGCGCCACCTCCGATTCGGGTGGAAGCCGAAAGACTGAAATCCCTTAA 6116
QY 5692 AGCTTCGCTCCATCGCTGGTTCCTACTCTGTCAATAAAGCTCTCAGACTTAATGGTATG 5751
DB AGCTTCGCTCCATCGCTGGTTCCTACTCTGTCAATAAAGCTCTCAGACTTAATGGTAAA 6176
QY 5752 CGCATAGGAGACAGCTGAACTCCCATAAACCTTTATCTCTCACTGGTTAATTAAGTAC 5811
DB CGCTTGTGGAAGCGGCTGAACTCCCATAAACCTTTATCTCTCACTGGTTAATTAAGTAC 6236
QY 5812 TCCGCGACAGGTATTAATATCAACAACTCAAGGGAGGCTCTTTAGGAACTGGTGG 5871
DB TCCGCGACAGGTATTAATATCAACAACTCAAGGGAGGCTCTTTAGGAACTGGTGG 6296
QY 5872 CCTGATCTATAGTTCCTCAGATCAGTTATCTCTAGTCT-----GACCTCAACC 5922
DB CCTGATCTATAGTTCCTCAGATCAGTTATCTCTAGTCT-----GACCTCAACC 6356
QY 5923 CCAGATCTCTCCATGCTCAGGATTTTATGTTGCCAGGACCAACCAATAATGGAATA 5982
DB CCGATGACTTCCGTTTACGGGTTTACGGTTCAGGACCCCAATAATAAGAA 6416
QY 5983 CATTCGGAATCCAGAGATTTCTTTGTTAAACAAATGGAATCTGTTAACTCTTAATGAT 6042
DB TATTGTGGAATCTCTCAGGATTTCTTTGCAAGCAATGAGCTGCAATCTTAATGAT 6476
QY 6043 GGATATTGGAATGGCCAACTCTCAGCAGATAGGTAAAGTTTCTTATGTTCAACACC 6102
DB GGGAATTTGGAATGGCCAGTCTCTCAGCAAGCAGAGTAACTCTTTGTTAAACAT 6536
QY 6103 TATACAGCTCTGGAACAATTTAATTAACCTGATTTAGAACCTGGAAGGCCCAAG--- 6159
DB CTTACAGTTTAAATCAATTTAATTTATGCGCATGGAGATGGAAGATTGGCAACAGCGG 6596
QY 6160 -----TGCTCTCTTCAGACTAGATTACCTA 6186
DB GTACAAAAGATGTACGAAATAAGCAATAAGCTGTCAATTCGTTAGACTAGATTACTTA 6656
QY 6187 AAAATAAGTTTCACTGAGAAAGGAAACAAAGAAATATCTTAAATGGTAAATGGTATG 6246
DB AAAATAAGTTTCACTGAGAAAGGAAACAAAGAAATATCTTAAATGGTAAATGGTATA 6716
QY 6247 TCTTGGGAAATGGTATATTTATGGAGCTCGGTTAAACCAACAGGCTCAATCTAATATT 6306
DB TCTTGGGAAATAGTGTACTATGGAGCTCTGGAGAAAGAAAGGATCTGTTCTGACTATT 6776
QY 6307 GCGCTCAAAAT---AAACAGCTGGAGCTTCAATGGCTATAGNCCAAATACGCTCTTG 6363
DB GCGCTCAGAAATAGAACTCAGATGGAACCTTCGGTTGCTATAGGACCAATAAGGGGTTG 6836
QY 6364 ACGGCTCAAGACCCCAACCAAGGACAGGACCATCTCTTAAC----- 6408
DB GCGCAACAGGACCTTCAATCCAGAAACAGAGGCTATCTCTTAACCTCTGATTACAAT 6896
QY 6409 ATAACTTCTGGATCAGACCCCACTGAGTCTAACAGCAGACTTAAATGGGGCAAACTT 6468
DB ACAACCTCTGGATCAGTCCCCCAGCTTAACATCACTATTAATAAGGGCGGAACTT 6956
QY 6469 TTTAGCTCTATCCAGGAGCTTTTCAAGCTCTTAACTCCAGACTCCAGAGGCTACCTCT 6528

Db 1 GGATCTGTTGGTTTCTGTTTGGTGTCTTTGTCCTTGTGCGTCCTTGTCTACAGTTTAA 60
Qy 584 TATGGACACAGCGTGAACGACCCCTCTTAGTTTGACTCTCGACCAATGGACTGAAGTTAA 643
Db 61 TATGGACACAGCGTGAACGACCCCTCTAGTTTGACTCTCGACCAATGGACTGAAGTTAA 120
Qy 644 ATCCAGGGCTCATATTTGTCTAGTTTCAGGTTAAGAAAGGACCTTGGCAGACTTCTGTGT 703
Db 121 ATCCAGGGCTCATATTTGTCTAGTTTCAGGTTAAGAAAGGACCTTGGCAGACTTCTGTGT 180
Qy 704 CTCTGAATGGCGACATTCGATGTTGGATGGCCATTCAGAGGGGACCTTTAAATCTGAGAT 763
Db 181 CTCTGAATGGCGACATTCGATGTTGGATGGCCATTCAGAGGGGACCTTTAAATCTGAGAT 240
Qy 764 TATCCTGGCTGTTAAAGCAGTTTATTTTTCAGACTGGACCCGGCTCTCATCCGATCAGGA 823
Db 241 TATCCTGGCTGTTAAAGCAATTTATTTTCAGACTGGACCCGGCTCTCATCCCAATCAGGA 300
Qy 824 GCCCTATATCTTACGTGGCAAGATTTGGCAGAGGATCTCCGGCATCGGTTTAAACCATG 883
Db 301 GCCCTATATCTTACGTGGCAAGATTTGGCAGAGGATCTCCGGCATCGGTTTAAACCATG 360
Qy 884 GCTGAATAGCCAGAAAGCCAGGTCCTCCGAATCTTGGCTCTTGAGAGAGAAAACAAACA 943
Db 361 GCTGAATAGCCAGAAAGCCAGGTCCTCCGAATCTTGGCTCTTGAGAGAGAAAACAAACA 420
Qy 944 CTCCGCTGAAAAGTCAAGCCCTCTCTCATATCTACCCCGAGATTTGAGGAGCCACCGGC 1003
Db 421 CTCCGCTGAAAAGTCAAGCCCTCTCTCATATCTACCCCGAGATTTGAGGAGCCACCGGC 480
Qy 1004 TTGGCCGGAAACCCATCTGTTCCCGACCCCTTATCTGGCACAGGGTCCGCGAGGG 1063
Db 481 TTGGCCGGAAACCCATCTGTTCCCGACCCCTTATCTGGCACAGGGTCTGCGAGGG 540
Qy 1064 ACCCTTTGCCCTCTCTGAGCTCCGCGGTGAGGAGCTGCTGAGGAGCTCGAGCG 1123
Db 541 ACCCTTTGCCCTCTCTGAGCTCCGCGGTGAGGAGCTGCTGAGGAGCTCGAGCG 600
Qy 1124 GAGGGCGCACCCCGGAGCGACAGACGAGATTCGCGACATTTACCGCTGCGCACGTACGG 1183
Db 601 GAGGGCGCACCCCGGAGCGACAGACGAGATTCGCGACATTTACCGCTGCGCACGTACGG 660
Qy 1184 CCCTCCACACCGGGGGGCAATTTGAGCCCTTCAGTATTTGGCCCTTTCTTCTGCGAGA 1243
Db 661 CCCTCCACACCGGGGGGCAATTTGAGCCCTTCAGTATTTGGCCCTTTCTTCTGCGAGA 720
Qy 1244 TCTCTATATTTGMAAACTAAACCATCCCTTTCTCGGAGGATCCCAACGCTCACCGG 1303
Db 721 TCTCTATATTTGMAAACTAAACCATCCCTTTCTCGGAGGATCCCAACGCTCACCGG 780
Qy 1304 GTTGTGGAGTCCCTTATGTTCTCTCACGAGCTACTTGGGATGATTTGTCAACAGCTGCT 1363
Db 781 GTTGTGGAGTCCCTTATGTTCTCTCACGAGCTACTTGGGATGATTTGTCAACAGCTGCT 840
Qy 1364 GCAGACACTCTTCAACCGAGGAGCGAGAGAAATTCATTATAGGGCTAGAAAAAATGT 1423
Db 841 GCAGACACTCTTCAACCGAGGAGCGAGAGAAATTCATTATAGGGCTAGAAAAAATGT 900
Qy 1424 TCTTGGGGCGAGGGCGAGCCACCGGTTGCAAAATGAGATTGACATGGGATTTCCCTT 1483
Db 901 TCTTGGGGCGAGGGCGAGCCACCGAGTTGCAAAATGAGATTGACATGGGATTTCCCTT 960
Qy 1484 AACTCGCCCCGGTTGGGACTACAACCGGCTGAAGTAGGGAGAGCTTGAAAAATCTATCG 1543
Db 961 GACTCGCCCCGGTTGGGACTACAACCGGCTGAAGTAGGGAGAGCTTGAAAAATCTATCG 1020
Qy 1544 CCAGGCTCTGGTGGGGTCTCCGGGGCGCTTCAAGACGGCCCACTAAATTTGGCTAAGGT 1603
Db 1021 CCAGGCTCTGGTGGGGTCTCCGGGGCGCTTCAAGACGGCCCACTAAATTTGGCTAAGGT 1080
Qy 1604 AAGAGAGTGATGCGAGGACCGAATGAACCCCTCTGTTTCTTGAGAGGCTCTTGA 1663
Db 1081 AAGAGAGTGATGCGAGGACCGAATGAACCCCTCTGTTTCTTGAGAGGCTCTTGA 1140

Qy 1664 AGCCTTCAGGCGGTACACCCCTTTTGATCCACCTCAGAGGCCCAAAAAGCCTCAGTGGC 1723
Db 1141 AGCCTTCAGGCGGTACACCCCTTTTGATCCACCTCAGAGGCCCAAAAAGCCTCAGTGGC 1200
Qy 1724 TTTGGCCTTTATAGGACAGTCAGCTTGGATATTAGAAAAGAGCTTCAGAGACTGGAAAG 1783
Db 1201 TTTGGCCTTTATAGGACAGTCAGCTTGGATATTAGAAAAGAGCTTCAGAGACTGGAAAG 1260
Qy 1784 GTTACAGAGGCTCAGTTTACGTGATCTAGTGAAGGAGCGCAGAGAAAGTATATTACAAAG 1843
Db 1261 GTTACAGAGGCTCAGTTTACGTGATCTAGTAAAGGAGCGCAGAGAAAGTATATTACAAAG 1320
Qy 1844 GGAGACAGAAAGAAAGGGAACAAAGAAAGAGAGAGAAAGAGAGGAAAGGAGGAAAG 1903
Db 1321 GGAGACAGAAAGAAAGGGAACAAAGAAAGAGAGAGAAAGAGAGGAAAGGAGGAAAG 1380
Qy 1904 ACGTAAATAAACCGCAAGAGAGAAATTTGACTTAAGATCTTTGGCTCAGTGGTTGAAGGAA 1963
Db 1381 ACGTAAATAAACCGCAAGAGAGAAATTTGACTTAAGATCTTTGGCTCAGTGGTTGAAGGAA 1440
Qy 1964 AAGCAATACGGAAAGAGAGAGAGATTTTAGGAAAATTTAGGTCAGGCCCTAGACAGTCAAG 2023
Db 1441 AAGCAATACGGAAAGAGAGAGAGATTTTAGGAAAATTTAGGTCAGGCCCTAGACAGTCAAG 1500
Qy 2024 GAACTGGGCAATTAGGACCCCACTCGACAGGACCAATTCGCATATTGTAAAGAAAGAG 2083
Db 1501 GAACTGGGCAATTAGGACCCCACTCGACAGGACCAATTCGCATATTGTAAAGAAAGAG 1560
Qy 2084 ACACCTGGCAGGAACTGCCCCAAGAGAGGGAACAAAGGACCAAGGATCCTAGCTCTAGA 2143
Db 1561 ACACCTGGCAGGAACTGCCCCAAGAGAGGGAACAAAGGATCTGAAGTCTTAGCTCTGGA 1620
Qy 2144 AGAAGATAAAGATTAGGAGGAGACGGGTTTCGGAACCCCTCCCGAGGCCAGGGTAACTTT 2203
Db 1621 AGAAGATAAAGATTAGGAGGAGACGGGTTTCGGAACCCCTCCCGAGGCCAGGGTAACTTT 1680
Qy 2204 GAAAGTGAGGGGCAACCGATTTGATTCCTGGTTGATACCGGAGGGAACATTCAGTGCT 2263
Db 1681 GAAAGTGAGGGGCAACCGATTTGATTCCTGGTTGATACCGGAGGGAACATTCAGTGCT 1740
Qy 2264 ACTACAGCAATTAGGAAAACCTAAAAGATAAAAAATCTTGGGTGATGGGTGCCACAGGCA 2323
Db 1741 ACTACAGCAATTAGGAAAACCTAAAAGATAAAAAATCTTGGGTGATGGGTGCCACAGGCA 1800
Qy 2324 ACAACAGTATCCATGGACTACCCGAGAACACAGTTTGACTTTGGGAGTGGGACGGTAAACCA 2383
Db 1801 ACAACAGTATCCATGGACTACCCGAGAACACAGTTTGACTTTGGGAGTGGGACGGTAAACCA 1860
Qy 2384 CTGCTTCTGTCATACCTGAGTGGCCAGCACCCCTCTTAGGTAGAGACTTTATTTGACCAA 2443
Db 1861 CTGCTTCTGTCATACCTGAGTGGCCAGCACCCCTCTTAGGTAGAGACTTTATTTGACCAA 1920
Qy 2444 GATGGAGCACAAATTTCTTTTGAACAGGGAACCCAGAGTGTCTGCAAAATAACAAACC 2503
Db 1921 GATGGAGCACAAATTTCTTTTGAACAGGGAACCCAGAGTGTCTGCAAAATAACAAACC 1980
Qy 2504 TATCACTGTGTGACCCCTCCCAATTTAGATGACGAATATCGACTATACTCTCCCTTAGTAA 2563
Db 1981 TATCACTGTGTGACCCCTCCCAATTTAGATGACGAATATCGACTATACTCTCCCTTAGTAA 2040
Qy 2564 GCCTGATCAAAATATACAAATTTCTGCTTGGAAACAGTTTCCCAAGCTGGGAGAAACCGC 2623
Db 2041 GCCTGATCAAAATATACAAATTTCTGCTTGGAAACAGTTTCCCAAGCTGGGAGAAACCGC 2100
Qy 2624 AGGGATGGGTTGGCAAGCAAGTTCGCCCAACAGTTATTCAACTGAAGGCCAGTGCCAC 2683
Db 2101 AGGGATGGGTTGGCAAGCAAGTTCGCCCAACAGTTATTCAACTGAAGGCCAGTGCCAC 2160
Qy 2684 ACCAGTGTCACTCAGACAGTACCCCTTGAGTAAAGAGAGCTCAAGAGGAATTCGGCCGCA 2743
Db 2161 ACCAGTGTCACTCAGACAGTACCCCTTGAGTAAAGAGCTCAAGAGGAATTCGGCCGCA 2220

Qy	2744	TGTCCTCAAGATTAAATCCAAACAGGCGATCCCTAGTTCCTGTCCAAATCTCCCTCGGAATATCTCC	2803	Db	3301	CCATGCGTTGGAGAACATCGTTTCGGCAGGCCCCAGACCGATGGATGATCCAAAGCCCGCAT	3360
Db	2221	TGTCCTCAAGATTAAATCCAAACAGGCGATCCCTAGTTCCTGTCCAAATCTCCCTCGGAATATCTCC	2280	Qy	3884	GACCCACTATCAAGAGCTGCTTCTCACAGAGAGGGTCACTGCTCGCTCCACAGCCGCTCT	3943
Qy	2804	CTTGCTACCGGTTAGAAAGCCTGGGACTAATGACTATCGACCGAGTACAGGACTTGAGAGA	2863	Db	3361	GACCCACTATCAAGAGCTGCTTCTCACAGAGAGGGTCACTGCTCGCTCCACAGCCGCTCT	3420
Db	2281	CTTGCTACCGGTTAGAAAGCCTGGGACTAATGACTATCGACCGAGTACAGGACTTGAGAGA	2340	Qy	3944	CAACCTGCGCACTCTTCTGCTGGAAGAGACTGATGAACAGTGAATCATGATTTGCCATCA	4003
Qy	2864	GGTCATTAACAGGGTGCAGGATATACACCAACAGTCCCGAACCTTTATTAACCTCTTGTC	2923	Db	3421	CAACCTGCGCACTCTTCTGCTGGAAGAGACTGATGAACAGTGAATCATGATTTGCCATCA	3480
Db	2341	GGTCATTAACAGGGTGCAGGATATACACCAACAGTCCCGAACCTTTATTAACCTCTTGTC	2400	Qy	4004	ACTATTGATTGAGGAGACTGGGGTCCGCAAGGACTTACAGACATACCGCTGACTGAGAGA	4063
Qy	2924	TGCTCTCCCAACCCCAACCGAGCTGGTATACAGTATTGGAATTAAGAGTCCCTTCTTCTG	2983	Db	3481	ACTATTGATTGAGGAGACTGGGGTCCGCAAGGACTTACAGACATACCGCTGACTGAGAGA	3540
Db	2401	TGCTCTCCCAACCCCAACCGAGCTGGTATACAGTATTGGAATTAAGAGTCCCTTCTTCTG	2460	Qy	4064	AGTGCTAAACCTGCTTCACTGACGGAAGAGCTATGTGTGGTGAAGGTAAGAGGATGGCTGG	4123
Qy	2984	CTTGAGATTAACCCCAACTAGCCAAACCACTTTTGGCTTCCGATGGAGAGATCCAGGTAC	3043	Db	3541	AGTGTTAACTGCTTCACTGACGGAAGAGCTATGTGTGGTGAAGGTAAGAGGATGGCTGG	3600
Db	2461	CTTGAGATTAACCCCAACTAGCCAAACCACTTTTGGCTTCCGATGGAGAGATCCAGGTAC	2520	Qy	4124	GGCGGCGTGGTGGAGCGGACCCGACGATCTGGGCCAGCGCTGCGGGAAGAACTTC	4183
Qy	3044	GGGAGAACCGGCGAGCTCACTGGACCGGACTGCCCCNAGGGTTCAAGAACTCCCGGAC	3103	Db	3601	GGCGGCGTGGTGGAGCGGACCCGACGATCTGGGCCAGCGCTGCGGGAAGAACTTC	3660
Db	2521	GGGAGAACCGGCGAGCTCACTGGACCGGACTGCCCCNAGGGTTCAAGAACTCCCGGAC	2580	Qy	4184	AGCACAAAAGCTGAGCTCATGCGCCTCAGCGAAGCTTTGCGGCTGCGGCGGAGGAAATC	4243
Qy	3104	CATCTTTGACGAAGCCCTACACAGAGACCTGGCCAACTTCAGGATCCAAACACCTCTCAGGT	3163	Db	3661	AGCACAAAAGCTGAGCTCATGCGCCTCAGCGAAGCTTTGCGGCTGCGGCGGAGGAAATC	3720
Db	2581	CATCTTTGACGAAGCCCTACACAGAGACCTGGCCAACTTCAGGATCCAAACACCTCTCAGGT	2640	Qy	4244	CATTAACATTTATACGAGCAGAGGTATGCTTTGCGACTGACACGTACATGCGGGCCAT	4303
Qy	3164	GACCTCTCCAGTACGTGATGACTGCTTCTGGCGGAGGCCAACAAACAGGACTGCTT	3223	Db	3721	CATTAACATTTATACAGACAGCAGGTATGCTTTGCGACTGACACGTACATGCGGGCCAT	3780
Db	2641	GACCTCTCCAGTACGTGATGACTGCTTCTGGCGGAGGCCAACAAACAGGACTGCTT	2700	Qy	4304	CTATAAACAAAGGGGTTGCTTACCTCAGCAGGAGGAGGAAATAAAGAACAAAGAGGAAAT	4363
Qy	3224	AGAAGCACAGAGCATACTGCTGGAAATGCTGACTAGGCTACAGAGCCTCTGCTAA	3283	Db	3781	CTATAACAAAGGGGTTGCTTACCTCAGCAGGAGGAGGAAATAAAGAACAAAGAGGAAAT	3840
Db	2701	AGAAGCACAGAGCATACTGCTGGAAATGCTGACTAGGCTACAGAGCCTCTGCTAA	2760	Qy	4364	TCTAAGCCTATTAGAAAGCCGTACATTTTGCCTTAATAAGAGGCTAGCTATTATACATGCTCTGG	4423
Qy	3284	GAAGGCCAGATTTGACGAGAGAGGTAAACATCTGGGGTACAGTTTGGGAGCGGCA	3343	Db	3841	TCTAAGCCTATTAGAAAGCCGTACATTTTGCCTTAATAAGAGGCTAGCTATTATACATGCTCTGG	3900
Db	2761	GAAGGCCAGATTTGACGAGAGAGGTAAACATCTGGGGTACAGTTTGGGAGCGGCA	2820	Qy	4424	ACATCAGAAAGCTAAAGATCTCATATCCAGAGAAACCCAGATGGCTGACCGGGTTGCAAA	4483
Qy	3344	GCGATGGCTGACGAGGAGCAGGAAAGAACTGTAGTCCAGATACCGGCCCAACACAGC	3403	Db	3901	ACATCAGAAAGCTAAAGATCTCATATCCAGAGAAACCCAGATGGCTGACCGGGTTGCAAA	3960
Db	2821	GCGATGGCTGACGAGGAGCAGGAAAGAACTGTAGTCCAGATACCGGCCCAACACAGC	2880	Qy	4484	GCAGGACGCCAGGGTGTAAACCTTCTGCTTAATAAGAGGCTAGCTATTATACATGCTCTGG	4543
Qy	3404	CAAAACAAATGAGAGAGTTTTTGGGGACAGCTGGATTTTGCAGACTGGATCCGGGGTT	3463	Db	3961	GCAGGACGCCAGGGTGTAAACCTTCTGCTTAATAAGAGGCTAGCTATTATACATGCTCTGG	4020
Db	2881	CAAAACAAATGAGAGAGTTTTTGGGGACAGCTGGATTTTGCAGACTGGATCCGGGGTT	2940	Qy	4544	CAGACGACAGTACACCTTAGAAGACTGGCAAGAGATTAAGAAAGATAGACAGTTCTCTGA	4603
Qy	3464	TGCGACCTTAGCAGCCCACTCTACCCGCTAACCAAGAAAGAGGAAATTTCTCTGGGC	3523	Db	4021	CGGACGACAGTACACCTTAGAAGACTGGCAAGAGATTAAGAAAGATAGACAGTTCTCTGA	4080
Db	2941	TGCGACCTTAGCAGCCCACTCTACCCGCTAACCAAGAAAGAGGAAATTTCTCTGGGC	3000	Qy	4604	GACTCCGGAAGGAGCCTGCTATACCTCAGATGGGAGGAAATCTCTGCCCAAGAGG	4663
Qy	3524	TCCTGAGCACACAGAGGCAATTTGATGCTATCAAAAGAGCCCTGCTGAGCGCACTGCTCT	3583	Db	4081	GACTCCGGAAGGAGCCTGCTATACCTCAGATGGGAGGAAATCTCTGCCCAAGAGG	4140
Db	3001	TCCTGAGCACACAGAGGCAATTTGATGCTATCAAAAGAGCCCTGCTGAGCGCACCTGCTCT	3060	Qy	4664	GTTAGAAATATGTCACACAGATACATCGCTAAACCCACTAGGAACTAAACACCTGAGCA	4723
Qy	3584	GGCCCTCTCAGTAACTAAACCTTTACCTTTATGTGATGAGCGTAAAGGAGTAGC	3643	Db	4141	GTTAGAAATATGTCACACAGATACATCGCTAAACCCACTAGGAACTAAACACCTGAGCA	4200
Db	3061	GGCCCTCTCAGTAACTAAACCTTTACCTTTATGTGATGAGCGTAAAGGAGTAGC	3120	Qy	4724	GTTGGTCAGAACATCCCTTTATCATGTTCTGAGGCTACAGGAGTGGCTGACTCGGTGGT	4783
Qy	3644	CCGGGAGTTTAAACCAACCCCTAGGACCATGAGAGAGCCTGTGCGCTACCTGTCAAA	3703	Db	4201	GTTGGTCAGAACATCCCTTTATCATGTTCTGAGGCTACAGGAGTGGCTGACTCGGTGGT	4260
Db	3121	CCGGGAGTTTAAACCAACCCCTAGGACCATGAGAGAGCCTGTGCGCTACCTGTCAAA	3180	Qy	4784	CAAAACATTTGTCCTGCGCAGCTGTTAATGCTTAATCTTCCAGATGCTCTCCAGGAA	4843
Qy	3704	GAAGCTCGATCTGTAGCCAGTGGTTGGCCCATATGCTGAAGGCTATCGCAGCTGTGGC	3763	Db	4261	CAAAACATTTGTCCTGCGCAGCTGTTAATGCTTAATCTTCCAGATGCTCTCCAGGAA	4285
Db	3181	GAAGCTCGATCTGTAGCCAGTGGTTGGCCCATATGCTGAAGGCTATCGCAGCTGTGGC	3240	Qy	4844	GAGACTAAGGGAAGCCACCCAGCGCTCACTGGGAAGTGGACTTCACTGAGGTAAAGCC	4903
Qy	3764	CATACTGTCAAGGACGCTGACAAATTTGAGCTTTGGGACAGAAATATACTGTAATAGCCCC	3823	Db	4286	-----GGTAAGCC	4294
Db	3241	CATACTGTCAAGGACGCTGACAAATTTGAGCTTTGGGACAGAAATATACTGTAATAGCCCC	3300	Qy	4904	GGCTAAATACGGAACAAATACCTTAATTTGTTTGTAGACACCTTTTTCAGGATCGGTAGA	4963
Qy	3824	CCATGCTTGAGAAACATCGTTTCGGCAGCCCCCAGACCGATGGATGACCAACGCGCGCAT	3883				

Db 4295 GCGTAAATACGGAAACAAATATCTATTGGTTTTTTGTAGACACCTTTTCAGGATGGGTAGA 4354
Qy 4964 GCGTTATCTCTACTAAGAAAGAGACTTCAACCGTGGTGGCTAAAAAATACTGGAA -GAAA 5022
Db 4355 GCGTTATCTCTACTAAGAAAGAGACTTCAACCGTGGTGGCTAGAAAAATACTGAGGGAAA 4414
Qy 5023 TTTTTCGAAGATTGGAAATACCTAAGGTAAATAGGTCAGACAAATGGTTCAGCTTTTGTG 5082
Db 4415 TTTTTCGAAGATTGGAAATACCTAAGGTAAATAGGTCAGACAAATGGTTCAGCTTTCGTTG 4474
Qy 5083 CCCAGTAACTCAGGACTGGCCAGATATCGGGATTTCGGAACCTGCAATGTCAT 5142
Db 4475 CCAGGTAACTCAGGACTGGCCAGATATCGGGATTTCGGAACCTGCAATGTCAT 4534
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Qy 5263 TTAGGTTTAGAACACCCCTGGACAGTTTGGGCTGACCCCTATGNAATTACTCTACGGGG 5322
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Qy 5803 ATTACTGACTCCGGCAGAGTATTAATATCAACACACTCAAGGGAGGCTCTTTAGGA 5862
Db 5195 CTTTACTGACTCCGGTACAGGTATTAATATTAACAGCACTCAAGGGAGGCTCCCTTGGGG 5254
Qy 5863 ACCTGTGGCTCATCTATACGTTTGGCTCAGATCAGTTATTCTCTAGTCTCT-----G 5913
Db 5255 ACCTGTGGCTGAAATTAATATGCTGCCCTCGATCAGTAATCCCTGTCTCAATGACCAG 5314
Qy 5914 ACCTCAACCCAGATATCTCCATGCTCAAGGATTTTATGTTTCCAGGACCAACCAAT 5973
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Qy 6034 TCTAATGATGATATTGGAATGGCCAACTCTCTAGCAGGATAGGGTAAGTTTTCCTAT 6093
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Db 5615 GATTACTTTAAAAATAAGTTTCTCAGTAAAAAGGAAAACAAAGAAAATATTCAAAGTGGTA 5674
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Db 5915 GCGAACTTTTAACTCATCCAGGAGCTTTTCAAGCTCTTAACTCCAGACTCCAGAG 5974
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Db	6515	CTACATCGAATTTGTAAACGGAAGATCTCCAAAGCCCTAGAAAAAATCTGTCACTAGTAACCTGGAG	6574
Qy	7120	GAATCCCTAACCTCCTTTATCTGAAGTAGTCTCTACAGNATAGAGAGGGTTAGATTTTATTA	7179
Db	6575	GAATCCCTAACCTCCTTTATCTGAAGTAGTCTCTACAGAAACAGAGGGGGTTAGATCTGTGA	6634
Qy	7180	TTTTCTAAAGAGAGGAGGATTTATGTGTAGCCTCTGAAGGAGGAATGCTGTGTTTTTATGTGGAT	7239
Db	6635	TTTTCTAAAGAGAGGAGGATTTATGTGTAGCCTCTGAAGGAGGAATGCTGTGTTTTTATGTGGAT	6694
Qy	7240	CATTCAAGGCGCCATCAGAGACTCCATGAAACA	7270
Db	6695	CATTCAAGGCGCCATCAGAGACTCCATGAAACAAGCTTAGAGAAAGGACTGGAGAGCGCCCG	6754
Qy	7271	-----	7270
Db	6755	CGGGTCTCGAACCAACCAGACAGGGTTGCTTTGTTTCAATTAAGAACTGTCGAAGTAACCG	6814
Qy	7271	-----AGCTTTAGAGAAAGGTTGGAGAAGCGTCCGAAGGGAAAAAGGAAACTTACT	7317
Db	6815	CTGAGCTAAAGCCAGCTTTAGAGAAAGGTTGGAGNAGCGTCGAAGGGNAAAGGAAACTACT	6874
Qy	7318	CAAGGGTGGTTTGAGGGATGGTTCACACAGGTCCTCTTTGGTTGGCTACCCCTACTTTCTGCT	7377
Db	6875	CAAGAGTGGTTTGAGGGATGGTTCACACAGGTCCTCTTTGGTTGGCTACCCCTACTTTCTGCT	6934
Qy	7378	TTAAACAGACCCCTTAATATGTCCTCTCTCTGTTACTCACAGTTGGGCCCATGTATTTTAAC	7437
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Qy	7438	AAGTTAATTTGCTCTCATTTAGAGAACGAATAAGTGCAGTCCAGATCATGGTACTTTAGACAA	7497
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Qy	7498	CAGTACCAAAAGCCGCTCTAGCAGGGAAGCTGGCCGCTAGCTCTACCAAGTTCTTAAGATTAG	7557
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Qy	7608	-----AAGCTAATAGAGAAGCTTAAATTTGTTCTTGAAATCCAGAGTTTGTTCCTTAT	7658
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Qy	7659	AGGTAAAGATTTAGGTTTTTTTGCTGTTTTTAAATATGCTG	7696
Db	7235	AGGTAAAGATCATACTTTTTGTCTGTTTTAGGGCTGCTTTCTGCTCTGTACAAAACCTTT	7294
Qy	7697	-----GGAAGTAAATATAGCCCTGAGTACATGTCCTTAGGCATGAAACTTTTGAAACT	7750
Db	7295	GTCGAAGGGGAAAAACAGGCCCTCTGAGTATGTGCTCTATGCTTTGAAACTTCTTGAAACT	7354
Qy	7751	ATTTGAGATAACAAGAAAAGGAGTTTCTTAACCTGCTTTGTTTA	7792
Db	7355	GCTCCTAATCTGCTTTGTTGGCTTCTGTAAACCTGCTTGCTGCTAAGATAAAAGAGGAGAAG	7414
Qy	7793	-----GCTTCTGTAAAACTGGTTGCGCCATAAAGATGTTGAAATGTTGATACACATATC	7846
Db	7415	TCAATTGCTTAACCGACCCCAAGTAAGATCGGGTGTAACAAAATGTTGAAACACATATC	7474
Qy	7847	TTGGTGACAAACATGTCCTCCCCACCCCGAACAATGTCGGCAATGTGAATCTTAACAACAT	7906
Db	7475	TTGGTGACAAACATGTCCTCCCCACCCCGAACAATGTCGGCAATGTGAATCTTAACAACAT	7534
Qy	7907	TTAAATTAATTTGGTCCAGAAAGCGGGCTCTCGAAGTGTTTTAAATTTGACTGTTTTGTGAT	7966
Db	7535	TTAAATTAATTTGGTCCAGAAAGCGGGCTCTCGAAGTGTTTTAAATTTGACTGTTTTGTGAT	7594
Qy	7967	ATTTTGAATGATTTGGTTTGTAAAGCGCGGGCTTTGTTGTGAACCCCATAAAGCTGTCC	8026

Db	7595	ATTTTGAATGATGTTGTTGTAAGCGCGGCTTTTGTGTAAACCCCATAAAGCTGTCC	7654
Qy	8027	CGACTCCACACTCGGGCGCGCAGTCTCTACCCCTCGTGGTGTACGACTGTGGGCCCA	8086
Db	7655	CGACTCCACACTCGGGCGCGCAGTCTCTACCCCTCGTGGTGTACGACTGTGGGCCCA	7714
Qy	8087	GCSCGGTTGAATAAAATCCTCTTCTGCTGTTGCATCAAAA	8127
Db	7715	GCSCGGTTGAATAAAATCCTCTTCTGCTGTTGCATCAAGA	7755
RESULT 15	AF435967	8911 bp DNA linear	VRL 14-MAR-2002
LOCUS	Porcine endogenous retrovirus isolate Bac-PERV-A(151B10) group		
DEFINITION	specific antigen (gag), pol protein (pol), and envelope protein (env) genes, complete cds.		
ACCESSION	AF435967		
VERSION	AF435967.1	GI:19422005	
KEYWORDS	Porcine endogenous retrovirus		
SOURCE	Porcine endogenous retrovirus		
ORGANISM	Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae; Gammaretrovirus; 1-Mammalian type C virus group.		
REFERENCE	1 (bases 1 to 8911)		
AUTHORS	Niebert.M., Rogel-Galliard,C., Chardon,P. and Tonjes,R.R.		
TITLE	Characterization of chromosomally assigned replication-competent gamma porcine endogenous retroviruses derived from a large white pig and expression in human cells		
JOURNAL	J. Virol. 76 (6), 2714-2720 (2002)		
PUBMED	11861838		
REFERENCE	2 (bases 1 to 8911)		
AUTHORS	Niebert.M., Rogel-Galliard,C., Chardon,P. and Tonjes,R.R.		
TITLE	Direct Submission		
JOURNAL	Submitted (19-OCT-2001) Medical Biotechnology, Paul-Ehrlich-Institut, Paul-Ehrlich-Str 51-59, Langen, Hessen 63225, Germany		
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QY	3707	GCTCGATCCTGTAGCCAGTGGTTGGCCCATATATCCCTGAAGGCTATGCGAGCTGTGCGCCAT	3766	QY	4787	ACATTTGTGTGCTGCCAGCTGGTTAATGCTTAATCCTTCCAGAAATGCCCTCCAGGGNAGAG	4846
Db	4267	GCTCGATCCTGTAGCCAGTGGTTGGCCCATATATCCCTGAAGGCTATGCGAGCTGTGCGCCAT	4326	Db	5347	ACATTTGTGTGCTGCCAGCTGGTTAATGCTTAATCCTTCCAGAAATGCCCTCCAGGGNAGAG	5406
QY	3767	ACTGGTCAAGGAGCGTGAACAATTTGACTTTTGGGACAGAAATATACTGTAAATAGCCGCCCA	3826	QY	4847	ACTAAGGGGAAGCCACCCAGGGCGCTCACTGGGAAGTGGACTTCACTAGAGTTAAAGCCGCGC	4906
Db	4327	ACTGGTCAAGGAGCGTGAACAATTTGACTTTTGGGACAGAAATATACTGTAAATAGCCGCCCA	4386	Db	5407	ACTAAGGGGAAGCCACCCAGGGCGCTCACTGGGAAGTGGACTTCACTAGAGTTAAAGCCGCGC	5466
QY	3827	TGCATTTGGAAGACATCGTTTGGCAGCCGCCAGACCGATGATGACCAAGCCCGCATGAC	3886	QY	4907	TAAATACCGGAAAACAAATACCTATTGCTTTTGTAGACACCTTTTTCAGGATGGGTAGAGGC	4966
Db	4387	TGCGTTTGGGAACAATCGTTTGGCAGCCGCCAGACCGATGATGACCAAGCCCGCATGAC	4446	Db	5467	TAAATACCGGAAAACAAATACCTATTGCTTTTGTAGACACCTTTTTCAGGATGGGTAGAGGC	5526
QY	3887	CCATATCAAAGCCTGCTTCTCACAGAGAGGCTCAGTTTCGCTCCACAGCCGCTCTCAA	3946	QY	4967	TTATCCTACTAAGAAAAGAGACTTCAACCGTGTGTGCTAAAGAAAATACTCGAAGAAATTTT	5026
Db	4447	CCATATCAAAGCCTGCTTCTCACAGAGAGGCTCAGTTTCGCTCCACAGCCGCTCTCAA	4506	Db	5527	TTATCCTACTAAGAAAAGAGACTTCAACCGTGTGTGCTAAAGAAAATACTCGAAGAAATTTT	5586
QY	3947	CCCTGCGACTCTTCTGCTGGAAGAGACTGATGAACAGTGACTCATGATGCGATCAACT	4006	QY	5027	TCCAGAGATTTGGAATACCTTAAGGTATAGGTGAGACAAATGCTCAGACCTTTTGTGTCGCCA	5086
Db	4507	CCCTGCGACTCTTCTGCTGGAAGAGACTGATGAACAGTGACTCATGATGCGATCAACT	4566	Db	5587	TCCAGAGATTTGGAATACCTTAAGGTATAGGTGAGACAAATGCTCAGACCTTTTGTGTCGCCA	5646
QY	4007	ATTGATTGAGGAGACTGGGGTCCGCAAGGACCTTACAGACATACCGCTGACTGGAGAAT	4066	QY	5087	GGTAAGTCAAGGAGCTGGCCAGAGATATTGGGGATTGATTGGAAACTGCAATTTGTCATACAG	5146
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QY	4067	GCTAACCTTGTTCACTGACCGAAGCAGCTATGTGTGGAGGTAAAGAGATGGCTGGGGC	4126	QY	5147	ACCCCAAAGCTCAGGACAGGTAGAGAGATGAATAGAACCATTAAGAGACCTTTACTTAA	5206
Db	4627	GGTAACCTTGTTCACTGACCGAAGCAGCTATGTGTGGAGGTAAAGAGATGGCTGGGGC	4686	Db	5707	ACCCCAAAGCTCAGGACAGGTAGAGAGATGAATAGAACCATTAAGAGACCTTTACTCAA	5766
QY	4127	GGCGGTGTGAGCGGAGCCCGACAGATCTGGGCGAGCAGCTTGCAGGAGGAACCTTCAGC	4186	QY	5207	ATTGACCGGAGAGCTGGGTTAATGATTGGATAGCTCTCCCTGCTTTGCTTTTGTAG	5266
Db	4687	CGCGGTGTGAGCGGAGCCCGACAGATCTGGGCGACCAACCTCGCCGGAAGGACTTCTTC	4746	Db	5767	ATTGACCGGAGAGCTGGGTTAATGATTGGATAGCTCTCCCTGCTTTGCTTTTGTAG	5826
QY	4187	ACAAAGGCTGAGCTATGCGCTCACGCAAGCTTTGCGGCTGGCGGAGGGAATCCAT	4246	QY	5267	GGTTAGGAACACCCCTGGACAGTTTGGGCTGACCCCTATGAATTAATCTACGGGGGAGC	5326
Db	4747	ACAAAGGCTGAGCTATGCGCTCACGCAAGCTTTGCGGCTGGCGGAGGGAATCCAT	4806	Db	5827	GGTTAGGAACACCCCTGGACAGTTTGGGCTGACCCCTATGAATTAATCTACGGGGGAGC	5886
QY	4247	AAACATTTATAGGACAGCAGGTATGCTTTGCGACTGCACACGTACATGAGGGGCCATCTA	4306	QY	5327	CCCCCATTTGTTAGAAAATTTGCTTGTATCATAGTGTGAGCTGCTTTTCCAGGCTTT	5386
Db	4807	AAACATTTATAGGACAGCAGGTATGCTTTGCGACTGCACACGTACATGAGGGGCCATCTA	4866	Db	5887	CCCCCATTTGTTAGAAAATTTGCTTGTATCATAGTGTGAGCTGCTTTTCCAGGCTTT	5946
QY	4307	TAAACAAAGGGGTTGCTTACTCTCAGCAGGGAGGGAATTAAGAAACAAAGAGAAATTTCT	4366	QY	5387	GTCTCTTAGGCTCAAGGCACTTTGAGTGGGTGAGACAAAGAGCTGGAGGCAACTCCGGGA	5446
Db	4867	TACGCAAGAGGGGTTGCTTACTCTCAGCAGGGAGGGAATTAAGAAACAAAGAGAAATTTCT	4926	Db	5947	GTCTCTTAGGCTCAAGGCACTTTGAGTGGGTGAGGAGCAGGCTGGAGCAGCTCCGGGA	6006
QY	4367	AGGCTATTAGAGCGGTACATTTACCAAAAGGCTAGCTATTATACATGCTCTGGACA	4426	QY	5447	GGCCTACTCAGGAGGAGGAGACTTGCAGATCCCAATCGTTTCCAAAGTGGAGATTCAGT	5506
Db	4927	AGGCTATTAGAGCGGTACATTTGCAAAAGGCTAGCTATTATACATGCTCTGGACA	4986	Db	6007	GGCCTACTC--AGGAGGAGACTTGCAAGTTCCACATCGCTTCCAAAGTTGGAGATTCAGT	6063
QY	4427	TCAGAAAGCTAAAGATCTCATATCCAGAGAAACCAAGATGGGTGACCGGGTTGCCAAGCA	4486	QY	5507	CTACGTTAGACGCCACCGTGCAGGAAAACCTCGAGACTCGGTGGAAGGGCCCTTATCTCGT	5566
Db	4987	TCAGAAAGCTAAAGATCTCATATCCAGAGGGAACCAAGATGGGTGACCGGGTTGCCAAGCA	5046	Db	6064	CTATGTTAGACGCCACCGTGCAGGAAAACCTCGAGACTCGGTGGAAGGGACCTTATCTCGT	6123
QY	4487	GGCAGCCAGGGTGTAACTTCTGCTATATAGAAAATGCCAAAGGCCCGAAGCCAG	4546	QY	5567	ACTTTTGGACCAACCAAGGCTGTGAAGTCCGAAGGAATCTCCACCTGATCCATGCATC	5626
Db	5047	GGCAGCCAGGGTGTAACTTCTGCTATATAGAAAACCAAGAGCCCGAAGCCCG	5106	Db	6124	ACTTTTGGACCAACCAAGGCTGTGAAGTCCGAAGGAATCCCCACCTGATCATGCAT	6183
QY	4547	ACGACAGTACACCTTAGAGACTGGGCAAGAGATAAAAGATAGACAGTTCTCTGAGAC	4606	QY	5627	CCACGTTAAACCGCGGCCACCTCCCGATTCCGGGTGGAAAGCCGAAAAGACTGAAAATCC	5686
Db	5107	ACGACAGTACACCTTAGAGACTGGGCAAGAGATAAAAGATAGACAGTTCTCTGAGAC	5166	Db	6184	CCACGTTAAACCGCGGCCACCTCCCGATTCCGGGTGGAAAGCCGAAAAGACTGAAAATCC	6243
QY	4607	TCCGGAAGGAGCCTGCTATACCTCAGATGGGAAGGAAATCCCTGCCCCCAAGAAAGGGTT	4666	QY	5687	CTTTAAGCTTCGCTCCATCGCGTGGTTCCTTACTCTGTCTGTCAATTAATCTCTCAAGTTAATG	5746
Db	5167	TCCGGAAGGAGCCTGCTATACCTCAGATGGGAAGGAAATCCCTGCCCCCAAGAAAGGGTT	5226	Db	6244	CCTTAAGCTTCGCTCCATCGCGTGGTTCCTTACTCTGTCTGTCAATTAATCTCTCAAGTTAATG	6303
QY	4667	AGAATATGCCAAGACATCGTCTAAACCCACTTAGGAACTTAAACAACCTGAGCAGTT	4726	QY	5747	GTATGGCATAGGAGACAGCTGAACTCCCATTAACCTTTATCTCTCACTGGTTAATTA	5806
Db	5227	AGAATATGCCAAGACATCGTCTAAACCCACTTAGGAACTTAAACAACCTGAGCAGTT	5286	Db	6304	GTAAAGCGCTTGTGGACAGCCGGAACCTCCCATTAACCTTTATCTCTCACTGGTTACTTA	6363
QY	4727	GGTCAGAAATCCCTTATCATGTTCTGAGGCTTACAGAGGTGGCTGACTCGGTGGTCAA	4786	QY	5807	CTGACTCCGGCAGAGTATTAATATCAACAACACTCAAGGGGAGGCTCTCTTAGGAACTCT	5866
Db	5287	GGTCAGAAATCCCTTATCATGTTCTGAGGCTTACAGAGGTGGCTGACTCGGTGGTCAA	5346	Db	6364	CTGACTCCGGTACAGGTATTAATATTAACAGCACTCAAGGGGAGGCTCTCTTAGGAACTCT	6423
				QY	5867	GGTGGCCTGATCTATACGTTTGCCTCAGATCAGTTATTCTTAGTCT-----GACCT	5917

[illegible]

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Db	8703	GGCTTTGTTGTGAACCCCATAAAGCTGTCCGACTCCACACTCCGGGGCCGAGTCCTCT	8762
Qy	8056	ACCCCTGCGTGTGTACGACTGTGGGCCCGAGCGCTTTGGAATAAAAAATCCTTTGCTG	8115
Db	8763	ACCCCTGCGTGGGTACGACTGTGGGCCCGAGCGCTTCGGAATAAAAAATCCTTTGCTG	8822
Qy	8116	TTTGATCAAAA	8127
Db	8823	TTTGATCAAGA	8834

Search completed: February 4, 2006, 23:52:44
Job time : 26242 secs

QY	1620	GGACCGAATGAAACCCCTCTGTTTTCTTTGAGAGCTCTTGGAAAGCCTTTCAGCGGTAC	1679
DB	1718	GGACCTGATGAGTCCCTCTCAGCTTCTTAGAGAGACTCAAGGAAGCCTTATCGCAGATAC	1777
QY	1680	ACCCCTTTTGATCCCACTCAGAGGCCAAAGAGCCTCAGTGGCTTTGGCCCTTTATAGGA	1739
DB	1778	ACTCCTTATGATCTCGAGGACCTTGGGCAAGAAACGAATGTATCTATGTCTATCTCTGG	1837
QY	1740	CAGTCAGCCTTGGATATTAGAAAGAGCTTCAGAGACTGGAAGGGTTTACAGGAGGCTGAG	1799
DB	1838	CAGTCGCGCTCCAGACATTTGTCGAAAGTTTAGAGCGGTTTAGAGACTTTAAAGATGAAACT	1897
QY	1800	TTACGTGATCTAGTGAAGGAGGAGAGAAAGTATATTTACAAAGGGAGAGACAGAAAGAA	1859
DB	1898	TTAGGAGATTTAGTGAGAGAGCGGAAGGATCTTTAATAAAGAGAAACTCCAGAGAA	1957
QY	1860	AGGGAACAAAGAAAGAGAGAAAGAGAGAAAGGAGGAGAAAGAGCTTATTAACCGGAA	1919
DB	1958	AGAGAGAGCGCTTAGGAGGAGAGACAGAGGAAAGAGAGCGGCTTAGGGCAGAGAG	2017
QY	1920	GAGAGAAATTTGACTAAGATCTTGGCTGCAAGTGGTTGAAGGGAAGCAATACGGAAGA	1979
DB	2018	GAGCAGAAAGAGAAAGAGAGGACCGTAGAGAGACATAGAGAAATGAGCAAACTTTTGGCC	2077
QY	1980	GAGAGAGATTTTAGGAAATTTAGTGTAGGCGCTTAGACAGTCAAGGAAACCTTGGSCAATAG	2039
DB	2078	ACCGTAGTTAGTGAAGACAGACAGGATAGAC-----AGGGGGAGAGCGAAGGAG	2128
QY	2040	ACCCACTCGACAAGGACCAATGTGCATATTTAAAGAAAGAGACACTGGGCAAGAAC	2099
DB	2129	CCCCAACTTGACAGGATCAATGTGCTACTGTGTAAGAAAGAGACACTGGGCTAAAGAC	2188
QY	2100	TGCCCCAAGAGGAAACAAAGNACCAAGGATCCTA-----GCTCTAGAAGAAGAT	2150
DB	2189	TGCCCAAGAAGCCACGGGTGCCCGAGGACCGGACCCCAAGACCTTCTCTGACTTTA	2248
QY	2151	AAAGATTAGGGGAGACGGGGTTCCGAGCCCTTCCCGAGCCAGGGTAACTTTGAAGGGTG	2210
DB	2249	GACGACTAGGGGGTCAAGGTCAGAGGCCCTCCCTGAAACCCAGGATACCTCACTGTC	2308
QY	2211	GAGGGCAACAGTTGATGTTCTGGTTGATACCGGAGCGAAACATTCAGTGTCTACTACAG	2270
DB	2309	GGGGGGCAACCCGTCACCTTCTGTTGGATCTGCGGCCCAACACTCCGTCGTGACTCAA	2368
QY	2271	CCATTAGGAAACCTAAAGATAAAATCTGGGTGATGGTGCCACAGGGCAACACAG	2330
DB	2369	AATCCTGGGGCCCTTAAGTGAAGCTCGGCTTGGGTCCAGGGGGCTACTGGAGAAAGCGG	2428
QY	2331	TATCCATGAGCTACCCGAAGAAAGTTGACTTTGGGAGTGGGACGGGTAAACCCACTCGTTT	2390
DB	2429	TATCGTGGACCAAGATCGCAGAGTACACTAGTACCAGGTAGTTATCTCACTCTTTC	2488
QY	2391	CTGGTCACTACCTGAGTGCCACGACCCCTCTTAGGTAGAGACTTTATGACCAAGATGGGA	2450
DB	2489	CTCCATGTGCCAGACTGCCCTACCCCTTGTCTAGGAAGAGACTTTGTTAACTAAACTAAAA	2548
QY	2451	GCACAAATTTCTTTTGA---ACAAGGGAACCAAGAGTGTCTGCAATATACAACTATC	2507
DB	2549	GCCCAGATCCACTTTGAGGGATCAGGAGCCAGGTTTGGGACCAAAAGGACAGCCTCTA	2608
QY	2508	ACTGTGTTGACCTCCCAATTAGATGACGAATATCGACTATATCTCTCCCTAGTAAAGCCT	2567
DB	2609	CAGGTGTTGACCTTAAACCTTAGAAGATGAGTATCGGCTTATGAGACTCAGCAGAGCCG	2668
QY	2568	GA---TCAAAATATACAAATCTGTTGGAAACAGTTTTCCCAAGCCTCGGCGAGAAACCGCA	2624
DB	2669	GAAGCTTCTCTGGGTCCACTGGCTTTCCGACTTTCCCGAGGCTTGGGAGAAACCGGG	2728
QY	2625	GGGATGGGTTTGGCAAGCAAGTTTCCCCCAACAGTTTATTCAACTGAAGGCCAGTGCCACA	2684
DB	2729	GGCATGGGACTGGCAGTTTCGCGAGCGGCTCTAATCATACCTCTGAAGGCAACCTCCACC	2788

QY	5894	GATCAGTTATTCTAGTCTGACCTCACCCAGATATCTCTCCATGCT-----	5940
Db	6081	CCGGGGCCCCCTGCTGTTCAGGAAGCAGCGACTCCACGCCAGGTGTTCAGAGATTG	6140
QY	5941	-----CACGGATTTTATGTTTGGCCAGGACACCAATAATAGGAACAATGCGGAA	5992
Db	6141	TGAGGAGCCCTGACTTCATATACTCCCGGTGCAATACGCGCTGGAAACAGACTTAAGTT	6200
QY	5993	ATCCAGAGATTTCTTTGTAACNATGGAACTGTGTAACTCTAATGATGGATATTGA	6052
Db	6201	ATCTAAAGTGACACATGCCCCACAAATGAAGGATTTCTATGTCGCCGGGCCACATCGCCC	6260
QY	6053	AATGGCCAACTCTCAGCAGATAGGTAAAGTTTCTTATGT-----CMA	6098
Db	6261	CCGGTGGGCCCGGTGGTGGTCCAGAACTCTTCTATTTGTGGCTCTTGGGGCTCGGA	6320
QY	6099	CACCTATACAGCTCTGGACAATTTAATTAACCTGACCTGATTAAGTAAGTGAAGCCCAA	6158
Db	6321	AACACAGGCGGAGCATCTCTGGAAACCCTCTGCTCTGGGACTACATCACAGTAAGCA	6380
QY	6159	GTGCTCTCTTACAGCTAGATTACCTTAAATAAAGTTTCACTGAGAAAGAAACAAGA	6218
Db	6381	CAATCTAACTCAGACCGAGCAACCCCAAGTATGCAAAAGGTAATAGTGGTGCACCTCT	6440
QY	6219	AAATATCC-----TAAATGGGTAAATGATGTCTCTTGGGGATGGTAT	6262
Db	6441	AATATCCGGTTCACGAGCTTTGAAACACAGGCCACTCTCTGGGTACAGGCCATTTGGT	6500
QY	6263	ATTATGG-----AGGCTCGGTAAACCAACAGGCTCCATTTCTAACTATTGCGCTCAA	6314
Db	6501	GGGATTTGGGCTATACGTCTCTGGACATGACCCAGGGCTCATCTTTGGGATCCGACTAA	6560
QY	6315	AATAAACCAAGCTGGAGCTCCAAATGCTATAGGACCAAAATACGGTCTTGAAGGGTCAAAG	6374
Db	6561	AATTACAGACTCGGGGCCCGGGTCCCAATAGGGCCAAACCCGCTCTTTGTGACACCGACG	6620
QY	6375	ACCCCAACCAAGGACAGGACCATCTCTTAACATTAATCTTGATGACAGACCCCACTGA	6434
Db	6621	ACCACCTTCGCGGCTAGACCCACAGATCTCCCGCGCTTCAAACTCCACCCCAACCGA	6680
QY	6435	GTCTAACAGACG-----ACTAAATGGGGGCAAAACTTTTAGCCT	6476
Db	6681	GACACCCCTCACCTCTCCCGAACCCCGCCAGCGGGAGTCGAACCGATTTAAATCT	6740
QY	6477	CATCCAGGAGCTTTTCAAGCTTTAACTCCAGCTCCAGCTCCAGAGCTACTCTTCTTTGTTG	6536
Db	6741	AGTAAAGGAGCCTTACCAAGCCCTCAACCTCACCAGTCTCTGATATAAAACCCAAAGAGTCTG	6800
QY	6537	GCTATGCTTAGCTTCGGGCCCACTTACTATGAAGGAATGGCTAGAGGGGAATTCAA	6596
Db	6801	GTTATGCTTAGTATCGGGACCCCATACTACGAGGGGGTTGCCCTCTAGGTACTACTCT	6860
QY	6597	TGTGACAAAAGAACATAGAGACCAATGCACATGGGGATCCCAAAATAAGCTTTACCCCTAC	6656
Db	6861	CAACCAATCTTCTGCCCAGCTAATGCTCTGTGGCTCTCAACACAAATGACCTTGTG	6920
QY	6657	TGAGGTTTCTGAAAAGGACCTTCGATAGGAAGGTTCCCCCATCCCAACCAACCTTTG	6716
Db	6921	CGAAGTGACCGACAGGAGCTCTGCATAGGAGCGTCCCTAAACCCCATCAAGTCTTTGTG	6980
QY	6717	TAAACACATGAAGCTTTAATCAAACTCTGAGAGTCAATATCTGGTACTCTGGTTAGA	6776
Db	6981	TAATACCAACCAA-----AAGACAAGCGATGGGTCTCTACTATTTTGGCCGCTCCACAGG	7034
QY	6777	CAGGTGGGGCATCTAATCTAGATTAACCCCTTGTTTCCACCTTGTTTAAACCA	6836
Db	7035	AACCTACCTGGGCTGTAGTACTGGACTCACTCCCTGTATCTCAACCACTACTTGACCT	7094
QY	6837	AACATAAGATTTTTCATTATGTTGGTCCAAATTTGTTCCCGAGTGATTAATCTCCCGAAA	6896
Db	7095	CACCACCGATTACTGTCTCTGGTCGAGCTTTGGCCAGGGGTGACCTACCATTCCTCCCTAG	7154
QY	6897	AGCAATCTTGTGATGATATGACTACAGAAATCATCGCAAAAGAGAGAACCCCATATCTCT	6956
Db	7155	TTATGTTTACCACCAATTTTGAAGACGAACCA-----ATATAAAAGAACCCGCTCTCACT	7211
QY	6957	GACACTTGTGTGATGCTCGGA-----CTTGGAGTGGCAGCAGGTGTAGGAAC	7004
Db	7212	AATCTGGGCCCTACTATTAGGAGACTCATATGGGGGGAATTTGCGCTGGAGTGGGAAC	7271
QY	7005	AGGAACAGCTGCGCTCGTCAACGGGACACAGCAGCTAGAAACAGGACTTAGTAACCTTACA	7064
Db	7272	AGGACTACCGCCCTAGTGGCCACTCAGCAGTTTCCAAACA-----CTCCA	7316
QY	7065	TCGAATGTAAACAGAAGATCTCCAGCCCTAGAAAAATCTGTAGTAACCTGGAGGATC	7124
Db	7317	GGCTGCCATGCACGATGACCTTAAAGAAGTTGAAAAGTCCATCACTAATCTAGAAAAATC	7376
QY	7125	CCTAACCTCTTATCTGAAGTAGTCTCTACAGAATAGAAGGGTTAGATTTATTTATTTCT	7184
Db	7377	TTTGACCTCTTGTCCGAAGTAGTGTTCAGAAATCGTAGAGGCTAGATCTACTATTCTCT	7436
QY	7185	AAAAGAAGGAGGATTTATGTAGCTTTGAAGGAGGAATGCTGTTTTTATGTGATCAATTC	7244
Db	7437	AAAAGAAGGAGGTTTGTGTGCTGCTTAAAGAAGAATGCTGTTTCTTCTATCCGACCAAC	7496
QY	7245	AGGGGCCATCAGAGACTCCATGAACAAAGCTTAGAGAAAGGTTGGAGAGCGTCGAAGGGA	7304
Db	7497	AGGATTTGGTACGGGATAGCATGGCCAAACTTAGAGAAAGATTTGAGTCAGAGACAAAGCT	7556
QY	7305	AAAGGAAACTACTCAAGGGTGGTTGAGGATGGTTCAACAGGCTCTCTTTGGTTGGCTAC	7364
Db	7557	CTTTGAATCCCAACAGGGTGGTTGAAGGGCTGTTTAAAGTCCCTTTGGTTCCACCAC	7616
QY	7365	CCTACTTTCTGCTTTAACAGGACCTTAAATAGTCTCTCTCTCTCTACAGTTGGGCC	7424
Db	7617	CTGTATATCACCATCATGSGTCCCTGTATATCTCTTGTAAATTTACTCTTTGGGCC	7676
QY	7425	ATGTATTATTAAACAAGTTAAATGCTTTCATTAGAGAACGAATAGTCGAGTCCAGATCAT	7484
Db	7677	TTGTATTCTCAATCGCCTGGTCCAGTTTATCAAGACAGGATTTCCGTTAGTCGAGGCCCT	7736
QY	7485	GGTACTTAGACACAGTATACCA 7505	
Db	7737	GGTTCTGACTCAACAAATATCA 7757	
RESULT 2			
AK090127	8268 bp	mRNA	linear
LOCUS	mus musculus brain CRL-1443 BC3H1 cDNA, RIKEN full-length enriched		
DEFINITION	library, clone:G431002F22 product:gene e1 protein, full insert		
ACCESSION	AK090127		
VERSION	AK090127.1	GI:26354960	
KEYWORDS	HTC; CAP trapper.		
SOURCE	Mus musculus (house mouse)		
ORGANISM	Mus musculus		
REFERENCE	1		
AUTHORS	Carninci, P. and Hayashizaki, Y.		
TITLE	High-efficiency full-length cDNA cloning		
JOURNAL	Meth. Enzymol. 303, 19-44 (1999)		
PUBMED	10349636		
REFERENCE	2		
AUTHORS	Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,		
TITLE	Itoh, M., Konno, H., Okazaki, Y., Muranatsu, M. and Hayashizaki, Y.		
JOURNAL	Normalization and subtraction of cap-trapper-selected cDNAs to		
PUBMED	prepare full-length cDNA libraries for rapid discovery of new genes		
REFERENCE	Genome Res. 10 (10), 1617-1630 (2000)		
AUTHORS	3		
TITLE	Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P.,		

Db 1403 CTCAACACACACAGCCACCTGGATGATTGCCAGCAATTAATTAGGGAATCTGCTTACC 1462
Qy 1380 ACCGAGGCGAGAGAAATCTTATTAGAGCTAGAAAAATCTTCTGGGGCGGACGGG 1439
Db 1463 GGGGAAGAGAGAGAGCGGGTCTCTGGAAGCCGGAAGAGCTTCCGGGCAACGATGGG 1522
Qy 1440 CGACCCACGGGTTCGAAAAATGAGATTGACATGGGATTTCCCTTAACTCCGCCCGGTGG 1499
Db 1523 CGCCCAACCACTGCCACAGGTTGACGCTGCTTTTCCCTTGAACGTCGGAATGG 1582
Qy 1500 GACTACAAACCGCTGAGGTAGGAGAGCTTGAAAAATCTATCGCAGGCTCTGGTGGCG 1559
Db 1583 GATTACACCAACCAAGAGAGGTAGGAACCACTAGTTCTCTATCGCCAGTTGCTTTAGCG 1642
Qy 1560 GGTCTCGGGGGCGCTCAAGACGGCCCACTAAATTTGGCTAAGTGAAGAGTGTGTCAG 1619
Db 1643 GGTCTCCAAACCGGGCCGAGCCCAACAAATTTGGCCAAAGGTAAAGGAATAACCCAG 1702
Qy 1620 GGACCGAATCAACCCCTCTGTTTTTCTTTGAGAGGCTCTTGAAGGCTTCAGCGGTAC 1679
Db 1703 GGACCTGATGAGTCCCCCTCAGCCTTCTTAGAGACTCAAGGAGCTATCGCAGATAC 1762
Qy 1680 ACCCTCTTTGATCCACCTCAGAGGCCCAAAAGCCCTCAGTGGCTTTGGCTTTATAGGA 1739
Db 1763 ACTCTTATGATCTCTGAGGACCTTGGCAAGAAAGAAATGTATCTATGTCAATCATCTGG 1822
Qy 1740 CAGTCAGCTTTGATATATAGAAAGAGCTTCAGAGACTGGAAGGTTTACAGGAGCTGAG 1799
Db 1823 CAGTCCCTCCAGACATTTGTCGAAAGTTAGAGCGGTTAGAGAGCTTTAAAAAGTAAAACT 1882
Qy 1800 TTACGTGATCTAGTGAAGGAGGAGAGAAAGTATATTACAAAAGGGAGACAGAGAAGAA 1859
Db 1883 TTAGGAGATTTAGTGAGAGAGCCGAAAGAGATCTTTTAAAGAGAAATCTCAGAAAGAA 1942
Qy 1860 AGGGAAACAAAGAAAGAGAGAGAGAGAAAGGGAGGAGAAAGACGTAATAAACCGCAA 1919
Db 1943 AGAGAGAGCGCTTAGGAGGGAGACAGAGGAAAGAGAGCGGCTAGGGCAGAGAG 2002
Qy 1920 GAGAGAAATTTGATTAAGATCTTGGCTGAGTGTGTTGAGGGAAGAAAGCAATACGGAAGA 1979
Db 2003 GAGCAGAAAGAGAAAGAGAGGAGCGCTAGGAGACATAGAGAAATAGACAACTTTTGGCC 2062
Qy 1980 GAGAGATTTTAGGAAATTTAGTCTAGGCGCTAGACAGTCAGGGAACCTGGCAATAGG 2039
Db 2063 ACCGTAGTTAGTGACAGACAGATAGAC-----AGGGGGAGAGCGAAGGAGG 2113
Qy 2040 ACCCCACTCGACAAGGACCAATGTGCATATTGTAAAGAGAGACACTGGGCAAGGAAC 2099
Db 2114 CCCCACTTGACAAGGATCAATGTGCTTCTGTAAAGAAAGAGACACTGGGCTAAGAC 2173
Qy 2100 TGCCCCAAGAGGGAACAAAGGACCAAGGATCCTA-----GCTCTAGAGAAGAT 2150
Db 2174 TGCCCCAAGAGACCGGGTCCCGGAGACCGGACCCAGACCTCCCTCTGACTTA 2233
Qy 2151 AAGATTTAGGGAGAGCGGGTTTCGACCCCTCCCGAGCCAGGGTAACTTTGAAAGTG 2210
Db 2234 GACGACTAGGGGGTTCAGGGTTCAGGAGCCCGCCCTGAAACCCAGGATAACCCCTCACTGTC 2293
Qy 2211 GAGGGCAACCACTGAGTTGAGTCTCTGTTGATACCGGAGGAAACATTCACTGCTACTACAG 2270
Db 2294 GGGGGCAACCCGTCACCTTCTGTTGATATCTGGGGCCCAACACTCGTCTGACTCA 2353
Qy 2271 CCATTTAGGAAACTAAAAAGATAAAAAATCCTGGGTGATGGGTGCCACAGGGCAACAACAG 2330
Db 2354 AATCTGGGCCCTTAAGTGAAGGTCTGGCTTGGGTCCCAAGGGCTACTTGGAGGAAGCGG 2413
Qy 2331 TATCATGGAATACCCGAGAAACAGTTGACTTTGGAGGTGGGACGGGTAAACCACTCGTTT 2390
Db 2414 TATCGCTGGAACACAGATCGCAAGGTACACCTAGCTACCGGTAAAGGTCACTCACTCTTTC 2473
Qy 2391 CTGGTCATACCTGAGTCCGACGACCCCTCTTAGTAGAGACTTATTGACCAAGATGGGA 2450
Db 2474 CTCCATGTGCCAGACTGCCCTTACCTTGTCTAGGAAGAGACTTGTTAACATAAATAA 2533
Qy 2451 GCACAAATTTCTTTTGA---ACAAAGGAAACAGAAAGTGTCTGCAATAACAACCTATC 2507
Db 2534 GCCCAGATCCACTTTTGGGGATCAGGAGCCAGGTTGTGGGACCAAAAGAGACAGCTCTA 2593
Qy 2508 ACTGTGTTGACCTTCAATTAGATGACGAATATCGACTATCTCTCCCTAGTAAAGCCT 2567
Db 2594 CAGGTGTTGACCTTAAACCTTAGAAGATGAGTACGGCTTCATGAGACCTCAGACAGCCG 2653
Qy 2568 GA---TCAAAAATATACAAATTTCTGTTGGMAACAGTTTCCCCCAAGCCTGGGAGAAACCGCA 2624
Db 2654 GAAGCTTCTCTGGGTCCACCTGGCTTTCGACTTTCCCCAGGCTGGGAGAAACCGGG 2713
Qy 2625 GGATGGGTTTGGCAAGCAAGTTTCCCCCAACAAGTTTATCAATGAAGGCGCAGTGCCACA 2684
Db 2714 GGATGGGACTGGCAGTTTCCGAGGCGCTCTAATCATACCTCTGAAAGCAACCTCCACC 2773
Qy 2685 CCAAGTCTAGTCAGACAGATACCCCTTGTAGTAAAGAGCTCAAGAGAAATTCGGCCGAT 2744
Db 2774 CTTGTGTCCATAAAACAATACCCCATGTCAACGGAAGCCAGACTGGGGATCAAGCCCCAC 2833
Qy 2745 GTCGAAGATTAATCCAACAGGCGCATCTAGTTTCTGTCCAATCTCCCTGGAATACCTCCC 2804
Db 2834 ATACAGAGGCTGTGGACCCAGGGAATACTGTACCTCCGAGTCCCCCTGGAATACACCC 2893
Qy 2805 CTGCTACCGGTTAGAAAGCCTGGGACTTAATGACTATCGACAGTACAGGACTTGAAGAG 2864
Db 2894 CTGCTACCGGTTAAGAAACCAAGNACTAACGATTATAGGCTGTGTCAGGATCTGAGAA 2953
Qy 2865 GTCAAATAACCGGTGAGGATATACCCCAACAGTCCCGAAACCTTTATACCTCTTGTGT 2924
Db 2954 GTCAAACAGCGGTGGAAGACATCCACCCACCGTGCCTCAATCTTATACCTCTCAAGT 3013
Qy 2925 GCTCTCCACCCCAACGAGCTGTATACAGTATTTGACTTTAAAGGATGCTCTTCTGCG 2984
Db 3014 GGGCTCCACCGTCCCAACCGGTGTATCTGTGCTGATTATTAAGGATGCTCTTCTGCG 3073
Qy 2985 CTGAGATTACACCCCACTAGCCAACTTTTGGCTTTGCAATCGAGAGATCCAGGTACG 3044
Db 3074 CTGAGACTCCACCCCACTAGCTCTCTTCCGCTTCGAGTGGAGAGATCCAGGATG 3133
Qy 3045 GGAAGAACCGGGCAGCTCACCTGGACCCGACTGCCCCCAAGGGTTCAAGAACTCCCGACC 3104
Db 3134 GGAATCTCAGACAAATTAACCTGGACCACTCCCAACAGGGTTTCAAAAACAGTCCCA 3193
Qy 3105 ATCTTTGACGAAGCCCTACACAGAGACTGGCCAACTTCAGGATCCCAACCTCAGGTG 3164
Db 3194 CTGTTGATGAGGCATACACAGAGACTTAGCAGACTTCGGGATCCAGACCCAGACTTG 3253
Qy 3165 ACCCTCTCCAGTACGTGGATGACCTGCTTCTGGCGGAGGACCAACACAGAGACTGCTTA 3224
Db 3254 ATCTGTCTACAGTACGTGGATGACATCTACTTGGCCGCCACTTTCTGAGCTCGACTGCA 3313
Qy 3225 GAAGCAGCAAGGACTACTGCTGGAATTTGTGACCTTAGGCTACAGAGCTCTGCTAAG 3284
Db 3314 CAAGTACTCGGGCCCTGTTACTAAACCTAGGAAACCTCGGGTATCGGGCTCGGCCAAG 3373
Qy 3285 AAGCCCAAGATTTCCAGAGAGAGGTAAACATCTTTGGGTACAGTTTTCGGGAGCGGAG 3344
Db 3374 AAAGCCCAACTTTGCCAAGAACAGGTCAAGTCACTTGGGGTATCTCTAAAAAGAGGTG 3433
Qy 3345 CGATGGCTGAGGAGGACGGAAGAACTCTAGTCCAGATACCGGGCCCAACACACAGCC 3404
Db 3434 AGATGGCTGACTGAGGCGCAGAAAGAGACTGTGATGGGGAGCCCTACTTCGAGACCCCT 3493
Qy 3405 AAAAATAATGAGAGAGTTTTCGGGACAGCTGGATTTTTCAGACTGTGTGATCCCGGGTTT 3464
Db 3494 CGACAACTAAGGGAGTTCTTAGGAGCGCAGGCTTCTGTCCCTCTGATCCCTGGGTTT 3553
Qy 3465 GCGACCTTTAGCAGCCCCCACTCTACCCGCTAAACCAAGAAAAAGGGGAATTTCTCTGGGT 3524
Db 3554 GCGGAATGGCAGCCCCCTTGTATCTCTTACCAAAACGGGAGCTCTGTTCAATTTGGGCG 3613

QY	3525	CCTGAGCACGAGAGGCATTTGATGCTATCAAAAAGGCCCTGCTGAGCGCACTGCTCTG	3584	QY	4590	GACCAAGTTCTCTGAGACTCCGGAAGGACCTGCTATACCTCAGATGGGAAGAAATCCTG	4649
Db	3614	CCAGACCCAGCAAAAGGCCCTATCAAGAAATCAAAACAGGCCCTCTTAACCTGCCCGCCCTG	3673	Db	4691	GGGGCCACTATAACACAGAGCAAGGATACCTGGGT---CTTCCAAGGCAAGCGGTGATG	4747
QY	3585	GCCTCCCTGACGTAACTAAACCCCTTTACCCCTTTATGTGGATGAGCGTAAAGGATAGCC	3644	QY	4650	CCCCCAAGAAGGGTTAGAATATGTCCAACAGATACATCGTCTAAACCCACCTAGGAAC	4709
Db	3674	GGATTGCCAGATTGACTAAGCCCTTTGAACCTCTTTGTGCGAGAGAGCAGGGCTACGCC	3733	Db	4748	CCCGACCAATTTGTATTTTGAATGTTAGACTCAGCTCCACCGGCTCACCCACCTCGGCTAC	4807
QY	3645	CGGGAGAGTTTAAACCCCAACCCCTAGGACCATGAGAGAACCTGTGCGCTACCTGCTCAAAAG	3704	QY	4710	AAACACCTGCGACAGTTGGTCA-----GAACATCCCTTTATCATGTGTTCTGAGGCTACCA	4763
Db	3734	AAAGGCTCTTAACGCAAAAACCTGGACCTTTGGCGTCCGCGTGGCTTACCTGTCTCCAAA	3793	Db	4808	CAGAAAAATGAAGCACTCCTTGACAGAGGAGAAAGCCCTACTACTCATGTCTAAACCGGAC	4867
QY	3705	AAGTCGATCTGTAGCAGTGGTTGGCCCATATGCTGAAAGCTATGCGAGCTGFGCC	3764	QY	4764	GGAGTGGCTGACTCGGTGGTCAAAATTTGTGTGCTCCCTGCGAGCTGGTTAATGCTAATCCT	4823
Db	3794	AAGCTAGACCAAGTCAGCTGGGTGGCCCTTGTCTACGGATGGTAGCCATTTGCC	3853	Db	4868	AAAAACCTCCAAATATGTGCGAGATTCTTGCACGGCTGTGTGCCCAAGTAATAATCCAGCAA	4927
QY	3765	ATACTGGTCAAGGACGCTGACAAATTTGACTTTTGGGACAGAAATATAACTGTAATAGCCCC	3824	QY	4824	TCCCAATGCTCTCAGGGAAGAGACTAAGGGGAAGCCACCCAGGCGCTCACTTGGGAAGTG	4883
Db	3854	GTCTGACAAAAGATGACGGCAAGCTAACTATGGGACAGCCGCTAGTCACTCTGGCCCCC	3913	Db	4928	GCTAAATCGGGGAGGAGTGAGAGTACGAGGACATCGGCCAGGCACCCATTTGGGAGATC	4987
QY	3825	CATGCATTCGAGAAACATCTGTCGGCAGCCCCCAGACCCGATGGATGACCAACGCCGATG	3884	QY	4884	GACTTCACTGAGGTAAAGCCGCTAAATAACGAAACAAATACCTATTGGTTTTTGTAGAC	4943
Db	3914	CATGAGTAGAGCACTGTCAAGCAACCCCTGACCGCTGGCTATCCAAACGCCCGCATG	3973	Db	4988	GATTTTACAGAAATCAAGCCAGGCTGTATGGGTACAAGTACCTCTCTGGTATTTCTGGTAC	5047
QY	3885	ACCCACTATPCA---AAGCCTGCTTCTACAGAGAGGGTCAAGTTGCTCCACAGCCGCT	3941	QY	4944	ACCTTTTCAGGATGGGTAGAGGCTTATCCTACTAAGAAAGAGACTTCAACCTGTGGTGGT	5003
Db	3974	ACCCACTACAGCAATGCTCTAGACACTGACCGAGTTCAGTTTCGGACAGTGTGTGGCC	4033	Db	5048	ACCTTTCTCTGGTGGGTGGAAGCCTTTCCAACCAAGAGAGAAACACAGAGTCTGTGCTCC	5107
QY	3942	CTCAACCTTGCCACTCTTCTGCTGAGAGACTGATGAACCAAGTCACTCATGTTGCCAT	4001	QY	5004	AAAAAAATACGGAAGAAATTTTCCAAGATTTGGAATACCTTAAGTAAATAGGTCAGAC	5063
Db	4034	CTCAATCTCTGCCACCTTACTCCCT---CTCCCGGAAGAGGAGCCCCCATGATTTGCCCTC	4090	Db	5108	AAGAAATTTGCTGGAAGAAATATTTCCGAGATTTGGAATGCCACAGGTATTTGGGATCTGAT	5167
QY	4002	CAACTATTGATTTAGGAGACTGGGGTCGCAAGGACCTTTACAGACATACCGCTGACTGGA	4061	QY	5064	AATGTCAGAGCTTTTGTGCCAGAGTAAGTCAGGGAAGTGGCCAAAGATATTTGGGGAATTGAT	5123
Db	4091	GAGATCTTGGCTGAACGATGGAACAGACCGGATCTCACGACAGGCCATCCAGAC	4150	Db	5168	AAAGGCTGCTTCACTCCAGGTAACTCGGTGGCCGATTTTACTGGGGATCGAT	5227
QY	4062	GAGTGTCTAACCTGGTTCACTGACGGAAGCAGCTATGTGGTGAAGGTAAAGGATGGCT	4121	QY	5124	TGGAATCTGATTTGTGCTATACAGACCCCAAGCTCAGGACAGGTAGAGGATGAATAGA	5183
Db	4151	GCCGACCACACCTGTGTATACCGATGGGAGCAGCTTTTTCGAAGAGGACAGCGGAAGGCT	4210	Db	5228	TGGAATTTACATTTGTGCTTATAGACCCCAAGAGTTCAAGTTCAGGTAGAGAAATGAATAGA	5287
QY	4122	GGGGCGGGTGGTGAAGGGACCCGACGATCTGGGCGAGCAGCCTGCGGGAAGGAATCT	4181	QY	5184	ACCATTAAGAGACCCCTTACTAAATTTGACCGGAGACTGGCGTTAAATGATTTGGATAGCT	5243
Db	4211	GGGGCAGCGGTGACCACTGAGACCCGAGGTAATCTGGGCAAGGGCACTGCGCGCTGGAACA	4270	Db	5288	ACCATCAAGGAGACTTAACTAAATTTAACGCTTGACGCTGGCAGCTAGAGACTGGGTACTC	5347
QY	4182	TCAGCAAAAGGCTCAGCTCATGGCCCTCAGCAAGCTTTTGGGCTGGCCGGAAGGAAA	4241	QY	5244	CTCTGCCCCCTTTGTGCTTTTAGGGTTAGGAACACCCCTGGACAGTTGGGCTGACCCCC	5303
Db	4271	TTTGCCCAAGGGCCGAACTGATAGCACTCACTCAAGCCTTAAGATGGCAGAGGTAG	4330	Db	5348	CTACTCCCCCTTAGCTCTCTACCGACCGGAAACACTCCGGGCCCCCATGATTTGACTCCG	5407
QY	4242	TCCATAAACATTATACGGACAGCAGGTATGCTTTTGGACTGCAACGATACATGGGGCC	4301	QY	5304	FATGAATTTACTACGGGGACCCCCCATTTGGTAGAAATTTGCTTCTGTCTATAGTGTCT	5363
Db	4331	AGGCTAAACGTTTACACTGACAGCCGATATGCTTTTCGCACCGCCCATATCCATGGAGAG	4390	Db	5408	TATGAATTTCTTGTACGGGGCGCCCCCTGCCCCCTTGTCACTTCCATGTACCCCCGACATGTCA	5467
QY	4302	ATCTATAAACAAGGGGTTGCTTACTCAGCAGGAGGGAATTAAGAAACAAGAGGA	4361	QY	5364	GAGTGTGCTTTTCCAGCCTTTTCTTAGGCTCAAGGCACCTTGAGTGGGTGAGACAA	5423
Db	4391	ATCTTAGGAGGCGGGTTGCTTAACCTCAGAGGGTAGAATAAATAAACAAGAGCGAG	4450	Db	5468	GAAATTAATAATAGCCATCTCTCCGAGCTCACTTACAGGCCCTCCAAACGCTGACGCGA	5527
QY	4362	ATTCTAAGCCTATTAGAAGCGTACATTTTACCAAAAGGCTAGCTATTATATACATGTCCT	4421	QY	5424	CGAGCGTGGAGCAACTCCGGAGGCTTACTCAGGAGGAGGAGACTTGC---AGATCCCA	5480
Db	4451	ATCCTGGCTTTACTGAAAGCTCTTTTCTGCCAAAAGAGCTCAGTATATATCCACTGCTG	4510	Db	5528	GAAATTTGGAACCACTGCGCGAGGCTTACCGGGACCCCTAGACCAACAGTGTATCCG	5587
QY	4422	GGACATCAGAAAGCTTAAGATCTCATATCCAGAGGAAACAGATGGCTGACCGGTTGCC	4481	QY	5481	CATCGTTTCCAAAGTGGGAGATTCACTTACGTTTAGACGCCACCGTGCAGGAAACCTCGAG	5540
Db	4511	GGGCATCAAAAGGAGATAGTGCAGGCTAGGGGCAACCGCTTAGCAGACCAAGCGGCC	4570	Db	5588	CACCCCTTCCGATTTGGAGACTCCGTTGGGTGCGCGCGCACAGACCAAAAACTTAGAA	5647
QY	4482	AAGAGGAGCC-----CAGGGTGTTAACCTTCTGCTTATATAGAAATGCCCC	4529	QY	5541	ACTCGGTGGAAGGGCCCTTATCTCTGCTACTTTTGACCAACCAACGCTCTGAAAGTCGAA	5600
Db	4571	CGGGAGGCGCCATAAAGACGCTCCAGATACATCCACTCTCTCTCATAGAGGATTTCAAC	4630	Db	5648	CCTCGTGAAGGAGCCCTTACCGCTCTTACTGACCAACCCCAACCGCTCTCAGGTAGAC	5707
QY	4530	AAAGCCCCAGAACCCAGACGACAGTACCCCTAGAAAGCTGGCAAGAGATAAAGAGATA	4589	QY	5601	GGAAATCTCCACCTGGATCCATGCTATCCCAAGTTAAACCGGCGCCACCTCCC-----GAT	5654
Db	4631	CCATATACGCTGCTCTATTTTCCATTTACTGAAAACAGATCTTAAAGAACTCAGAGCTT	4690	Db	5708	GGCATCTCTGCATGTGATACACGCCGCCCAAGTCAAGGACGACGACACACCCCCGATAAAA	5767
				QY	5655	TCGGGGTGGAAAGCCGAAAGAACTGAAAAATCCCTTAAAGCTTCCGCTCCATCGCTGGT	5714

Db	5768	CCATCATGGAGAGTACAAACGCTCTCAAAACCCCTTTAAATAATCAGGTTAAACCCGCTGGGGCC	5827
Qy	5715	CTTACTCTCTCAATAACCTCTCAGACTAATGATGCGCATAGGACAGCCTGAATC	5774
Db	5828	CCCTAATGCTCTTCTGATTTCTCGGA--GGGGTCAACCCCGCTGGTGGGAAACAGCCC	5885
Qy	5775	CCATAAACCTTATCTCTCACTGGTTAAATTACT-----GACTCGCGCACAGG	5822
Db	5886	CCACCAAGTTTAACTCACTGGGAAGTGACTAATGGAGACCGAGAAACGGTGTGGGC	5945
Qy	5823	TATTAATATCAACAACACTCAAGG-----	5846
Db	5946	AATAACCGGCAATCAACCTCTGTGGACTTGTGGCTGTGACCTCACACAGATCTCTGTAT	6005
Qy	5847	-----GGAGGCTCCTTTAGGAACCTGGTGGCTGTATATAGTTTGGCTCA	5893
Db	6006	GTTGGCCCTCCACGGGCGCTCTATTTGGGCGCTAGAAATATCGGGCTCTTTTCTCTCTCC	6065
Qy	5894	GATCAGTTATTCCTAGTCTGACCTCACCCCGAGATATCTCTCCATGCT-----	5940
Db	6066	CCCGGGCCCCCTGTCTGTTTCAGGAACAGGACTCCACGCGAGCTGTTCCAGGATGT	6125
Qy	5941	-----CACGGATTTTATGTTTGTCCAGGACCAACCAATAATAGGAAAAATTCGGGAAA	5993
Db	6126	GAGGAGCCCCGCTGACTCATATCTCCCGGTGCAATACGGCTCGGAACAGACTTAAGTTA	6185
Qy	5994	TCCAGAGATTTCTTTTGTAAACAAATGGAACCTGTGTAACCTCTAATGATGGATATTGAA	6053
Db	6186	TCTAAAGTGACATATGCGCCCAATGAAGGATTTCTATGCTGCCCCGGGCGCACATCGCCCC	6245
Qy	6054	ATGCCAACCTCTCAGCAGGATAGGTAAGTTTCTTATGT-----CAAC	6099
Db	6246	CGTGGGCCCGCTCGTGTGGTGTCCAGAACTCTTATGTGCTCTTGGGGCTGGAA	6305
Qy	6100	ACCTATACCAAGCTCTGGACAAATTTAATTTACCTGACCTGGATAGAACTGGAAGCCCCAAG	6159
Db	6306	ACCACAGCCGAGCATCTCGGAACCATCTCTGCTCGTGGACTACATCACAGTAAGCAAC	6365
Qy	6160	TGCTCTCTTCAGACCTAGATTACTTAAATAAGTTTCACTGAGAAAGGAAACAGAA	6219
Db	6366	AATCTAACCTCAGACCAAGCAACCCAGTATGCAAGGTAATGAGTGGTGCAACTCTCTTA	6425
Qy	6220	AATATCC-----TAAATGGTAAATGGTATGCTTTGGGGAATGGTATA	6263
Db	6426	ACTATCCGGTTTCAGAGCTTTGAAAAACAGGCCACCTCTCGGTGCACAGGCCATGTGG	6485
Qy	6264	TTATGG-----AGCTCGGGTAAACAAACAGGCTCCATTTCTAACTATTCGCTCAAA	6315
Db	6486	GGATTGGCCCTATACGTTCTGGACATGACCCAGGGCTCATCTTTGGGATCCGACTTAAA	6545
Qy	6316	ATAAACAGCTGGAGCCTCCAAATGGCTATAGGACAAATACGGTCTTGACGGGTCAAAGA	6375
Db	6546	ATTACAGACTCGGGGCCCGGGTCCCAATAGGGCCAAACCCGCTTTGTTCAGACCGACGA	6605
Qy	6376	CCCCCAACCAAGACCGHAGACATCTCTTAACATACTTCTGGATCAGACCCCACTGAG	6435
Db	6606	CCACCTTCCCGGCCCTAGACCCACCAAGATCTCCCCCGCTTCAAACTCCACCCCAACCGAG	6665
Qy	6436	TCTAACAGCA-----CGACTAAATGGGGGCAAAACTTTTATAGCTC	6477
Db	6666	ACACCCCTCACCTCCCGCAACCCCGCCAGGGAGTCGAAACCGATTTGTTAAATCTA	6725
Qy	6478	ATCAGGGAGCTTTTCAAGCTCTTAACCTCCAGACTCCAGAGGCTACCTCTTCTTGTGG	6537
Db	6726	GTAAGAAGGCTTACCAAGCCCTCAACCTCACAGTCTGATATAAAACCAAGAGTGTCTGG	6785
Qy	6538	CTATGCTTAGTTCGGGCCCACTTACTATGAGGAATGGCTAGAGAGGGAATTCAT	6597
Db	6786	TTATGCTTAGTATCGGACCCCACTACTACGAGGGGGTGGCGCTCTAGGTACCTACTCC	6845
Qy	6598	GTGACAAAGAACATAGAGACCAATGCATGGGATCCCAAAATAAGCTTACCTTACT	6657

RESULT 3
AK090126
LOCUS
DEFINITION Mus musculus brain CRL-1443 BC3H1 cDNA, RIKEN full-length enriched library, clone:G431002E14 product:gene e1 protein, full insert sequence.
ACCESSION AK090126
VERSION AK090126.1 GI:26105743
KEYWORDS HTC; CAP trapper.
SOURCE Mus musculus (house mouse)

Db	1418	CTCACCACCACACAGCCACCTGGGATGATTCGCCAGCAATATTATAGGAGCTCTGCTTACC	1477
Qy	1380	ACCGAGGAGCGAGAGAGAAATTTCTATTAGAGCTAGAAAATAATCTTCTGGGGCCGACGGG	1439
Db	1478	GGGGAAGAGAGACAGCGGGTCTCTCGAAGCCGGAAGAGCTCTCGGGGCAACGATGGG	1537
Qy	1440	CGACCCACGCGGTTGCAAAATGAGATTTGACATGGGATTTCCCTTAACTCGCCCGGTTGG	1499
Db	1538	CGCCCCACCACTGCCCAACGAGGTTGACGCTGCTTTTCCCTTGAAACGTCCCGATTTG	1597
Qy	1500	GACTACAAACGCGCTGAGGTAGGAGAGCTTGAAATCTATCGCAGGCTCTGGTGGG	1559
Db	1598	GATTACACCAACCAAGAGTAGGAGCCACTAGTTCTCTATCGCAGTTGCTTTTAGCG	1657
Qy	1560	GGTCTCGGGGGCCCTCAACAGCGCCCACTAAATTTGGCTAAGTAAAGAGAAAGTATGCAG	1619
Db	1658	GGTCTCAAAACGGGCGAGCCCAACCAATTTGGCCAAAGGTAAAGGAATAACCCAG	1717
Qy	1620	GGACCGAATGAACCCCTCTGTTTTTTTGAGAGGCTCTTGAAGGCTTTCAAGCGGTATC	1679
Db	1718	GGACCTGATGATCCCTCTCAGCTTCTTAGAGAGACTCAAGGAAGCCTATCGCAGATAC	1777
Qy	1680	ACCCCTTTTATCCCACTCAGAGGCCCAAAAGCCTCAGTGGCTTTGGGCTTTATAGGA	1739
Db	1778	ACTCTTATGATCTCGAGGACCTCGGGCAAGAAACGAATGTATCTATGTCAITCTCTGG	1837
Qy	1740	CAGTCAGCTTGGATATTAGAAAGAGCTTCAGAGACTGGAAGGTTTACAGGAGGCTGAG	1799
Db	1838	CAGTCGCGCTCCAGACATTTGTGCAAGTTAGAGCGGTTAGAAGACTTTAAAGTAATACT	1897
Qy	1800	TTACGTGATCTAGTGAAGGAGGACAGAAAGTATATTACAAAAGGGAGACAGAAAGAA	1859
Db	1898	TTAGGAGATTAGTGAGAGAGCCGAAGGATCTTTAATAAAGAGAACTCCAGAGAA	1957
Qy	1860	AGGGAACAAAGAAAGAGAGAGAAAGAGAGAAAGGAGGAAGACGTAATAAAGGCAA	1919
Db	1958	AGAGAGAGCGGTTAGGAGGAGACAGAGGAAGAAAGAGCGGCTAGGGCAGAGAG	2017
Qy	1920	GAGAGAAATTGATAGATCTTGGCTGAGTGTGGAAGGGAAGAAACATACGGAAGA	1979
Db	2018	GAGCAGAAAGAGAAAGAGAGGACCGTAGGAGACATAGAGAAATGAGCAAACTTTTGGCC	2077
Qy	1980	GAGAGACATTTAGGAAAATTTAGGTCAAGGCCCTAGACAGTCAGGGAACCTGGGCAATAGG	2039
Db	2078	ACCGTAGTTAGTGAACAGACAGGATAGAC-----AGGGGGAGAGAGGAGG	2128
Qy	2040	ACCCCACTCGACAGGACCAATGTGCATATTGTAAGAAAGAGAGACACTGGGCAAGGAAC	2099
Db	2129	CCCCAACTTGACAAAGGATCAATGTGCTACTGTAAAGAAAGGACACTGGGCTAAAAGAC	2188
Qy	2100	TGCCCCAAGAGGAAACAAAGGACCAAGGATCCTA-----GCTCTAGAGAAGAT	2150
Db	2189	TGCCCAAGAGGCCACCGGGTCCCGAGGACCGGACCCCAAGACCTCCCTCTGACTTTA	2248
Qy	2151	AAAGATTAGGGAGACGGGTTGGGACCCCTCCCGAGCCGAGGTAACCTTTCAAGGTG	2210
Db	2249	GACCACTAGGGGGTCAAGGTCAGAGCCCGCCCTGAAACCAAGATAAACCTCACTGTC	2308
Qy	2211	GAGGGCAACCAAGTTGAGTTCTCTGTTGATACCGGAGCGAAACATTCAGTGTCTACTACAG	2270
Db	2309	GGGGGGCAACCCGTCACTTCTGTTGATACGCGGCCCCAACACTCGGTGCTGACTCAA	2368
Qy	2271	CCATTAGGAAACTTAAAGATAAATAATCTTGGGTGATGGGTGCCACAGGCAACACAG	2330
Db	2369	AATCTGGGCCCTTAAGTGAACAGGTCTGGCTTGGGTCCAAAGGGGCTACTGGAGGAAGCGG	2428
Qy	2331	TATCCATGGAATAACCGGAACAGCTTGGCTTGGAGTGGGCAAGGCTAACCTCGTTT	2390
Db	2429	TATCGCTGGACCAAGATCGCAAGGTACACCTAGCTACCGGTAAAGGTCACTCTTTC	2488
Qy	2391	CTGGTCACTACCTGAGTGCCAGCACCCCTCTTAGGTAGAGACTTTATTGACCAAGATGGGA	2450
Db	2489	CTCCATGTGCCAGACTGCCCCCTACCCCTTGTCTAGGAAGAGACTTGTTAACCTAAACTAAA	2548
Qy	2451	GCACAAATTTCTTTTGA----ACAAAGGAAACCAAGAGTGTCTGCAATTAACAAACCTATC	2507
Db	2549	GCCAGATCCACTTTTGGGGATCAGAGCCCAAGGTTGTGGGACCAAAAGAGACAGCTCTTA	2608
Qy	2508	ACTGTGTTGACCTCCAAATTTAGATGACGAATATCGACTATACTCTCCCTTAGTAAAGCCCT	2567
Db	2609	CAGGTGTTGACCTTAAACCTAGAGATGAGTATCGGCTTCATGAGACCTCAGCAGAGCCG	2668
Qy	2568	GA----TCAAAAATATACAATTTCTGTTTGGAAACAGTTTCCCAAGCCTGGGCGAGAAACGCGCA	2624
Db	2669	GAAGCTTCTCTGGGTCACCTGGCTTCCGACTTTTCCCGAGGCTGGGCGAGAAACCGGG	2728
Qy	2625	GGATGGGTTGGCAAGCAAGTTTCCCAACAAGTTATTCAACTGAAGGCCAGTGCCACA	2684
Db	2729	GGCATGGGACTGGCAGTTGGCCAGGGCGCTCTAATCATACTCTCTGAAGGCAACTTCCACC	2788
Qy	2685	CCAGTCTCAGTCAGACAGTACCCCTTGTAGTAAAGAAAGCTCAAGAAGGAAATTCGGCCGCAT	2744
Db	2789	CTGTGTCCATAAAAACAATACCCCAATGTCAAGAAAGCAGACTGGGGATCAAGCCCCAC	2848
Qy	2745	GTCCAAAGATTTAATCCAAACAGGGCATCCTAGTTCTGTCCAATCTCCCTGGAATACTCCC	2804
Db	2849	ATACAGAGGCTGTTGGACAGGGAATACTGTGTACCTGTCAGTCCCTCGAATACACCC	2908
Qy	2805	CTGCTACCGGTTAGAAAGCCTGGGACTAATGACTATCGACCAAGTACAGGACTTTGAGAGAG	2864
Db	2909	CTGCTACCCGTTAAGAAACCAGGAACTTAACGATTTATAGGCTGTCTCCAGGATCTGAGAGAA	2968
Qy	2865	GTCAATAACGGGTGAGGATATACACCAACAGTCCCGAACCTTATAACCTCTTCTGT	2924
Db	2969	GTCAA--CAAGGGGTGGAAGACATCCACCCCGTCCCAATCTTTATAACCTCTTAAGT	3027
Qy	2925	GCTCTCCACCCCAACGGAGCTGTATACAGTATTGGACTTTAAAGGATGCTCTTCTTCG	2984
Db	3028	GGGCTCCACCGTCCACCGTGGTATCTGTGCTTGAATTTAAAGGATGCTTTTCTGCG	3087
Qy	2985	CTGAGATTACACCCCACTAGCCAAACCTTTTGGCTTTGAAATGGAAGAGATCCAGGTACG	3044
Db	3088	CTGAGACTCCACCCCACTGACGCTCTCTCGCTTCGAGTGGAGAGATCCAGGGATG	3147
Qy	3045	GGAAAGAACCGGAGCTCACTGGACCGGATGCCCAAGGTTCAAGAACTCCCGGAC	3104
Db	3148	GGAACTCTCAGGACAAATTAACCTGGACAGACTCCACAGGGTTTCAAAAACAGTCCAC	3207
Qy	3105	ATCTTTGACCAAGCCCTACACAGAGACTCGCCAACTTCAGGATCCCAACCCCTCAGGTG	3164
Db	3208	CTGTTGATGAGGACACTTACACAGAGACTTAGCAGACTTCGGATCCAGCACCCAGACTTG	3267
Qy	3165	ACCTCTCTCAGTACGTGGATGACCTGCTTTCTGGCGGAGCCCAACACAGGACTGTGTTA	3224
Db	3268	ATCTGCTACAGTACGTGGATGACATACTACTGGCCGCCACTTCTGAGCTGACTGCCAA	3327
Qy	3225	GAAGGACGAAAGGACCTACTGCTGGAAATGTCTGACCTAGGCTACAGAGCTCTGCTAAG	3284
Db	3328	CAAGGTACTCGGGCCCTGTTACTAAACCTTAGGAAACCTCGGGTATCGGGCTTCGGCCAA	3387
Qy	3285	AAGGCCAGATTTGACAGGAGAGGTAACATACTTGGGTACAGTTTGGCGGAGCGGGCAG	3344
Db	3388	AAAGCCCAACTTTGCCAGAAACAGGTCAAGTACTTGGGTATCTCTTAAAGAGGGTCTAG	3447
Qy	3345	CGATGGCTGACGGAGGACGAAAGAAACTGTAGTCCAGATACCGGGCCCCAACCAACGCC	3404
Db	3448	AGATGGCTGACTGAGGCCAGAAAGAGACTGTGTATGGGCGAGCTTACTCCGAGAGCCCT	3507
Qy	3405	AAACAAATGAGAGAGTTTGGGACAGCTGGATTTTGCAGACTGTGTGATCCCGGGTTT	3464
Db	3508	CGACAACTAAGGGAGTTCTTAGGACGCGAGGCTTCTGTGCTCTCTGATCCCTGGGTTT	3567
Qy	3465	CGGACCTTAGCAGGCCCACTCTACCCGCTAACCAAGAAAGAGGGAATTTCTCTGGGCT	3524
Db	3568	GCGGAAATGGCAGCCCCCTTGTATCTCTTACCAGAAACGGGGACTCTGTTCAATTTGGGC	3627

5782 CCATCGAGAGTACAAAGCTCTCAAAACCCCTTTAAATATCAGGTTAAACCCGTGGGCC 5841
5715 CTTTACTCTCTCAATAACCTCTCAGACTAATGATGCGCATAGGACAGCCTGAATC 5774
5842 CCCTAATGTCCTTCTGATTTCTCGGA--GGGGTCAACCCCGTGGTGGGAAACAGCCC 5899
5775 CCATAAACCTTATCTCTCACTCGTGGTAAATTAATGACTCCGGCACAGGTATTAATCA 5834
5900 CCACAGGTTTAAACCTCACTCGGAGTGAATGACTAATGGAGACCGAGAAACGGTGGGC 5959
5835 CAACACTCAAGGGAGGCTCTTTAGGAACTGGTGGCCCTGATC----- 5878
5960 AATAACCC--GGCAATCACCTCTGTGGACTTGGTGGCCTGACCTCACACAGATCTCTG 6016
5879 -----TATACGTTTGGCTCAGATCAGTTATTCCTAGTCTGAC 5916
6017 TATGTTGGCCCTCAACGGGCCGCTTATATGGGCTTAGAATATCGGGCTCTTTTCTCC 6076
5917 TCACCC----- 5929
6077 TCCCCGGGGCCCCCTGCTGTTTCAGGAAGCAGGACTCCACGCCAGGCTGTTCCAGAGA 6136
5930 TCCTCCATGCTACGGATTTTATGTTTGGCCAGGACCAACAAATAATGGAACATTCG 5989
6137 TTGTGAGGAGCCCTGACTTTCATATCTCCCGTGCAATACGGCCTGGAACAGACTTAA 6196
5990 GAAATCCAGAGATTTCTTTTGTAAACATGGAAGTGTGTAACCTTAATGATGGATTT 6049
6197 GTTATCTAAAGTGACACATGCCCAATGAAGGATTTCTATGCTGCCCCGGGCCACATCG 6256
6050 GGAATGGCCAACTCTCAGCAGGATAGGTAAAGTTTCTTATGT----- 6095
6257 CCCCCGGTGGCCCGCTGTTGTTGTTGTCAGAACTCCTTATTTGTCCTTGGGGCTG 6316
6096 CAACACCTATACAGCTCTGACAAATTAATTAATCTGACCTGGATTAGAACTGGAAGCCC 6155
6317 CGAAACACAGGCGGAGCATCTGGAAACCATCTCTGCTGGGACTACATCACAGTAAG 6376
6156 CAAGTGTCTCTTCAGACCTAGATTACCTTAAATAAGTTTCTACTGAGAAAGGAACA 6215
6377 CAACAAATTAACCTCAGACAGGCAACCCAGTATGCAAAAGGTAATGAGTGGTGCACCTC 6436
6216 AGAAATATCC-----TAAATGGGTAAATGTTATGCTTTGGGGAATGG 6259
6437 CTTAACTATCGGTTACAGAGCTTTGGAAACAGGCCACCTCTGGGTACAGGCCATTG 6496
6260 TATATTATGG-----AGCTCGGTAAACACACAGGCTCCATTCTAACTATTCGCT 6311
6497 GTGGGATTTGGCCTATACGTTCTCTGGACATGACCCAGGGCTCATCTTTGGATCCGACT 6556
6312 CAATAATAACAGCTGGAGCTTCAATGGCTATAGGACCAATAACGGTCTTGGCGGTCA 6371
6557 TAAATTTACAGACTCGGGGCCCCGGTCCCAATAGGGCCAAACCCCTCTTGTGACAGCCG 6616
6372 AAGACCCCAACCAAGGACAGGACCATCTCTTAAATAACTTCTGATCAGACCCAC 6431
6617 ACGACCACTTCCCGGCTAGACCCACAGATCTCCCGGCTTTCAAACTCCACCCCAAC 6676
6432 TGAGCTTAAACAGCA-----CGACTAAATGATGGGGCAAACTTTTATG 6473
6677 CGAGACACCTCTACCTTCCCGGAACCCCGCCAGCGGAGTCGAAACCGATTGTAA 6736
6474 CCTCATCCAGGAGCTTTTCAAGCTCTTAACTCCACGACTCCAGAGGCTACCTCTTCTG 6533
6737 TCTAGTAAAGAGGCTTACCAAGCCCTCAACCTCACCAGTCTCTGATATAAACCCCAAGAGT 6796
6534 TTGCTATGCTAGTTCGGGCCCCACCTTACTATGATGAGGATGCTAGAGAGGGAATT 6593
6797 CTGTTATGCTAGTATGAGGACCCCGTACTACAGGGGGTTCGCGCTCTGATACCTA 6856
6594 CAATGTGACAAAGAACATAGAGACCAATGACATGGGATGCCAAATAAGCTTACCT 6653
6857 CTCCAACCATCTTCTGCCCCAGCTAATGCTCTGTGGCTCTCAACAAATTTGACCTT 6916

QY 6654 TACTGAGGTTTCTGHAAGGACCTGCTATGAGAAAGGTTCCCCATCCACCAACACCT 6713
Db 6917 GTCCGAAGTGACGGGACAGGACTCTGCTATAGGAGCGTCCCTAAAACCCATCAAGTCTT 6976
QY 6714 TTGTAAACCACTAGGAGCCTTTAATCAAACTCTGAGAGTCAATATCTGTAAGTCTGTTA 6773
Db 6977 GTGTAAATACCAACCAA-----AAGACAAGCGATGGTCTCTACTATTTGGCCGCTCCAC 7030
QY 6774 TGACAGGTGGTGGCATGTAATACTGATTAACCCCTTGTGTTTCAACCTTTGGTTTTAA 6833
Db 7031 AGAAGCTACTCGGGCTTGTAGTACTGACTCCTCTGTATCTCAACCACTACTTGA 7090
QY 6834 CAAAATTAAGATTTTGTCAATATGTTTCCAAATTTGTTCCCGAGTGTATTACTATCCCGA 6893
Db 7091 CCTCACCAACCGATTACTGTCTCGAGCTTTGGCCAAAGGTGACCTACCATTCCTCC 7150
QY 6894 AAAAGCAATCTTGTATGAAATATGACTACAGAAATCATCGACAAAGAGAGAACCCATATC 6953
Db 7151 TAGTTATGTTTACCAACCAATTTG-----AAAGACGAGCCAAATATAAAGAGAGACCCGCTC 7207
QY 6954 TCTGACACTGTGCTGATGCTCGA-----CTTGGAGTGGCAGCAGGTGTAGG 7001
Db 7208 ACTAATCTGCGCCTACTATTAGGAGACTCATATGGCGGGAATTCGCCCTGGAGTGG 7267
QY 7002 AACAGGAACAGCTGCGCTGTGTACCGGACCCACAGCAGCTAGAAACAGGACTTAGTAACCT 7061
Db 7268 AACAGGACTACCGCCTTAGTGCCACTCAGCAGTTCCACAA-----CT 7312
QY 7062 ACATCGAATTTGAACAGAGATCTCCAAGCCCTAGAAATCTGTGTAAGTAACTGGAGGA 7121
Db 7313 CCAGGCTGCCATGCAACGATGACCTTAAAGAAAGTTGAAAGTCCATCACTAATCTAGAAAA 7372
QY 7122 ATCCCTAACTCTTATCTGAAGTAGTCTTACAGAAAGAGAGGTTAGATTATTT 7181
Db 7373 ATCTTTGACCTCTTGTCCGAAGTAGTTTACAGAACTCGTAGAGGCTTAGACTACTATT 7432
QY 7182 TCTAAAGAGAGGAGGATTATGTGTAGCTTTGAAGGAGGAATGCTGTTTTATGTGATCA 7241
Db 7433 CCTTAAAGAGGAGGTTTGTGTCTGCTTAAAGAGAAATGCTGTTCTATGCCGACCA 7492
QY 7242 TTCAGGGCCCATCAGAGACTCCATGAACAAAGCTTAGAGAAAGGTTGAGAGAGCGTCAAG 7301
Db 7493 CACAGGATTGGTACGGGATAGCATGCGCAAACTTAGAGAAAGATTGAGTCAGAGACAAAA 7552
QY 7302 GGAAGAGAAACTACTCAAGGTGTTGAGGATGTTCAACAGGTCTCTTTGGTTGGC 7361
Db 7553 GCTCTTTGAATCCCAACAGGGTGGTTGAAGGGCTGTTTAAAGTCCCTTGGTTAC 7612
QY 7362 TACCCTACTTTCTGCTTTTAAACAGACCCCTTAAATAGTCTCTCTCTTACTCAGATTGG 7421
Db 7613 CACCTGATATCACCATCATGGTCCCTGTATATCTCTTGTATTTTACTCTTTGG 7672
QY 7422 GCCATGTTATTAAACAAAGTTAATGCTTCTATTAGAGAAAGAAATAGTGAGTCCAGAT 7481
Db 7673 GCCTTGTATTCTCAATGCGCTGGTCCAGTTTATCAAGAGCAGGATTTCCGTTAGTGACGC 7732
QY 7482 CATGGTACTTAGAACACAGTACCA 7505
Db 7733 CTTGGTTCTGACTCAACAAATATCA 7756

RESULT 4

AK090125 12349 bp mRNA linear HTC 03-APR-2004
LOCUS Mus musculus brain CRL-1443 BC3H1 cDNA, RIKEN full-length enriched
DEFINITION library, clone:G431002D05 product:gene e1 protein, full insert
sequence.
ACCESSION AK090125
VERSION AK090125.1 GI:26354958
KEYWORDS HTC; CAP trapper.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

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Nature 420, 563-573 (2002)
6 (bases 1 to 12349)

Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hangsaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ono, M., Ohsato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sobabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.
Direct Submission

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COMMENT
cDNA library was prepared and sequenced in Mouse Genome Encyclopedia project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
Please visit our web site for further details.
URL: <http://genome.gsc.riken.jp/>
URL: <http://fantom.gsc.riken.jp/>
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QY	5541	ACTCGGTGGAAGGCGCTTATCTCGTACTTTTGACACACCAACCGCTGTGAAAGTCGAA	5600	Db	9804	AGTAAAGGAGCGCTACCAAGCCCTCAACCTCAGCTCCTGTATATAAACCCCAAGAGTGTG	9863
Db	8726	CCTCGCTGGAAGGAGCCCTACACCGCTCTACTGACACCCGCCACACCCCGATATAAA	8785	QY	6537	GCTATCTTAGCTTCGGGCCCACTTACTATGAAGAAATGGCTAGAAGAGGGAATTCAA	6596
QY	5601	GGAATCTCCACCTGGATCCATGCCAGTTCACCGTTAAACCGCGCCACCTCCC-----GAT	5654	Db	9864	GTTATGCTTAGTATCGGACCCCATACTACGAGGGGTTGCCGTCTAGGTACCTACTC	9923
Db	8786	GGCATCTCTGATGATACACCGCGGCCACGTCAGGCGAGCGACCAACCCCGATATAAA	8845	QY	6597	TGTGACAAAAGAAATAGAGACCAATGCAATCGGCATCGGGATCCCAAAATAAGCTTACCCTTAC	6656
QY	5655	TGCGGGTGGAAAGCGGAAAGAGATGAAATTCGCCCTTAAAGCTTCGCCCTCCATCGGTGTT	5714	Db	9924	CAACCATACTTCTGCGCCAGCTAACTGCTCTGTGGCTCTCAACACAAATGACCTTGTG	9983
Db	8846	CCATCATGGAGAGTACAAACGCTCTCAAAACCCCTTAAATAATCAGGTTTAAACCGTGGGCC	8905	QY	6657	TGAGGTTTCTGGAAGGCACTGTCATAGAAAGTTTCCCCCATCCCAACCAACACTTTG	6716
QY	5715	CCTTACTCTGCTCAATACCTCTCAGACTAATGTTATGCGCATAGGAGACAGCCTGAACTC	5774	Db	9984	CGAAGTGACCGGACAGGACTCTGCA-AGGAGCGGTCCCTTAAACCCATCAAGTCTTGTG	10042
Db	8906	CCCTAATGTGCTTCTGATTCGGA--GGGGTCAACCCCGTTCGCTTGGGAAACAGCCC	8963	QY	6717	TAAACCACTGAAGCCCTTTAATCAACCTCTGAGACTCAATATCTGTACTCTGCTATGA	6776
QY	5775	CCATAAACCTTATCTCTCACCTGGTTAATTACT-----GACTCCGGCACAGG	5822	Db	10043	TAAATACCAACCAA-----AAGACAGCGATGGTCTCTACTATTGCGCGCTCCACAGG	10096
Db	8964	CCACCAGTTTAACTCTACCTGGGAAGTGACTAATGGAGACCGAAGAACGGTGTGGC	9023	QY	6777	CAGGTGTGGGCATGTAATACTGATTAAACCCCTGTGTGTTTCCACCTTGGTGTTTTAAACCA	6836
QY	5823	TATTAATATCAACAACTCAAGG-----	5846	Db	10097	AATCTCGGCTGTGTAGTACTGACTCACTCCTCTGTATCTCAACCACTACTTGTGACCT	10156
Db	9024	AATAACCGCAATCACCCTCTGTGGACTTGTGGCCTGACTCACACCAAGATCTCTGTAT	9083	QY	6837	AATCAAAGATTTTGTGCAATATGTGTCCAAATTTTCCCGAGTGTATTACTATCCCGAAAA	6896
QY	5847	-----GGAGGCTCTTTAGAACCTGGTGGCTGATCTATAGTTTGGCTCA	5893	Db	10157	CACCAACGATTAAGTGTCTGTCTGAGCTTTGGCCAAAGGTGACCTTACCACTCCCTAG	10216
Db	9084	GTTGGCCCTCCACGGGCGCTTATTTGGGCTTGAATATCGGCTCTTTTCTCTCTCC	9143	QY	6897	AGCAATCTTGTATGAAATATGACTACAGAAATCATCGACAAAGAGAGAAACCATATCTCT	6956
QY	5894	GATCAGTTATTCCTAGTCTGACTCACCCAGATATCTCCATGCT-----	5940	Db	10217	TTATGTTTACCAACCAATTTGAAAGAGAGAGCCAA---ATATAAAGAGAAACCCGCTCACT	10273
Db	9144	CCCGGGGCCCCCTGTGTTTCAGGAAGAGGACTCCACGGCAGCTTTCAGAGATTG	9203	QY	6957	GACACTGTCTGATGCTCGGACTT-----GGAGTGGCAGCAGGTGTAGAAC	7004
QY	5941	-----CAGGATTTTATGTTTGGCCAGGACCAACCAATTAATGGAATAATTCGGGAA	5992	Db	10274	ATCTGTGGCCCTACTATTAGGAGGACTCACTATGGGGGGAATTTGCCCTGGAGTGGGAC	10333
Db	9204	TGAGGACCCCTGACTTCATATACTCCCGGTGCAATACGCGCTTGAACAGACTTAAAGTT	9263	QY	7005	AGGAAACAGCTGCCCTGTGTACCGGACCAACAGCAGCTAGAAACAGGACTTAGTAACCTTACA	7064
QY	5993	ATCCAGAGATTTCTTTGTAAACATGGAACCTGTGTAACTCTTAATGATGATATTGGA	6052	Db	10334	AGGACTACCGCCCTAGTGGCCACTCAGCAGTTCCAAAC-----CTCCA	10378
Db	9264	ATCTAAAGTGACATGCCACAATGAAGATTCTATGCTGTGCCCGCGGCCACATCGCCC	9323	QY	7065	TCGAATTTGTAACAGAAAGATCTCCAAGCCCTAGAAAAATCTGTCAGTAACTCTGGAGGAATC	7124
QY	6053	AATGGCCAACTCTCAGCAGATAGGTAGTTTCTTATGT-----CAA	6098	Db	10379	GGCTGCCATGCAGTACCTTAAAGAAAGTTGAAAGTCCATCACTAATCTAGAAAAATC	10438
Db	9324	CCGTTGGGCGCGTGTGGTGTCCAGAAATCTTCTATTGTGCCCTTGGGGCTGCGA	9383	QY	7125	CCTTAACCTCTTATCTGAAGTAGTCTTACAGATAGAGAGGGTGTAGATTATTATTCT	7184
QY	6099	CACCTATACAGCTCTGACAAATTAATTAACCTGACCTGGATTAGAACTGGAAGCCCAA	6158	Db	10439	TTTGACCTCTTGTTCGAAAGTAGTGTTCAGAAATCTGAGAGGCTTAGACTTACTTCTCT	10498
Db	9384	AACACAGGCGCAGCATCTCGAAACCAATCTCTGCTGGGACTACATCAGTAAGCA	9443	QY	7185	AAAAGAGGAGGATTATGTGTAGCTTTGAAGGAGAAATGCTGTTTTTATGTGGATCAATC	7244
QY	6159	GTGCTCTCTTCAGACCTTAGATTACTTAAATAATAGTTTCTCAGAAAGGAAACAAAGA	6218	Db	10499	AAAAGAGGAGGTTTGTGCTGCTTTAAAGAGAAATGCTGTTCTATGCCGACACAC	10558
Db	9444	CAATCTAACCTCAGACAGGCAACCCAGTATGCAAGAGTAAATGAGTGTGCAACTCCTT	9503	QY	7245	AGGGGCCATCAGAGACTCCATGAACAAAGCTTTAGAGAAAGTTGAGAGCGCTCGAAGGGA	7304
QY	6219	AAATATCC-----TAAATGGTAAATGTTATGCTCTTGGGGAATGTTAT	6262	Db	10559	AGGATTGTCAGGGATAGCATGGCCAACTTAGAGAAAGATTGAGTCAGAGACAAAGCT	10618
Db	9504	AACATCCGGTTTACAGAGCTTTGAAACACAGGCCACCTCTCGGGTCACAGGCCAATGGT	9563	QY	7305	AAAGGAACTACTCAAGGGTGGTTTGAAGGATGTTTCAACAGTCTCTTTGTTGGCTTAC	7364
QY	6263	ATTATGG-----AGCTCGGGTAAACAAACAGGCTCCATTTCTAATTTCCGCTCAA	6314	Db	10619	CTTTGAATCCCAACAAGGGTGGTTTGAAGGGCTCTTTAATAGTCCCTCTGGTCCACCAC	10678
Db	9564	GGGATTGGCCCTATACGCTCTGAGACATGACCCAGGGCTCATCTTTGGGATCCGACTTAA	9623	QY	7365	CCTACTTCTGCTTTTAAACAGGACCTTAAATAGTCTCTCTCTGTACTCTACAGTTTGGGCC	7424
QY	6315	AATAAACAGCTGGAGCCTCCAAATGGCTATAGGACCAATACGGTCTTTCAGCGGTCAAAG	6374	Db	10679	CCTGATATCCACCATCATATGGGTCCCTGATTAATCTCTGTTAATTTTACTCTTTGGGCC	10738
Db	9624	AATTACAGACTCGGGGCCCCGGTCCCAATAGGGCCAAACCCCGTCTTGTTCAGACCGAGC	9683	QY	7425	ATGTATTATTAAACAAAGTTAATTTGCTTCTTATTAGAGAACGAATAAGTGCAGTCCAGATCAT	7484
QY	6375	ACCCCCAACCAAGGACCGAGCCATCTCTTAACATTAATCTCTGTGATCAGACCCCACTGA	6434				

Db	1176	GAAGAGCCACCTCTCACTTCTGAGATTCCTGCCCTCTCTCCCATAGTGTCTCGCTGCGG	1235
Qy	1141	AGCGGACAGACGAGATCGCAGCATTTACCGCTGCGCAGTACGGCCCTCCACACCGGGG	1200
Db	1236	GGCAAAAGAGAGACCCCGCGGAGATTCACACCTCTCGGGCTTCCCACTCCGTTTG	1295
Qy	1201	GCCAATTGCAG-CCCTCCAGTATGCGCCCTTTCTCTCGAGATCTCTATAATTTGAAA	1259
Db	1296	GGGGTAATGGTCAGTTGCACTGCGCGGTTTTCTCTCTGATCTATATAACTGGAA	1355
Qy	1260	ACTAACCATCCCTTTCTCGAGGATCCCAAGCCCTCAGCGGGTTGGTGGAGTCCCTT	1319
Db	1356	AATAAATACTCTCTCTCGAGGATCCAGGTAACCTGACTGCAATTTGATTTGATCTGTC	1415
Qy	1320	ATGTTCTCTCACCAGCTCTGCGGATGATTGTCAACAGCTGTGCGAGACACTCTTCACA	1379
Db	1416	CTACACACCACAGCCCACTGGGATGATTGCCAGCAATTTATTAGGACTCTGCTTACC	1475
Qy	1380	ACCAGGAGCGAGAGAGAAATTTCTATTAGAGCTAGAAAAAATGTTCTGGGGCGGACGG	1439
Db	1476	GGGGAAGAGAGACGCGGTCTCTTGAAGCCCGAAAAAGCTGTCGGGGCAACGATGG	1535
Qy	1440	CGACCCACGGGTTGCCAAAATGAGATTGACATGGGATTTCCCTTAACTCGCCCGGTTGG	1499
Db	1536	CGCCCAACCAACTGCCCAACGAGGTTGACGCTGCTTTTCCCTTGAACGTCGCCGATTGG	1595
Qy	1500	GACTACAAACGGCTGAGGTAGGAGAGCTTGAANAATCTATGCCAGGCTCTGGTGGCG	1559
Db	1596	GATTACACACCCAAAGAGGTAGGAACCACTAGTTCTCTATGCCAGTTGCTTTTAGCG	1655
Qy	1560	GGTCTCGGGCGCTCTCAAGACGGCCCACTAATTTGGCTAAGGTAAGAGAGTGAATGACG	1619
Db	1656	GGTCTCTCAAAACGGCGCGAGCCCAACCAATTTGGCCAGGTAAAGGATAAACCCAG	1715
Qy	1620	GGACCGAATGAACCCCTCTGTTTTTTCTTGAGAGGCTCTTGAAGCCTTCAGCGGTAC	1679
Db	1716	GGACCTGATGATCCCCCTCAGCCTTCTAGAGAGACTCAAGGAAGCCTATCGCAGATAC	1775
Qy	1680	ACCCCTTTTGTATCCCACTCAGAGGCCCAAAAGCCTCAGTGGCTTTGGCTTTTATAGGA	1739
Db	1776	ACTCCTTATGATCTGAGGACCTTGGGCAAGAAACGAATGTATCTATGTCATTCATCTGG	1835
Qy	1740	CAGTCAGCTTGGATATTAGAAAGAGCTTCAGAGACTTGAAGGTTTACAGGAGCTGAG	1799
Db	1836	CAGTCGCTACAGACATTTGGTCGAAAGTTAGAGCGTTAGAAAGTCTTAAAGTATAAAT	1895
Qy	1800	TTAGCTGATCTAGTGAAGGCGCAGAGAAAGTATATTAACAAAGGAGACAGAGAGAA	1859
Db	1896	TTAGGAGATTTAGTGAGAGAGCCGAAAGGATCTTTAATAAAGAGAAACTCCAGAGAA	1955
Qy	1860	AGGAAACAAAGAAAGAGAGAGAAAGAGAGGAAAGGAGGAAAGACGTATAAAGCGCAA	1919
Db	1956	AGAGAAGACCGCTTAGGAGGAGACAGAGGAAAGGAGGCGGTAGGCGAGAGAG	2015
Qy	1920	GAGAAGATTTGACTAGATCTTGGCTGACGTGTTGAAGGAAAGCAATACGGAAGA	1979
Db	2016	GAGCAGAAAGAAAGAGAGGAGACCGTAGGGGACATAGAGAAATGAGCAAACTTTTGCC	2075
Qy	1980	GAGAGAGATTTTAGGAAATTTAGTTCAGGCCCTAGACAGTCAAGGAACTCGGCAATAGG	2039
Db	2076	ACCGTAGTTAGTGACAGACAGGATAGAC-----AGGGGGAGAGCGAAGGAG	2126
Qy	2040	ACCCCACTCGAAGAGCAATGTGCATATTGTAAAGAAAGAGGACACTGGGCAAGGAAC	2099
Db	2127	CCCCAATTTGACAGGATCAATGTGCTTACTGTAAAGAAAGAGACACTGGGCTAAAGAC	2186
Qy	2100	TGCCCCAAGAGAGGAAACAAAGGACCAAGGATCTCTA-----GCTCTAGAGAGAT	2150
Db	2187	TGCCCCAAGAGAGGACCGGGTCCCCGAGGACCGGACCCAGACCTCCCTCTGACTTTA	2246
Qy	2151	AAAGATTAGGAGAGCGGGTTCCGACCCCTCCCGAGCCCGAGGTAACCTTGAAGGTG	2210
Db	2247	GACGACTAGGGGGGTCAGGGTCAGGAGCCCCCTGAAACCCAGGATAAACCTCTACTGTC	2306
Qy	2211	GAGGGCAACCAAGTTGAGTTCTGTTGATACCGGAGCGAAACATTCAGTGTCTACTACAG	2270
Db	2307	GGGGGGCAACCCGTCACCTTCTCTGGTGATCTGGGGCCCAACACACTCGTGTGACTCAA	2366
Qy	2271	CCATTAGGAAACCTAAAGATAAAAATCCTGGGTGATGGTCCACAGGCGCAACAACAG	2330
Db	2367	AATCTGGGGCCCTAAAGTACAGGTGCGCTTCAGGGGCTACTGAGGAAAGGG	2426
Qy	2331	TATCCATGGACTACCCGAAAGACAGTTGACTTTGGGAGTGGGACGGGTAACCCACTCGTTT	2390
Db	2427	TATCGCTGGACCAAGATCGCAAGGTACACTAGCTACCGGTAAAGGTCACTCACTCTTTC	2486
Qy	2391	CTGGTCATACCTGAGTGGCCAGCACCCCTCTTAGGTAGAGACTTTATTGACCAAGATGGGA	2450
Db	2487	CTCCATGTGCAGACTGCCCTTACCCCTTGTCTAGGAAGAGACTTTGTTAACTTAAACTAAA	2546
Qy	2451	GCAAAATTTCTTTTGA---ACAAGGGAACACAGAGTGTCTGCAAAATAACAAACCTTATC	2507
Db	2547	GCCAGATCCACTTTGAGGATCAGGAGCCAGGTTGTGGACCAAAAGAGACGCTCTA	2606
Qy	2508	ACTGTGTGACCTTCCAAATTTAGATGACGAATATCGACTATATCTCTCCCTAGTAAAGCCT	2567
Db	2607	CAGTGTGACCTTAACTTAGAAGTATCGGCTTCTAGAGACTTCGGCAGAGCG	2666
Qy	2568	GA---TCAAAATATACAATTTCTGTTGGAAACAGTTTCCCAAGCCTGGGCGAGAAACCGCA	2624
Db	2667	GAAGCTTCTCTGGGTCCACTGCTTTCGACTTTCGCCAGCTTTCGCCAGGCTGGGCAAAACCGG	2726
Qy	2625	GGGATGGGTTGGAAAGCAAGTTTCCCCCAAGTTTATCACTGAAGGCCAGTGCACCA	2684
Db	2727	GGCATGGGACTGGGCTGCGCAGGCGCTCTAATCATACCTCTTAAAGGCAACCTCCACC	2786
Qy	2685	CCAGTGTCACTCAGACAGTACCCCTTCAGTAAAGAGCTCAAGAGGAATTCGGCGCAT	2744
Db	2787	CCTGTGTCCATAAAACAATATCCCATGTACAGGAGCCAGACTGGGATCAAGCCAC	2846
Qy	2745	GTCCAAAGATTAATCCAAACAGGCGATCTAGTTCTCTTCCAACTCTCCCTGGAATCTCCC	2804
Db	2847	ATACAGAGGCTGTGGACAGGGAATACTGTTACCTCGCAGTCCCTCTGGAATACACCC	2906
Qy	2805	CTGCTACCGTTAGAAAGCCTGGGACTTAATGACTATCGACAGTACAGGACTTGAGAGAG	2864
Db	2907	CTGCTACCGTTAGAAACCCAGGAATAACGATTTATAGGCTGTCCAGGATCTGAGAGAA	2966
Qy	2865	GTCAATAAACGGGTGCAGGATATACCCACAGTCCCGACCTTATAACCTCTTGTGT	2924
Db	2967	GTCAACAAAGCGGTGGAGACATCCACCCACCGTGCCTTATTAACCTCTTAAGT	3026
Qy	2925	GCTCTCCACCCCAACCGAGCTGGTATACAGTATTGGACTTTAAAGGATGCTCTTCTGTC	2984
Db	3027	GGGCTCCACCGTCCCAACCGGTGTACTGTGTGTTGATTTAAAGGATGCTCTTCTGTC	3086
Qy	2985	CTGAGATTTACACCCCACTAGCCAAACCACTTTTTCGCTTCGAATGGAGAGATCCAGGTAG	3044
Db	3087	CTGAGACTCCACCCCAACCACTGAGCTCTCTTCGCTTCGAGTGGAGAGATCCAGGGATG	3146
Qy	3045	GGAAAGACCGGGGAGCTCAGCTGAGCCGACTGCCCCCAAGGGTTCAAGAACTCCCGGACC	3104
Db	3147	GGAACTCTCAGGACAATTAACCTGGACAGACTCCCAAGGGTTTCAAAAACAGTCCCACC	3206
Qy	3105	ATCTTTGACGAAGCCCTACACAGAGACTGCGCAACTTCAGGATCCCAACACCTCAGGTG	3164
Db	3207	CTGTTTGTATGAGGCACTACACAGAGACTTAGAGACTTCGGATCCAGCAACCGACTTG	3266
Qy	3165	ACCCTCTCTCAGTACGTGGATGACTGCTTCTGGGGGAGGCCAACAAACAGGACTGCTTA	3224
Db	3267	ATCTCTACAGTACGTGGATGACATACTACTTGGCGGCACTTCTGAGCTCGACTGCCAA	3326
Qy	3225	GAAGGCAAGAGGCACTACTCTCGAATTTGTCTGACCTTAGGCTACAGAGCTCTGCTAAG	3284
Db	3327	CAAGGTACTCGGGGCTTGTACTTAACCTTAGAAACCTTCGGGTATTCGGGCTCGGCCAAG	3386

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Qy
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Db
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Db
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Db
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Qy
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Db
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5894 GATCAGTTATTCCTAGTCTGACCTCACCCACAGATATCTCTCAATGCT-----5940
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3300 ACCCTGACCAAGAGGAGAAATTCATTTGGACTCTGATTTTCAAGAGCA-TTG 3358
QY 3547 ATGCTATCAAAAAGGCCCTGCTGAGCGCACTCTCTGCGCCCTCCCTGACGTAACATAAC 3606
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3359 ACAAAATCAAAACAGTCTATTGTGAGCTCCAGCTTGGCTTGGCTTGTGCTGATTTAACTAAGC 3418
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3539 GCTGGCCATCGTCTTAAAGCTATCGCTGAGTGGCCATGTTGGTCAAGATGCGAGATA 3598
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3839 CCTGTGCTAATTGTGGGATCATCATATGGGCTG- - -AAGCCCAACTGTGATACCGATG 3895
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RESULT 7
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LOCUS
DEFINITION 916502 MARC 4PIG Sus scrofa cDNA 3', mRNA sequence.
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ACCESSION CK455881
VERSION CK455881.1 GI:40803095
KEYWORDS EST.
SOURCE Sus scrofa (pig)
ORGANISM Sus scrofa
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
Sus.
REFERENCE 1 (bases 1 to 848)
AUTHORS Smith,T.P.L., Freking,B.A., Ford,J.J., Vallet,J.L., Wise,T.A.,
Noneman,D.J., Wray,J.E. and Keele,J.W.
TITLE Porcine EST collection using a normalized library constructed from
embryos representing early developmental stages
JOURNAL Unpublished (2003)
COMMENT Contact: Smith-TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called with phred v0.020425.c and
trimmed with the aid of the trim_alt option. Vector identified with
cross_match v0.990329.
Plate: TMW8027 row: F column: 1
Seq primer: TAGAAGCACAGTCGAGG.
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Library made with combined RNA from day-10, day-13,
day-15, day-25, and day-30 whole embryos."
ORIGIN
Query Match 10.1%; Score 825.2; DB 7; Length 848;
Best Local Similarity 98.5%; Pred. No. 5.4e-223;
Matches 833; Conservative 0; Mismatches 13; Indels 0; Gaps 0;
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QY	2865	GTCATTAACCGGTGACGAGTATACACCCACAGTCCCGAACCTTATACCTTCTTGCT	2924
DB	128	GTCATTAACCGGTGACGAGTATACACCCACAGTCCCGAACCTTATACCTTCTTGCT	69
QY	2925	GCCTCTCCACCCCAACCGAGCTGGTATACAGTATTTGGACTTTAAAGGATGCCTTCTTCTGC	2984
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DEFINITION	CK454836		
ACCESSION	CK454836.1	GI:40802050	
VERSION			
KEYWORDS	EST.		
SOURCE	Sus scrofa (pig)		
ORGANISM	Sus scrofa		
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
	Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;		
	Sus.		
REFERENCE	1 (bases 1 to 836)		
AUTHORS	Smith,T.P.L., Freking,B.A., Ford,J.J., Vallet,J.L., Wise,T.A., Nonneman,D.J., Wray,J.E. and Keele,J.W.		
TITLE	Porcine EST collection using a normalized library constructed from embryos representing early developmental stages		
JOURNAL	Unpublished (2003)		
COMMENT	Contact: Smith TPL USDA, ARS, US Meat Animal Research Center PO Box 166, Clay Center, NE 68933-0166, USA Tel: 402 762 4366 Fax: 402 762 4390 Email: smith@email.marc.usda.gov Single pass sequencing. Bases called with phred v0.020425.c and trimmed with the aid of the trim_alt option. Vector identified with cross_match v0.990329. Plate: TW8027 row: F column: 1 Seq primer: GTAATACGACTCACTATAGG.		
FEATURES			
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ORIGIN			
Query Match	9.9%	Score 804;	DB 7; Length 836;

AUTHORS Smith, T.P.L., Preking, B.A., Ford, J.J., Vallet, J.L., Wise, T.A.,
Nonneman, D.J., Wray, J.E., and Keele, J.W.
TITLE Porcine EST collection using a normalized library constructed from
embryos representing early developmental stages
JOURNAL Unpublished (2003)
COMMENT Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called with phred v0.020425.c and
trimmed with the aid of the trim_alt option. Vector identified with
cross match v0.990329.
Plate: HHY8028 row: H column: 24
Seq primer: TAGAAGGCACAGTCGAGG.
Location/Qualifiers
1. .835
/organism="Sus scrofa"
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Library made with combined RNA from day-10, day-13,
day-15, day-25, and day-30 whole embryos."
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Best Local Similarity 96.3%; Pred. No. 1e-208;
Matches 807; Conservative 0; Mismatches 23; Indels 8; Gaps 1;
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DB 835 GCCAGGAGCCCTGGTGGTCTCTCTACTGTCGTCAGGACCAATCTGTCTCTGAAGC 776
QY 451 GAAAGCTTCCCTCCCGACCGCTCCGACCTCTTTTGGCTCTGTGGAAGACGTGACCG 510
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DEFINITION 1122855 MARC 4PIG Sus scrofa cDNA 3', mRNA sequence.
ACCESSION DN122618
VERSION DN122618.1 GI:59816897
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SOURCE Sus scrofa (pig)
ORGANISM Sus scrofa
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
Sus
1 (bases 1 to 793)
REFERENCE Smith, T.P.L., Preking, B.A., Ford, J.J., Vallet, J.L., Wise, T.A.,
Nonneman, D.J., Wray, J.E., and Keele, J.W.
TITLE Porcine EST collection using a normalized library constructed from
embryos representing early developmental stages
JOURNAL Unpublished (2003)
COMMENT Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called with phred v0.020425.c and
trimmed with the aid of the trim_alt option. Vector identified with
cross match v0.990329.
Plate: HHY8024 row: O column: 19
Seq primer: TAGAAGGCACAGTCGAGG.
Location/Qualifiers
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Library made with combined RNA from day-10, day-13,
day-15, day-25, and day-30 whole embryos."
ORIGIN
Query Match 9.4%; Score 761; DB 8; Length 793;
Best Local Similarity 97.5%; Pred. No. 1.1e-204;
Matches 773; Conservative 0; Mismatches 20; Indels 0; Gaps 0;
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DB 733 AAGGGAGACAGAGAAGAAAGGGAAACAAGAAAGAGAGAGAAAGAGAGAAAGGGAGGA 674
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Db 613 GAAAGCAATAGGAAGAGAGAGAGATTTTATAGGAAATAGGTGACGCCCTAGACAGTC 554
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Qy 2201 TTTGAAAGTGGAGGGGCAACAGTTGAGTTCTCTGTTGATACCGGAGCGAAACATTGAGT 2260
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Qy 2321 GCAACACAGTATCCATGACTACCGAGACACAGTTGACTTGGAGTGGACGCGGTAAC 2380
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Qy 2381 CCATCTGTTTCTGTTGATACCTGAGTGCCGAGCACCCCTCTTAGGTAGAGACTTATTGAC 2440
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Qy 2561 AAAGCTGATCAA 2573
Db 13 AAAGCTGAAAAA 1

RESULT 11
LOCUS AK089325 3442 bp mRNA linear HTC 03-APR-2004
DEFINITION Mus musculus B6-derived CD11 +ve dendritic cells cDNA, RIKEN
full-length enriched library, clone:F730005P06 product: murine
repeated virus, Y linked, full insert sequence.
ACCESSION AK089325
VERSION AK089325.1 GI:26105207
KEYWORDS HTC; CAP trapper.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Mus.
1
REFERENCE
AUTHORS Carninci, P., Shibata, Y., Hayateu, N., Sugahara, Y., Shibata, K.,
Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
TITLE High-efficiency full-length cDNA cloning
JOURNAL Meth. Enzymol. 303, 19-44 (1999)
PUBMED 10349636
2
REFERENCE
AUTHORS Carninci, P., Shibata, Y., Hayateu, N., Sugahara, Y., Shibata, K.,
Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
TITLE Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes
JOURNAL Genome Res. 10 (10), 1617-1630 (2000)
PUBMED 11042159

REFERENCE
AUTHORS Shibata, K., Itoh, M., Aizawa, K., Nagao, S., Sasaki, N., Carninci, P.,
Konno, H., Akiyama, J., Nishi, K., Kiteunai, T., Tashiro, H., Itoh, M.,
Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A.,
Yamanoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K.,
Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M.,
Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J.,
Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
TITLE RIKEN integrated sequence analysis (RISA) system--384-format
sequencing pipeline with 384 multicapillary sequencer
JOURNAL Genome Res. 10 (11), 1757-1771 (2000)
PUBMED 11076861
4
TITLE The RIKEN Genome Exploration Research Group Phase II Team and the
FANTOM Consortium.
AUTHORS Functional annotation of a full-length mouse cDNA collection
NATURE 409, 685-690 (2001)
5
TITLE The FANTOM Consortium and the RIKEN Genome Exploration Research
Group Phase I & II Team.
AUTHORS Analysis of the mouse transcriptome based on functional annotation
of 60,770 full-length cDNAs
NATURE 420, 563-573 (2002)
6 (bases 1 to 3442)
AUTHORS Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P.,
Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W.,
Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T.,
Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T.,
Kato, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M.,
Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M.,
Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N.,
Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N.,
Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T.,
Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akai, S.,
Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A.,
Muramatsu, M. and Hayashizaki, Y.
TITLE Direct Submission
JOURNAL Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of
Physical and Chemical Research (RIKEN), Laboratory for Genome
Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
Kanagawa 230-0045, Japan (E-mail: genome-res@gsc.riken.jp,
URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222,
Fax: 81-45-503-9216)
COMMENT cDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in RIKEN.
Division of Experimental Animal Research in Riken contributed to
prepare mouse tissues.
Tissues were provided by Dr. John Todd (Dept. of Medical Genetics
Wellcome Trust Centre for Molecular Mechanisms in Disease Wellcome
Trust/MRC building Addenbrookes Hospital Cambridge) whose
assistance we gratefully acknowledge.
Please visit our web site for further details.
URL: http://genome.gsc.riken.jp/
URL: http://fantom.gsc.riken.jp/
FEATURES
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/clone_lib="RIKEN full-length enriched mouse cDNA library"
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Best Local Similarity 59.4%; Pred. No. 2.5e-201;
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 Qy 2977 TCTTCTGCTGAGATTACACCCCACTAGCCCAACCACTTTTTCCTTCGAAATGAGAGATC 3036
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RESULT 12
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 DEFINITION
 ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 CR902227 797 bp DNA linear GSS 23-NOV-2004
 Sus scrofa BES, genomic survey sequence.
 CR902227.1 GI:56226724
 GSS; Bac-end sequence BES; Genome Survey Sequence.
 Sus scrofa (pig)
 Sus scrofa
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
 Sus.
 1 (bases 1 to 797)
 Rogel-Gaillard,C., Bourgeaux,N., Billault,A., Vaiman,M. and
 Chardon,P.
 Construction of a swine BAC library: application to the
 characterization and mapping of porcine type C endoviral elements
 Cytogenet. Cell Genet. 85 (3-4), 205-211 (1999)
 10449899
 2 (bases 1 to 797)
 Chardon,P., Iannuccielli,N., Roig,A., Dossat,C., Demars,J.,
 Rogel-Gaillard,C., Roy,A., Schibler,L. and Milan,D.
 A physical map of the swine genome
 Unpublished
 3 (bases 1 to 797)
 Genoscope.
 Direct Submission
 Submitted (18-NOV-2004) Genoscope - Centre National de Sequencage :

BP 191 91006 EVRY cedex - FRANCE (E-mail : sequef@genoscope.cns.fr
 - web : www.genoscope.cns.fr)
 Location/Qualifiers
 1. .797
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 /strain="Large White"
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 Qy 3725 TGGTTGGCCCATATGCTGAGGCTATGCGAGCTGTGGCCATCTGTTGTTCAAGGAGCGCTGA 3784
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RESULT 13
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LOCUS      733 bp      mRNA      linear      EST 02-APR-2004
DEFINITION 946489 MARC 4PIG Sus scrofa cDNA 5', mRNA sequence.
ACCESSION  CN157762
VERSION     CN157762.1 GI:46172192
KEYWORDS    EST.
SOURCE      Sus scrofa (pig)
ORGANISM    Sus scrofa
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
            Sus.
REFERENCE   1 (bases 1 to 733)
AUTHORS    Smith,T.P.L., Freking,B.A., Ford,J.J., Vallet,J.L., Wise,T.A.,
            Nonneman,D.J., Wray,J.E. and Keele,J.W.
TITLE      Porcine EST collection using a normalized library constructed from
            embryos representing early developmental stages
JOURNAL
COMMENT     Unpublished (2003)
            Contact: Smith TPL
            USDA, ARS, US Meat Animal Research Center
            PO Box 166, Clay Center, NE 68933-0166, USA
            Tel: 402 762 4366
            Fax: 402 762 4390
            Email: smith@email.marc.usda.gov
            Single pass sequencing. Bases called with phred v0.020425.c and
            trimmed with the aid of the trim_alt option. Vector identified with
            cross_match v0.990329.
            Plate: TW8053 row: M column: 24
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Query Match      9.0%; Score 730.4; DB 7; Length 733;
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Matches 731; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db      181  CATGATTGCCATCAACTATTGATTGAGGAGACTGGGGTCCGCAAGGACCTTACAGACATA 240

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Qy      4110  AAGNGATGCTGGGGCGGGTGGTGGAGCGGACCGGACCGACTCTGGGCCAGCAGCGCTG 4169
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Qy      4530  AAAGCCCCAGAA 4541
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CN159699      733 bp      mRNA      linear      EST 02-APR-2004
LOCUS      948793 MARC 4PIG Sus scrofa cDNA 3', mRNA sequence.
DEFINITION  CN159699
ACCESSION  CN159699
VERSION     CN159699.1 GI:46174129
KEYWORDS    EST.
SOURCE      Sus scrofa (pig)
ORGANISM    Sus scrofa
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
            Sus.
REFERENCE   1 (bases 1 to 733)
AUTHORS    Smith,T.P.L., Freking,B.A., Ford,J.J., Vallet,J.L., Wise,T.A.,
            Nonneman,D.J., Wray,J.E. and Keele,J.W.
TITLE      Porcine EST collection using a normalized library constructed from
            embryos representing early developmental stages
JOURNAL
COMMENT     Unpublished (2003)
            Contact: Smith TPL
            USDA, ARS, US Meat Animal Research Center
            PO Box 166, Clay Center, NE 68933-0166, USA
            Tel: 402 762 4366
            Fax: 402 762 4390
            Email: smith@email.marc.usda.gov
            Single pass sequencing. Bases called with phred v0.020425.c and
            trimmed with the aid of the trim_alt option. Vector identified with
            cross_match v0.990329.
            Plate: TW8053 row: M column: 24
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         Library made with combined RNA from day-10, day-13,
         day-15, day-25, and day-30 whole embryos."

ORIGIN
Query Match      9.0%; Score 730.4; DB 7; Length 733;
Best Local Similarity 99.9%; Pred. No. 5.9e-196;

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Qy 733 ACTGTAATAGCCCCCATGCAATTCGAGAACATCGTTGGCAGCCCCCAGACCCGATGATG 674
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Qy 3870 ACCAACGCCCGCATGACCCACTATCAAGCCCTGCTTCTCAGAGAGGGTCAAGTTCGCT 3929
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Db |||||
Qy 613 CCACAGCGCTCTCAACCCCTGCCACTTCTTGCTGCTGAAGAGCTGATGAACAGTGAAT 554
Db |||||
Qy 3990 CATGATTCGCATCAACTATTGATGAGGAGACTGGGTCCGCAAGGACCTTACAGACATA 4049
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Qy 553 CATGATTCGCATCAACTATTGATGAGGAGACTGGGTCCGCAAGGACCTTACAGACATA 494
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Qy 4050 CCGCTGACTGGAGAGTGTCAACCTGTTCACTGACGGAAGCAGCTATGTGGTGAAGGT 4109
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Qy 493 CCGCTGACTGGAGAGTGTCAACCTGTTCACTGACGGAAGCAGCTATGTGGTGAAGGT 434
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Qy 4110 AAGAGGATGGCTGGGGCGGCGGTGGTGAACGGGACCGGACCGATCTGGGCCAGCAGCTG 4169
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Qy 373 CCGNAGGAATCTCAGCACAAAGGCTGAGCTCATGGCCCTCAGCAGGCTTTCGGGCTG 314
Db |||||
Qy 4230 GCCNAGGGAATCCATAAACAATTTATACGGACAGCAGTATGCTTTGCCACTGCACAC 4289
Db |||||
Qy 313 GCCNAGGGAATCCATAAACAATTTATACGGACAGCAGTATGCTTTGCCACTGCACAC 254
Db |||||
Qy 4290 GTACATGGGGCCATCTATAAACAAGGGGTGTCTTACCTCAGCAGGAGGGAATAAAG 4349
Db |||||
Qy 253 GTACATGGGGCCATCTATAAACAAGGGGTGTCTTACCTCAGCAGGAGGGAATAAAG 194
Db |||||
Qy 4350 AACNAGGGAATCTTAAGCTTATTAGAAGCGGTACATTTTACCANAAGGCTAGCTATT 4409
Db |||||
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Db |||||
Qy 133 ATACACTGCTCTGGACATCAGAAAGCTAAAGATCTCATATCCAGAGGAACAGATGGCT 74
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Qy 4470 GACCGGGTTGCCAAGCAGGAGCCAGGGGTGTTAACTTCTGCTTATATAGAAATGCC 4529
Db |||||
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ACCESSION DN125059
VERSION DN125059.1 GI:59819338
KEYWORDS EST.
SOURCE Sus scrofa (pig)
ORGANISM Sus scrofa
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
Sus
1 (bases 1 to 867)
REFERENCE
AUTHORS Smith,T.P.L., Freking,B.A., Ford,J.J., Vallet,J.L., Wise,T.A.,
Nonneman,D.J., Wray,J.E. and Keele,J.W.
TITLE Porcine EST collection using a normalized library constructed from
embryos representing early developmental stages
JOURNAL Unpublished (2003)
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COMMENT

Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called with phred v0.020425.c and
trimmed with the aid of the trim_alt option. Vector identified with
cross match v0.990329.
Plate: HHV8029 row: C column: 1
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Location/Qualifiers
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/note="Vector: pCDNA3.1; Site 1: EcoRI; Site 2: NotI;
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FEATURES
source

ORIGIN

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Query Match 8.9%; Score 722; DB 8; Length 867;
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Matches 793; Conservative 0; Mismatches 65; Indels 12; Gaps 2;
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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

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Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

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Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0
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Post-processing: Maximum Match 0%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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ALIGNMENTS

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; Sequence 3, Application US/08766528
; Patent No. 6190861
; GENERAL INFORMATION:
; APPLICANT: Jay A. Fishman
; TITLE OF INVENTION: MOLECULAR SEQUENCE OF SWINE RETROVIRUS
; TITLE OF INVENTION: AND METHODS OF USE
; NUMBER OF SEQUENCES: 74
; CORRESPONDENCE ADDRESS: 74
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 60 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/766,528
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/572,645
; FILING DATE: 14-DEC-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Louis Myers
; REGISTRATION NUMBER: 35,965
; REFERENCE/DOCKET NUMBER: MGP-038CP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)227-5941
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8132 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-08-766-528-3

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Best Local Similarity 100.0%; Pred. No. 0;
Matches 8132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 2

US-09-661-858-3

; Sequence 3, Application US/09661858

; Patent No. 6699663

; GENERAL INFORMATION:

; APPLICANT: Jay A. Fishman

; TITLE OF INVENTION: MOLECULAR SEQUENCE OF SWINE RETROVIRUS

; AND METHODS OF USE

; NUMBER OF SEQUENCES: 74

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: LAHIVE & COCKFIELD, LLP

; STREET: 60 State Street

; CITY: Boston

; STATE: Massachusetts

; COUNTRY: USA

; ZIP: 02109-1875

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent in Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/661,858

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; ATTORNEY/AGENT INFORMATION:

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; INFORMATION FOR SEQ ID NO: 3:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 8132 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear		
; MOLECULE TYPE: cDNA		
; SEQUENCE DESCRIPTION: SEQ ID NO: 3:		
US-09-661-858-3		
Query Match 100.0%; Score 8132; DB 3; Length 8132;		
Best Local Similarity 100.0%; Pred. No. 0;		
Matches 8132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
QY	1	GCCTGTGTACGACTGTGGCCCCCAGCGCTTGGAAATAAAATCTCTTGCTGTTTGA 60
DB	1	GCCTGTGTACGACTGTGGCCCCCAGCGCTTGGAAATAAAATCTCTTGCTGTTTGA 60
QY	61	TCAAGACCGCTTCTCGTAGTGATTAAAGGGAGTCGCCCTTTTCCGAGCTGAGGTTCTT 120
DB	61	TCAAGACCGCTTCTCGTAGTGATTAAAGGGAGTCGCCCTTTTCCGAGCTGAGGTTCTT 120
QY	121	TTTGCTGGTCTTACATTTGGGGCTCGTCGGGATCTGCGGGCCACCCCTTAACACCG 180
DB	121	TTTGCTGGTCTTACATTTGGGGCTCGTCGGGATCTGCGGGCCACCCCTTAACACCG 180
QY	181	AGAACCGACTTGGAGGTAAAAAGGATCCTCTTTTAAACGTGTATGCATGTACCGCGCGC 240
DB	181	AGAACCGACTTGGAGGTAAAAAGGATCCTCTTTTAAACGTGTATGCATGTACCGCGCGC 240
QY	241	GTCTCTGTTCTGAGTGTCTGTTTTTTCAGTGTGCGCGCTTTTCGGTTTTGCAGCTGCTCTC 300
DB	241	GTCTCTGTTCTGAGTGTCTGTTTTTTCAGTGTGCGCGCTTTTCGGTTTTGCAGCTGCTCTC 300
QY	301	AGCCGTAAAGGCTGGGGACTGTGATCAGCAGACGTGCTAGGAGATCACAGGCTGCTG 360
DB	301	AGCCGTAAAGGCTGGGGACTGTGATCAGCAGACGTGCTAGGAGATCACAGGCTGCTG 360
QY	361	CCCTGGGGACGCCCGGGAGGTAGGAGACGAGGACGCGCTGCTCTCACTGTC 420
DB	361	CCCTGGGGACGCCCGGGAGGTAGGAGACGAGGACGCGCTGCTCTCACTGTC 420
QY	421	GGTCAGAGGACCGAAATTCGTTCTGTAAGCGAAGCTTCCCTCCGCGACGCTCCGACT 480
DB	421	GGTCAGAGGACCGAAATTCGTTCTGTAAGCGAAGCTTCCCTCCGCGACGCTCCGACT 480
QY	481	CTTTTGGCTGCTGTGGAGACGTGGACGGGTCACTGTGTCTGGAATCTGTGTTCTG 540
DB	481	CTTTTGGCTGCTGTGTGGAGACGTGGACGGGTCACTGTGTCTGGAATCTGTGTTCTG 540
QY	541	TTTGTGTGCTTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 600
DB	541	TTTGTGTGCTTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 600
QY	601	CGACCCCTCTTAGTTTGAATCTCGACCAATGGACTGAAGTTAAATCCAGGGCTCATATTT 660
DB	601	CGACCCCTCTTAGTTTGAATCTCGACCAATGGACTGAAGTTAAATCCAGGGCTCATATTT 660
QY	661	TGTCAGTTTCAAGTTAAGAGGACCTTTGGCAGACTTTCTGTGTCTCTGTAATGCCGACAT 720
DB	661	TGTCAGTTTCAAGTTAAGAGGACCTTTGGCAGACTTTCTGTGTCTCTGTAATGCCGACAT 720
QY	721	TCCATGTGATGCGCATCAGAGGGACCTTTTAAATCTCGAGATTATCTGGCTGTTTAAAG 780
DB	721	TCCATGTGATGCGCATCAGAGGGACCTTTTAAATCTCGAGATTATCTGGCTGTTTAAAG 780
QY	781	CAGTTATTTTTCAGACTGGACCGGCTCTCATCCCGATCAGGAGCCCTATATCTTTACGT 840
DB	781	CAGTTATTTTTCAGACTGGACCGGCTCTCATCCCGATCAGGAGCCCTATATCTTTACGT 840
QY	841	GGCAAGATTGGCAGAGGATCTCTCGCCATGGGTTAAACCATGGCTGAATAAGCCAGAA 900
DB	841	GGCAAGATTGGCAGAGGATCTCTCGCCATGGGTTAAACCATGGCTGAATAAGCCAGAA 900
QY	901	AGCCAGTCCCGAAATTCGGCTCTTGGAGAGAAACCAACACTCGGCTGAAAAGTCA 960
DB	901	AGCCAGTCCCGAAATTCGGCTCTTGGAGAGAAACCAACACTCGGCTGAAAAGTCA 960

QY	961	AGCCCTCTCTCATATCTACCCGAGATTGAGAGCCACCGCTTGGCGGAAACCCCAAT 1020
DB	961	AGCCCTCTCTCATATCTACCCGAGATTGAGAGCCACCGCTTGGCGGAAACCCCAAT 1020
QY	1021	CTGTTTCCCCACCCCTTATCTGGCACAGGGTGC CGCAGAGGACCCCTTTGCCCCCTCTG 1080
DB	1021	CTGTTTCCCCACCCCTTATCTGGCACAGGGTGC CGCAGAGGACCCCTTTGCCCCCTCTG 1080
QY	1081	GAGCTCCGCGGTGGAGGACCTGTGCAAGGACTCGGAGCCGAGGGCGCCACCCCG 1140
DB	1081	GAGCTCCGCGGTGGAGGACCTGTGCAAGGACTCGGAGCCGAGGGCGCCACCCCG 1140
QY	1141	ACGCGACAGACGAGATCGGCACATTTACCGCTGCGCACGTACGGCCCTCCACACCGGG 1200
DB	1141	ACGCGACAGACGAGATCGGCACATTTACCGCTGCGCACGTACGGCCCTCCACACCGGG 1200
QY	1201	GCCAATTTGAGCCCTTCCAGTATTGGCCCTTTTCTTCTGCAGATCTCTATAATTGAAAA 1260
DB	1201	GCCAATTTGAGCCCTTCCAGTATTGGCCCTTTTCTTCTGCAGATCTCTATAATTGAAAA 1260
QY	1261	CTAACCATCCCCCTTTCTCGGAGGATCCCAAACGCTCA CGGGTTGGTGGAGTCCCTTTA 1320
DB	1261	CTAACCATCCCCCTTTCTCGGAGGATCCCAAACGCTCA CGGGTTGGTGGAGTCCCTTTA 1320
QY	1321	TGTTCTCTCACAGCCTACTTGGGATGATTGTCAACAGCTGCTGCAGACACTTTCACAA 1380
DB	1321	TGTTCTCTCACAGCCTACTTGGGATGATTGTCAACAGCTGCTGCAGACACTTTCACAA 1380
QY	1381	CCGAGGAGGAGAGAGATTCTATTAGAGCTTAGAAAAAATGTTCTCTGGGGCGACGGGC 1440
DB	1381	CCGAGGAGGAGAGAGATTCTATTAGAGCTTAGAAAAAATGTTCTCTGGGGCGACGGGC 1440
QY	1441	GAACCAACGCGTGTGCAAAATGAGATTGACATGGGATTTCCCTTAACTCGCCCCGGTTGG 1500
DB	1441	GAACCAACGCGTGTGCAAAATGAGATTGACATGGGATTTCCCTTAACTCGCCCCGGTTGG 1500
QY	1501	ACTACAAACGCGCTGAGGTAGGAGAGCTTGAATAATTTGCTAAGGTAAAGAGAGTATCAGG 1560
DB	1501	ACTACAAACGCGCTGAGGTAGGAGAGCTTGAATAATTTGCTAAGGTAAAGAGAGTATCAGG 1560
QY	1561	GTCTCGGGGCGCTCAAGACGCGCCACTTAATTTGCTAAGGTAAAGAGAGTATCAGG 1620
DB	1561	GTCTCGGGGCGCTCAAGACGCGCCACTTAATTTGCTAAGGTAAAGAGAGTATCAGG 1620
QY	1621	GACCGAATGAACCCCTCTGTTTTTCTTGAGAGGCTCTTGAAGCCTTCAGGCGGTACA 1680
DB	1621	GACCGAATGAACCCCTCTGTTTTTCTTGAGAGGCTCTTGAAGCCTTCAGGCGGTACA 1680
QY	1681	CCCTTTTGTATCCCACTCAGAGGCCCAAAAAGCCTCAGTGGCTTTGGCTTTTATAGGAC 1740
DB	1681	CCCTTTTGTATCCCACTCAGAGGCCCAAAAAGCCTCAGTGGCTTTGGCTTTTATAGGAC 1740
QY	1741	AGTCAGCTTTGGATATTAGAAAGAGCTTTCAGAGACTGGAAGGTTTACAGGAGGCTGAGT 1800
DB	1741	AGTCAGCTTTGGATATTAGAAAGAGCTTTCAGAGACTGGAAGGTTTACAGGAGGCTGAGT 1800
QY	1801	TACGTGATCTAGTGAAGGAGGAGAGAAAGTATTATTAACAAAGGGAGACAGAGAAAGAAA 1860
DB	1801	TACGTGATCTAGTGAAGGAGGAGAGAAAGTATTATTAACAAAGGGAGACAGAGAAAGAAA 1860
QY	1861	GGGAAACAAAGAAAGAGAGAGAAAGGAGAAAGGAGAAAGACGTATTAACGCGCAAG 1920
DB	1861	GGGAAACAAAGAAAGAGAGAGAAAGGAGAAAGGAGAAAGACGTATTAACGCGCAAG 1920
QY	1921	AGNAGAAATTTGACTAAGATCTTGGCTGCAGTGTGTTGAAGGAAAAACCAATACGGAAGAG 1980
DB	1921	AGNAGAAATTTGACTAAGATCTTGGCTGCAGTGTGTTGAAGGAAAAACCAATACGGAAGAG 1980
QY	1981	AGAGAGATTTTGGAAAAATTTAGGCTCAGGCCCTTAGACAGTCAGGGAACCTGGGCAATAGGA 2040
DB	1981	AGAGAGATTTTGGAAAAATTTAGGCTCAGGCCCTTAGACAGTCAGGGAACCTGGGCAATAGGA 2040
QY	2041	CCCCACTCGACAGGACCAATGTGCAATTTGTTAAAGAAAGGACACTGGGCGAAGGACT 2100

Db	2041		CCCCACTCGACAGGACCAATGTGCATATTGTAAGAAAGAGGACACTGGGCAAGGAAC	2100	Db	3121	TACACAGAGACCTGGCCCACTTCAGGATCAACACACCTCAGGTGACCCCTCTCCAGTAGC	3180
Qy	2101		GCCCCAAGAGGGAACCAAGGACCAAGGATCCTAGCTCTAGAAAGAGATAAGATTAGG	2160	Qy	3181	TGGATGACTGCTTCTGGCGGGAGCCACCAACAGGACTGCTTAGAAGGCACGAGGCAC	3240
Db	2101		GCCCCAAGAGGGAACCAAGGACCAAGGATCCTAGCTCTAGAAAGAGATAAGATTAGG	2160	Db	3181	TGGATGACTGCTTCTGGCGGGAGCCACCAACAGGACTGCTTAGAAGGCACGAGGCAC	3240
Qy	2161		GGAGACGGGGTTCGGACCCCTCCCGAGCCGAGGGTAACCTTTGAAGGTGGAGGGCAAC	2220	Qy	3241	TACTGCTGGAAATTTGCTGACCTAGGCTACAGAGCCTCTGCTAAGAGGCCAGATTGCA	3300
Db	2161		GGAGACGGGGTTCGGACCCCTCCCGAGCCGAGGGTAACCTTTGAAGGTGGAGGGCAAC	2220	Db	3241	TACTGCTGGAAATTTGCTGACCTAGGCTACAGAGCCTCTGCTAAGAGGCCAGATTGCA	3300
Qy	2221		CAGTTGAGTTCTCTGGTTGATACCGGAGCGGAAACATTCAGTGTCTACTACAGCCATTAGGAA	2280	Qy	3301	GGAGAGAGGTAAACATCTCTGGGGTACAGTTTGGGGACGGCAGCGATGGCTGACCGAGG	3360
Db	2221		CAGTTGAGTTCTCTGGTTGATACCGGAGCGGAAACATTCAGTGTCTACTACAGCCATTAGGAA	2280	Db	3301	GGAGAGAGGTAAACATCTCTGGGGTACAGTTTGGGGACGGCAGCGATGGCTGACCGAGG	3360
Qy	2281		AACATAAGAGATAAAATCTCTGGGTGATGGGTGCCACAGGGCAACACAGTATCCATGGA	2340	Qy	3361	CACGGAGAAAACTGTAGTCCAGATACCGGCCCAACACACAGCCCAACAAATGAGAGAGT	3420
Db	2281		AACATAAGAGATAAAATCTCTGGGTGATGGGTGCCACAGGGCAACACAGTATCCATGGA	2340	Db	3361	CACGGAGAAAACTGTAGTCCAGATACCGGCCCAACACACAGCCCAACAAATGAGAGAGT	3420
Qy	2341		CTACCCGAAGAACAGTTGACTTGGGAGTGGGACGGGTAACCACTCGTTTCTGCTCATAC	2400	Qy	3421	TTTTGGGGAACAGCTGGATTTTGCAGACTGTGGATCCCGGGGTTTGCACCTTAGCAGCCC	3480
Db	2341		CTACCCGAAGAACAGTTGACTTGGGAGTGGGACGGGTAACCACTCGTTTCTGCTCATAC	2400	Db	3421	TTTTGGGGAACAGCTGGATTTTGCAGACTGTGGATCCCGGGGTTTGCACCTTAGCAGCCC	3480
Qy	2401		CTGAGTGCACGACCCCTCTTAGGTAGAGACTTATTGACCAAGATGGGAGCAAAATTTT	2460	Qy	3481	CACCTACCCGCTAAACCAAGAAAAAGGGGAAATTTCTCTGGGCTCTTGAGCACCAGAGG	3540
Db	2401		CTGAGTGCACGACCCCTCTTAGGTAGAGACTTATTGACCAAGATGGGAGCAAAATTTT	2460	Db	3481	CACCTACCCGCTAAACCAAGAAAAAGGGGAAATTTCTCTGGGCTCTTGAGCACCAGAGG	3540
Qy	2461		CTTTTGAACAGGGAACCAAGAGTGTGCAATATACAAACCTTACCTGTGTTGACCC	2520	Qy	3541	CATTGATGTATCAAAAGGCCCTGCTGAGCGCACCTGCTCTGGCCCTCCCTGACGTAA	3600
Db	2461		CTTTTGAACAGGGAACCAAGAGTGTGCAATATACAAACCTTACCTGTGTTGACCC	2520	Db	3541	CATTGATGTATCAAAAGGCCCTGCTGAGCGCACCTGCTCTGGCCCTCCCTGACGTAA	3600
Qy	2521		TCCAAATTAGATGACGATATCGACTATCTCTCCCTAGTAAAGCTGATCAAAATATAC	2580	Qy	3601	CTAAACCTTTTACCTTTTATGTGGATGAGCGTAAGGGAGTAGCCCGGGAGTTTTAAACC	3660
Db	2521		TCCAAATTAGATGACGATATCGACTATCTCTCCCTAGTAAAGCTGATCAAAATATAC	2580	Db	3601	CTAAACCTTTTACCTTTTATGTGGATGAGCGTAAGGGAGTAGCCCGGGAGTTTTAAACC	3660
Qy	2581		AATTTCTGGTTGGAAACAGTTTCCCAAGCTTGGGAGAAACCGAGGGATGGGTTTGGCAA	2640	Qy	3661	AAACCTTAGACCAATGAGAGAGACCTGTCGCCTACCTGTCAAGAACTCGATCCTGTAG	3720
Db	2581		AATTTCTGGTTGGAAACAGTTTCCCAAGCTTGGGAGAAACCGAGGGATGGGTTTGGCAA	2640	Db	3661	AAACCTTAGACCAATGAGAGAGACCTGTCGCCTACCTGTCAAGAACTCGATCCTGTAG	3720
Qy	2641		AGCAAGTTCCCCCAAGTTATTCAACTGGAAGGCAAGTCCGCGCATGTCACAAAGATTATCC	2700	Qy	3721	CCAGTGTGTGGCCCATATGCTGAAGCTATCGCAGCTGTGGCCATCTGCTCAAGGACG	3780
Db	2641		AGCAAGTTCCCCCAAGTTATTCAACTGGAAGGCAAGTCCGCGCATGTCACAAAGATTATCC	2700	Db	3721	CCAGTGTGTGGCCCATATGCTGAAGCTATCGCAGCTGTGGCCATCTGCTCAAGGACG	3780
Qy	2701		AGTACCCCTTCAGTAAAGAACTCAAGAGGAAATTCGGCCGATGTCACAAAGATTATCC	2760	Qy	3781	CTGACAAATTTGACTTTTGGGACAGAAATAACTGTAAATAGCCCCCATTCGATTTGAGAGA	3840
Db	2701		AGTACCCCTTCAGTAAAGAACTCAAGAGGAAATTCGGCCGATGTCACAAAGATTATCC	2760	Db	3781	CTGACAAATTTGACTTTTGGGACAGAAATAACTGTAAATAGCCCCCATTCGATTTGAGAGA	3840
Qy	2761		AACAGGGCATCTAGTTCTCTGCAATCTCCCTGGAATACCTCCCTGCTACCGGTTAGAA	2820	Qy	3841	TCGTTTGGGAGCCCCCAGACCGATGGATGACCAAGCCCGCATGACCCACTATCAAGGCC	3900
Db	2761		AACAGGGCATCTAGTTCTCTGCAATCTCCCTGGAATACCTCCCTGCTACCGGTTAGAA	2820	Db	3841	TCGTTTGGGAGCCCCCAGACCGATGGATGACCAAGCCCGCATGACCCACTATCAAGGCC	3900
Qy	2821		AGCCTGGGACTTAATGACTATCGACCAAGTACAGGACTTGAGAGAGGTCAATAACGGGTGC	2880	Qy	3901	TGCTTCTCAGAGAGGGGTACGTTCCCTCCACAGCCGCTCTCAACCTGCGCACTCTTC	3960
Db	2821		AGCCTGGGACTTAATGACTATCGACCAAGTACAGGACTTGAGAGAGGTCAATAACGGGTGC	2880	Db	3901	TGCTTCTCAGAGAGGGGTACGTTCCCTCCACAGCCGCTCTCAACCTGCGCACTCTTC	3960
Qy	2881		AGGATATACCCCAAGTCCGACCTTATACCTCTGTTGCTCTCCACCCCAAC	2940	Qy	3961	TGCCTGAAGAGACTGTAAACAGTCACTCATGATTGCCATCAACTATTGATTGAGGAGA	4020
Db	2881		AGGATATACCCCAAGTCCGACCTTATACCTCTGTTGCTCTCCACCCCAAC	2940	Db	3961	TGCCTGAAGAGACTGTAAACAGTCACTCATGATTGCCATCAACTATTGATTGAGGAGA	4020
Qy	2941		GGAGCTGTTATACAGTATTGACTTAAAGGATGCTTCTCTGCTGAGATTACACCCCA	3000	Qy	4021	CTGGGGTCCGCAAGGACCTTACAGACATACCGCTGACTGGAGAGTGTCTAACTGTTTCA	4080
Db	2941		GGAGCTGTTATACAGTATTGACTTAAAGGATGCTTCTCTGCTGAGATTACACCCCA	3000	Db	4021	CTGGGGTCCGCAAGGACCTTACAGACATACCGCTGACTGGAGAGTGTCTAACTGTTTCA	4080
Qy	3001		CTAGCCAAACCACTTTTTCCTTCGAAATGGAGAGATCCAGGTACCGGGAAGAACCGGGCAGC	3060	Qy	4081	CTGACGGNACGAGCTATGTGTGAAGGTAAAGAGATGGCTGGGGCGCGGTGGTGGACG	4140
Db	3001		CTAGCCAAACCACTTTTTCCTTCGAAATGGAGAGATCCAGGTACCGGGAAGAACCGGGCAGC	3060	Db	4081	CTGACGGNACGAGCTATGTGTGAAGGTAAAGAGATGGCTGGGGCGCGGTGGTGGACG	4140
Qy	3061		TCACCTGAGACCGGACCTGCCCCAAGGGTTCAAGAACTCCCGACCACTTTTGAAGAGGCC	3120	Qy	4141	GGACCCCAACGATCTGGGCCAGACGCTGCGGAAGGAACTTCAGCACAAAGGCTGAGC	4200
Db	3061		TCACCTGAGACCGGACCTGCCCCAAGGGTTCAAGAACTCCCGACCACTTTTGAAGAGGCC	3120	Db	4141	GGACCCCAACGATCTGGGCCAGACGCTGCGGAAGGAACTTCAGCACAAAGGCTGAGC	4200
Qy	3121		TACACAGAGACTGGCCAACTTCAGGATCCAAACCTTCAGGTGACCCCTCTCCAGTAGC	3180	Qy	4201	TCATGGCCCTCACGCAAGCTTTGCGGCTGGCCGGAAGGAAATCCATAAACATTTATACGG	4260
Db	3121		TACACAGAGACTGGCCAACTTCAGGATCCAAACCTTCAGGTGACCCCTCTCCAGTAGC	3180	Db	4201	TCATGGCCCTCACGCAAGCTTTGCGGCTGGCCGGAAGGAAATCCATAAACATTTATACGG	4260

QY 4261 ACAGCAGGTATGCTTTGGAGCTGCAACGTCATGGGCGCATCTATAAACAAGGGGT 4320
DB |||||
QY 4261 ACAGCAGGTATGCTTTGGAGCTGCAACGTCATGGGCGCATCTATAAACAAGGGGT 4320
DB |||||
QY 4321 TGCCTACCTCAGCAGGGAGGAAATAAGAAACAAAGAGGAAATCTTAAGCCTATTAGAG 4380
DB |||||
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DB |||||
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QY 4561 TAGAAGCTGGCAAGAGATAAAGATAGACAGCTTCTGAGACTCCGGAAGGACCT 4620
DB |||||
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QY 4621 GCTATACCTCAGATGGGAAGGAAATCCTGCCCCACAAGAGAGGTTAGAAATATGTCAC 4680
DB |||||
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QY 4681 AGATACATCGTCTAACCCACCTTAGGAACTAAACACCTGAGCAGTTGGTCAGAACTCCC 4740
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DB |||||
QY 5701 TCCATCGGTGTTTCTTACTCTGTCAATAAAGCTCTCAGACTTAATGGTATGGGCATAGGA 5760
DB |||||
QY 5701 TCCATCGGTGTTTCTTACTCTGTCAATAAAGCTCTCAGACTTAATGGTATGGGCATAGGA 5760
DB |||||
QY 5761 GACGCTGAACTCCCATAAACCTTATCTCTCAGCTGGTAAATTAATGACTCCGCGACA 5820
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QY 5761 GACGCTGAACTCCCATAAACCTTATCTCTCAGCTGGTAAATTAATGACTCCGCGACA 5820
DB |||||
QY 5821 GGTATTAATATCAACAACACTCAAGGGAGGCTCTTTTAGGAACCTGGTGGCTGATCTA 5880
DB |||||
QY 5821 GGTATTAATATCAACAACACTCAAGGGAGGCTCTTTTAGGAACCTGGTGGCTGATCTA 5880
DB |||||
QY 5881 TAGCTTTGCTCAGATCAGTTATTCTTAGTCTGAACCTCAACCCAGATATCTCCTGATCT 5940
DB |||||
QY 5881 TAGCTTTGCTCAGATCAGTTATTCTTAGTCTGAACCTCAACCCAGATATCTCCTGATCT 5940
DB |||||
QY 5941 CACGGAATTTATGTTTGGCCAGGACCAACCAATAATGGAATAACATTCGGAATCCAGA 6000
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DB |||||

Db 6421 TCACAGCCCACTGAGTCTTAACAGACAGCACTAAATAGGGGCAAACTTTTAGCCTCATC 6480
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Qy |||||

RESULT 3
US-09-171-553B-3
; Sequence 3, Application US/09171553B
; Patent No. 6756227
; GENERAL INFORMATION:
; APPLICANT: GALBRAITH, DANIEL N.
; APPLICANT: HAWORTH, CHRISTINE
; APPLICANT: LEE, GILLIAN M.
; APPLICANT: SMITH, KENNETH T.
; TITLE OF INVENTION: PORCINE RETROVIRUS
; FILE REFERENCE: CFV-5.01
; CURRENT APPLICATION NUMBER: US/09/171,553B
; PRIORITY FILING DATE: 1999-02-08
; PRIOR APPLICATION NUMBER: PCT/GB97/01087
; PRIOR FILING DATE: 1997-04-18
; PRIOR APPLICATION NUMBER: GB 9702668.6
; PRIOR FILING DATE: 1997-02-10
; PRIOR APPLICATION NUMBER: GB 9608164.1
; PRIOR FILING DATE: 1996-04-19
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 8209
; TYPE: DNA
; ORGANISM: Porcine retrovirus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (588)..(2159)
; NAME/KEY: CDS
; LOCATION: (2163)..(5744)

US-09-171-553B-3

Query Match		77.3%;	Score 6282.4;	DB 3;	Length 8209;
Best Local Similarity		87.1%;	Pred. No. 0;		
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QY	63	AAGACCGCTTCTCGTAGTGATTAAGGGAGTGCCTTTTCGAGGCTGAGG-----	115		
DB	61	AAGACCGCTTCTCGTAGTGATTAAGGGAGTGCCTTTTCGAGGCTGAGG-----	119		
QY	116	--TTCTTTTGTGCTTACATTTGGGGGCTCGTCCGGGATCTGTCCGGGCAACCCCTTA	173		
DB	120	TGTGCTTTTACTTGGGCTTTTCATTTGGTGGTGGCCGGGAAATCCTGCGACACCCCTT	179		
QY	174	ACACCCGAGAACCGACTTGGAGGTAAAAAGGATCCTCTTTTAAAGTGTATGATGTACC	233		
DB	180	ACACCCGAGAACCGACTTGGAGGTAAAGGATCCTCTTTTAAAGTGTATGATGTACC	236		
QY	234	GCGCGGCGTCTCTGTTCTGAGTGTCTGTTTTCAGTGGTGGCGGCTTTTCGTTTGCAGCTG	293		
DB	237	GCGCGGCGTCTCTGTTCTGAGTGTCTGTTTTCGTTGATGCGGCTTTTCGTTTGCAGCTG	296		
QY	294	TCTCTCAGGCCGTAAAGGCTGGGGACTGTGATCAGCAGAGTGTCTAGGAGATCACAG	353		
DB	297	TCTCTCAGACCCTAAGGACTTGAGGACTGTGATCAGCAGAGTGTCTAGGAGATCACAG	356		
QY	354	GCTGCTGCCCTGGGGGACGCCCGGAGGTGAGGAGCCAGGAGCCCTGTTGTTCTCC	413		
DB	357	GCTGCCACCTGGGGAGCCCGCGGAGTGGGGAGCCAGGAGCCCTGTTGTTCTCC	416		
QY	414	TACTGTGCGTACAGAGACCGAATTCCTGTTGCTGAAAGCGAAAGTTTCCCTTCGCGACCG	473		
DB	417	TACTGTGCGTACAGAGACCGAGTTCCTGTTGTTGAAAGCGAAAGTTTCCCTTCGCGGCGG	476		
QY	474	TCCGACTCTTTGCTGCTGTTGGAAGAGTGAACGGGTCACTGTTGATCTGGATCTGTTG	533		
DB	477	TCCGACTCTTTGCTGCTGTTGGAAGAGCAGCGGTCGCGTGTCTGGAATCTGTTG	536		
QY	534	GTCTCTGTTGTTGCTCTTTGTTGCTGTTGCTCTTGTCTTACAGTTTAAATATGGACAG	593		
DB	537	GTCTCTGTTGTTGCTCTTTGTTGCTGTTGCTCTTGTCTTACAGTTTAAATATGGACAG	596		
QY	594	ACGGTGAACCCCTCTTAGTTTGACTCTCGACCAATTGACCTGAAGTTAAATCCAGGGCT	653		
DB	597	ACAGTGACTACCCCTTCTAGTTTGACTCTCGACCAATTGACCTGAAGTTAGATCCAGGGCT	656		
QY	654	CATAATTTGTCAGTTTGAAGGGACCTTGGCAGACTTCTGTTCTCTGAATGG	713		
DB	657	CATAATTTGTCAGTTTGAAGGGACCTTGGCAGACTTCTGTTCTCTGAATGG	716		
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DB	717	CCAACTTCGATGTTGGATGCCCATCAGAGGGACCTTTAAATTCAGATATCTCTGGCT	776		
QY	774	GTTTAAAGCAATTTTTCAGATGAGACCCGGCTCTCATCCGATCAGGAGCCCTATATC	833		
DB	777	GTTTAAAGCAATTTTTCAGATGAGACCCGGCTCTCATCCGATCAGGAGCCCTATATC	836		
QY	834	CTTACGTGGCAAGTTTGGCAGAGGATCTCCGCCATGGGTTAAACATGGCTGAATAAG	893		
DB	837	CTTACGTGGCAAGTTTGGCAGAGGATCTCCGCCATGGGTTAAACATGGCTGAATAAG	896		
QY	894	CCAAGAAAGCAGGTCGCCGAAATTCGGCTCTTGGAGAGAAAAACAACACTCGGCTGAA	953		
DB	897	CCAAGAAAGCAGGTCGCCGAAATTCGGCTCTTGGAGAGAAAAACAACACTCGGCGGAA	956		
QY	954	AAAGTCAAGCCCTC-TCCTCATATCTAACCCGAGATTGAGGAGCCACCGGCTTGGCGGA	1012		
DB	957	AAAGTCAAGCCCTCTTCTCTGATATCTACCCCGAGATCGAGGAGCCGCGGCTTGGCGGA	1016		

QY	1013	ACCCCAATCTGTTCCCCACACCCCTTATCTGGCAAGGGTGCAGAGGGAGCCCTTTGC	1072
DB	1017	ACCCCAATCTGTTCCCCACACCCCTTATCTGGCAAGGGTGCAGAGGGAGCCCTTTGC	1075
QY	1073	CCCTCTCGAGCTCCGGGTGGAGGACCTGCTCAGGGACTCGGAGCGGAGGGGCGC	1132
DB	1076	CCCTCTCGAGCTCCGGGTGGAGGACCTGCTCCGGGACTCGGAGCGGAGGGGCGC	1135
QY	1133	CACCCCGAGCGGACAGACGAGATCGCGACATTAACCGTGGCGACGTACGGCCCTCCAC	1192
DB	1136	CACCCCGAGCGGACAGACGAGATCGCGATTAACCGTGGCGACCTATGGCCCTCCCAT	1195
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DB	1196	GCCAGGGGGCCAAATTCAGCCCTCCAGTATTTGGCCCTTTCTTTGAGATCTCTATAA	1255
QY	1253	TTGGAAAACTAACCATTCCTCGGAGATCCCAACGCTCAGGGGTGGTGA	1312
DB	1256	TTGGAAAACTAACCATTCCTCGGAGATCCCAACGCTCAGGGGTGGTGA	1315
QY	1313	GTCCCTTATGTTCTCTCACCGCTTCTTGGGATGATTTGTAACAGCTGCTCGACACT	1372
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QY	1373	CTTCAACCCGAGGAGGAGAGAAATCTATTAGAGGCTAGAAAAATTTCTCTGGGC	1432
DB	1376	CTTCAACCCGAGGAGGAGAGAAATCTATTAGAGGCTAGAAAAATTTCTCTGGGC	1435
QY	1433	CGAGGGGAGCCACCGGTTGCAAAATGAGATTCACATGGGATTTCCCTTAACCTGCC	1492
DB	1436	CGAGGGGAGCCACCGGTTGCAAAATGAGATTCACATGGGATTTCCCTTAACCTGCC	1495
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DB	1496	CGGTTGGGACTACACACCGCTGAAAGTAGGAGAGCTTTGAAAAATCTATCGCAGGCTCT	1555
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DB	1556	GGTGGCGGCTCTCCGGGCGCTCAAGACGGCCCACTAAATTTGGCTAAGTAAGAGGT	1615
QY	1613	GATGAGGAGCCGAATGAACCCCTCTGTTTCTTTGAGAGGCTTTGGAAGCTTCAG	1672
DB	1616	GATGAGGAGCCGAACGAACCTCCCTCGGTATTTCTTGAGAGGCTCATGGAAGCTTCAG	1675
QY	1673	GGGTTACACCCCTTTTGATCCACCTCAGAGGCCCAAAAAGCTCAGTGGCTTTGGCTTT	1732
DB	1676	GGGTTACACCCCTTTTGATCCCTCAGAGGCCCAAAAAGCTCAGTGGCTTTGGCTTT	1735
QY	1733	TATAGGACAGTCAGCCTTGGATATTAGAAAGAGCTTCAGAGACTGGAAGGGTTACAGGA	1792
DB	1736	CATTGGGCACTCGGCTCTGGATATCAGGAAGAAACTTCAGAGACTGGAAGGGTTACAGGA	1795
QY	1793	GGCTGATTTACGTGATCTAGTGAAGGAGCAGAGAAATATATTACAAAGGGAGACAGA	1852
DB	1796	GGCTGATTTACGTGATCTAGTGAAGGAGCAGAGAAAGTTATTACAGAAAGGGAGACAGA	1855
QY	1853	AGAAGAAAGGAAACAAAGAAAGAGAGAGAAAGGAGAGAAAGAGCGTAATAA	1912
DB	1856	AGAAGAAAGGAAACAAAGAAAGAGAGAGAAAGAGAGAGAAAGAGCGTAGTAG	1915
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DB	1916	ACGGCAAGAGAAAGAAATTTGACTTAAGATCTTGGCTGAGTGGTTGAAGGGAAGCAATAC	1975
QY	1973	GGAAAGAGAGAGATTTTAGGAAATTTAGGTCAGGCCCTTAGACACTCAGGGAACTGGG	2032
DB	1976	GGAAAGAGAGAGATTTTAGGAAATTTAGGTCAGGCCCTTAGACACTCAGGGAACTGGG	2035
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[illegible]

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Db 4316 AAGGGGTTTGCCTTACCTCAGCAGGGAGGAAATAAAGAAACAAAGAGGAAATTTCTAAGCCT 4375
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QY 4793 TGTGCCCTGCCAGCTGTTAAATGCTTAATCTTCCAGATGCCTCCAGGAAGAGACTAAG 4852
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Db 6392 CGGTGCCCAATTAACCTCGCTCGGCTGACATAACACAGCGCCCTAGCAACAGTACCA 6451

6416	CTGGATCAGACCCCACTGAGTCTAACAGCAGAC-----TAAATGGGG	6460	7532	TCATGGTACTTAGGCAACAGTACCGAGCCCTCTGAGCCAAAGGAGAACTGACCTCTAGC	7599
6452	CTGGATTTGATTCCTAACCAACGCGCTAGAAACTCCCGAGGTGTTCTGTTTAAAGACAGGAC	6511	7538	TCTACCAAGTCTTAAGATTAGAACTATTAAACAAGAGAAAGTGGGGAATGAAGAGATGAA	7597
6461	CAAAACTTTTATGCTCATCCAGGGAGCTTTTCAAGCTCTTAAGCTCCACGACTCCAGAGG	6520	7592	CTTCCAGTCTTAAGATTAGAACTATTAAACAAGACAAGAGTGGGAAATGAAGAGATGAA	7651
6512	AGAGACTCTTTCAGTCTCATCAGGAGGCTTTCCAAAGCCATCACTCCACCGACCTGTATG	6571	7598	AATACAACTTAAGCTAATGAGAGCTTAAATTTGTTCTTGAATTTCCAGAGTTTGTCTCTTA	7657
6521	CTACCTCTTCTTGTGGTATGCTTAGCTTCGGGCCCACTTACTATGAAGGAATGGCTA	6580	7652	AATGCAACTTAACCTCCAGAACCCAGGAAGTTAATAAAAGCTCTAAATGCCCCCGAA	7711
6572	CCACTCTCTTGTGGCTTGTCTATCTCAGGGCCCTCTTATTATGAGGGATGGCTA	6631	7658	TAGGTAAAAGATTAGGTTTTTGTGTTTTTAAATATATGCGAAAGTAAATAGGCCCTGAG	7717
6581	GAAGAGGGAATTTCAATGTGACAAAGAACATAGAGACCAATGACATGGGGATCCCAA	6640	7712	TTACAGACCTGCTGGCTGCCAGTAAATAGGTAGAAGCTCACACTTCTATTGTTCCAGG	7771
6632	AAGAAGAAAAATTCAATGTGACAAAGAGCATAGAAATCAATGTACATGGGGTCCCGAA	6691	7718	TACATGCTCTTAGGCATGAACCTTCTTGAACATTAATTTGAGATTAACAAGAAAGGAGTTT	7777
6641	ATAAGCTTACCCTTACTGAGTTTCTGAAAGGACCTGCATAGGAAGGTTTCCCCCAT	6700	7772	GCTGCTATCTGGCT--AAGTAAGATAACAGGAAATGAGTTGAC-----TAATCGCTTAT	7826
6692	ATAAGCTTACCCTCACTGAAGTTTCCGGGAAGGAGACATGATAGGAAGAGCTCCCCCAT	6751	7778	CTAACTGCTGTTTGTAGCTTCTGTAAAACTGGTTCGCCCATAAAGATGTTGAAATGTTGAT	7837
6701	CCACCAACACCTTTGTAAACCACTGAAGCGCTTTAATCAAACTCTGAGAGTCAATATC	6760	7827	CTGGATTCTGTAACCTGACCTGGCACCATAGAAGAAATTGAATTACACATTGACAGCCCTAG	7886
6752	CCACCAACACCTTTGTATAGTACTGTGTTTATGACAGCCCTCAGAAAAATCAGTATT	6811	7838	ACACATATCTTGGTGACAAATGCTCCCCCACCCGAAACATGCGCAAAATGTGTAACTC	7897
6761	TGGTACCTGGTTATGACAGGTGGTGGCAATGTAATATGAGATTAACCCCTGTGTTTCCA	6820	7887	TGACCTATCTCACTGCAATCTGTCACTCTGCCCAGAGGCCACGAGATGCGGACCTCC	7946
6812	TAGTACCTGGTTATAACAGGTGGTGGCAATGCAATCTGTTGTTAAACCCCTGTGTTTCCA	6871	7898	TAAAACAATTTAAATTAATTTGCTCCAGAGCGGGCTCTCGAAATTTTAAATTTGACTG	7957
6821	CTTGTGTTTAAACCAACTAAGATTTTGCATTTATGCTTAAATTTTCCCGAGTGT	6880	7947	GGAGCTATTTTAAATGATTGTTCCACGAGCGGGCTCTCGATATTTTAAATTTTAAATTTGAT	8006
6872	CCTCAGTCTTCAACCAATCCAAAGATTTCTGTGTCATGTTCAATGTTCCCGAGTGT	6931	7958	GT-----TTGTGATATTTTGAATGATTGTTTCTTAAAGCGCGGCTTTG	8002
6881	ATTACTATCCGAAAAAGCAATCTTTGATGATATGACTACAGAAATCATCGACAAAGA	6940	8007	GTCCATGGAGCGCGGCTCTCGATATTTTAAATGATTGTTTGTGACGACAGGCTTTG	8065
6932	ACTACATCTCGAGGAGTGTCTTGTATGATATGACTATCGGTATAACCGACCAAAA	6991	8003	TTGTCAACCCCATAAAAGCTGTCGCCGACTCCACACTCGGGGCCGAGTCTCTACCCCTG	8062
6941	GAGAACCCATATCTCTGACATTTGCTGTGATGCTCGGACTTGGAGTGGCAGCGGTAG	7000	8067	TTGTGAACCCCATAAAAGCTGTCGCCGATTCCGCACTCGGGGCCGAGTCTCTACCCCTG	8126
6992	GAGAACCCGTATCCCTTACCTTAGCTGTAATGCTCGGATTAGGGACGCGCTTGGCGTAG	7051	8063	CGTGTGTACGACTGTGGGCCCGGCGCTTGGAAATAAAATCCTCTTGTGTTTGCAT	8122
7001	GAACAGGACAGTCCCTGTTCCAGGACACACGACTAGAACAGGACTTAGTAACC	7060	8127	CGTGTGTACGACTGTGGGCCCGGCGCTTGGAAATAAAATCCTCTTGTGTTTGCAT	8186
7052	GAACAGGACAGTCCCTGTTCCAGGACACACGACTAGAACAGGACTTAGTAACC	7111	8123	CAAAAAAAA 8132	
7061	TACATCGAATTTGAACAGAGATCTCAGAGCCCTAGAAAAATCTGTCAAGTAACCTGGAGG	7120	8187	CAAAAAAAA 8196	
7112	TACTCGGCCCATGACAGAGATCTCCGAGCCTTAAAGGAGTCTGTTAGCAACCTAGAG	7171			
7121	AATPCCCTAACCTCTTATCTGAAGTAGTCTTACAGATAGAGAGGTTAGATTATAT	7180			
7172	AGTCCCTGACTCTTTGTTCTGAAGTGTCTTACAGAACCGGAGGGATTAGATCTGCTGT	7231			
7181	TTCTAAAGAGAGGATTTATGTAGCTTTGAAGGAGGATGCTGTTTTATCTGGATC	7240			
7232	TTCTAAAGAGAGGTTATGTAGCAGCCTTAAAGAGGATGTTGCTTCTATGTAGATC	7291			
7241	ATTGAGGGCCATCAGAGACTCCATGAACAGCTTAGAGAAAGTTGAGAGGCGTCCAA	7300			
7292	ACTGAGAGCCATCAGAGACTCCATGAACAGCTTAGAAGGTTAGAGAGGCGTCCAA	7351			
7301	GGGAAAGGAACTACTCAAGGGTGGTTGAGGGATGTTCAACAGGCTCTTTGGTTGG	7360			
7352	GGGAAAGAGAGGCTGACAGGGGTGGTTTGAAGGATGTTTCAACAGGCTCTCTTGGATGA	7411			
7361	CTACCTACTTTCTGCTTTAAAGGACCTTAATAGTCTCTCTCTGTTACTCACAGTTG	7420			
7412	CCACCTTCTTCTGCTGACAGGGGCCCTAGTAGTCTGCTCTCTGTTACTTACAGTTG	7471			
7421	GGGCATGTATTATTAACAAGTTAATTTAGCCCTTCAATTAGAGAAAGAAATAGTGCAGTCCAGA	7480			
7472	GGCTTGTCTTAATTAAGTTTGTGCTTTGTTGTTAGAGAACGAGTGAAGTGCAGTCCAGA	7531			
7481	TCATGGTACTTAGACAACAGTACCAAGCCGCTTAGC---AGGGAAGCTGGCCGCTAGC	7537			

US-09-171-553B-2

Query Match		76.8%;	Score 6248.4;	DB 3;	Length 8196;
Best Local Similarity		87.0%;	Pred. No. 0;		
Matches 7150;		Conservative 3;	Mismatches 929;	Indels 136;	Gaps 21;
QY	15	TGTGGGCCCCAGCGCCTTGGAAATAAAATTCCTTCTGCTGTTTGCATCAAGACCGCTTCT	74		
DB	1	TGTGGGCCCCAGCGCCTTGGAAATAAAATTCCTTCTGCTGTTTGCATCAAGACCGCTTCT	60		
QY	75	CGTAGTGATTAAGGGAGTCGCTTTTCCGAGCCTGGAGG-----TTCCTTTTTCG	125		
DB	61	CGTAGTGATTTGGGGTGTGCGCTCTTCCGAKCCCGGACGAGGGGATTTGTTCTTTTAC	119		
QY	126	TGCTCTTACATTTGGGGGCTCGTCCGGGATCTGTCCGGCCACCCCTAAACCCGAGAAC	185		
DB	120	TGGCCTTTTCATTTGGTGGCTTGGCCGGGAAATCCTTCGGACACCCCTTACACCCGAGAAC	179		
QY	186	CGACTTGGAGGT-AAAGGGATCCCTTTTGGAAACGTGTGTG--TGTGTCCGGCCGGCGTCTC	236		
DB	180	CGACTTGGAGGT-AAAGGGATCCCTTTTGGAAACGTGTGTG--TGTGTCCGGCCGGCGTCTC	236		
QY	246	TGTTCTGAGTGTCTGTTTTCAGTGGTCCGGCTTTCGGTTTGCAGCTGCTCTCAGGCC	305		
DB	237	TGTTCTGAGTGTCTGTTTTCAGTGGTCCGGCTTTCGGTTTGCAGCTGCTCTCAGACC	296		
QY	306	GTAAGGGCTGGGGGACTGTGATCAGCAGACGTGTCTAGGAGGATCACAGGCTGTGCTGCCCTG	365		
DB	297	GTAAGGACTTGGAGACTGTGATCAGCAGACGTGTCTAGGAGGATCACAGGCTGTGCTGCCACCTG	356		
QY	366	GGGGACCCCGGGAGGTGAGGAGAGCCAGGGACGCTCGTGTCTCTACTGTGCGTCA	425		
DB	357	GGGGACCCCGGGAGGTGAGGAGAGCCAGGGACGCTCGTGTCTCTACTGTGCGTCA	416		
QY	426	GAGGACCGAATTCGTGTTGCTGAAGCGAAAGCTTCCCCCTCCGGACCGTCCGACTCTTTT	485		
DB	417	GAGGACCGAATTCGTGTTGCTGAAGCGAAAGCTTCCCCCTCCGGACCGTCCGACTCTTTT	476		
QY	486	GCTCTGTTGGAAGACGTGGACGGGTCACTGTGTCTGTGATCTGTGTTGTTCTGTTTG	545		
DB	477	GCTCTGTTGGAAGACGTGGACGGGTCACTGTGTCTGTGATCTGTGTTGTTCTGTTTG	536		
QY	546	TGTGCTTTTGTCTGTGTGTCTGTCTACAGTTTTTAATATGGGACAGACGFTGACGACC	605		
DB	537	TGTGCTTTTGTCTGTGTGTCTGTCTACAGTTTTTAATATGGGACAGACGFTGACGACC	596		
QY	606	CCTCTTAGTTTGAATCTCGACCAATTCGACTGAAGTTAAATCCAGGCTCATTAATTTGTCA	665		
DB	597	CCTCTTAGTTTGAATCTCGACCAATTCGACTGAAGTTAAATCCAGGCTCATTAATTTGTCA	656		
QY	666	GTTTCAGTTTAAAGAGGACCTTGGCAGACTTTCTGTGTCTCTGAATGGCCGACATTCGAT	725		
DB	657	GTTTCAGTTTAAAGAGGACCTTGGCAGACTTTCTGTGTCTCTGAATGGCCGACATTCGAT	716		
QY	726	GTTTGGATGGCCATCAGAGGGACCTTTAAATTCGAGATTATCTGTGCTGTAAAGCAGTT	785		
DB	717	GTTTGGATGGCCATCAGAGGGACCTTTAAATTCGAGATTATCTGTGCTGTAAAGCAGTT	776		
QY	786	ATTTTTCAGACTGGACCCGGCTCTATCCGGATCAGGAGCCCTATATCTTACGTGGCAA	845		
DB	777	ATTTTTCAGACTGGACCCGGCTCTATCCGGATCAGGAGCCCTATATCTTACGTGGCAA	836		
QY	846	GATTTGGCAGAGGATCCTCCGCCATCGGTTTAAACCATGGCTGAATTAAGCCCAAGAAAGCCA	905		
DB	837	GATTTGGCAGAGGATCCTCCGCCATCGGTTTAAACCATGGCTGAATTAAGCCCAAGAAAGCCA	896		
QY	906	GGTCCCAGAAATCTGGCTCTTGGAGAGAAAAACAAACACTCGGCTGAAAAAGTCAAGCCCC	965		
DB	897	GGTCCCAGAAATCTGGCTCTTGGAGAGAAAAACAAACACTCGGCTGAAAAAGTCAAGCCCC	956		
QY	966	TC--TCCTCATATCTACCCGAGATTGAGGAGCCACCGGCTTGGCCGGGACCCCAATCTGT	1024		
DB	957	TCCTTCCTGTATCTACCCGAGATCGAGGAGCCGCGGACTTGGCCGGGACCCCAACCTGT	1016		

QY	1025	TCGCCACACCCCTTATCTGGGCA CAGGTTGCCCGCGAGGGGACCCCTTTTGCCTCTCTGGAGC	1084
DB	1017	TCGCCACACCCCTTATCTGGGCA CAGGTTGCCCGCGAGGGGACCCCTTTTGCCTCTCTGGAGC	1075
QY	1085	TCGGCGGTGGAGGACCTGTCTGAGGACTCGGAGCGGAGCGGGGCGCCACCCGAGCG	1144
DB	1076	TCGGGTGTGGAGGACCTGTCTGCGGACTCGGAGCGGAGCGGGGCGCCACCCGAGCG	1135
QY	1145	GACAGACGAGATTCGCGACATTTACCGCTGCGCACTGACGGCCCTCCACACCCGGGGGCCA	1204
DB	1136	GACAGACGAGATTCGCGATATTACCGCTGCGCACTATGGCCCTCCATGCGAGGGGGCCA	1195
QY	1205	ATTGAGCCCTCCAGTATTTGGCCCTTTCTTCTGCGAGATCTCTATAATTGGAATACTAA	1264
DB	1196	ATTGAGCCCTCCAGTATTTGGCCCTTTCTTCTGCGAGATCTCTATAATTGGAATACTAA	1255
QY	1265	CCATCCCTTTCTCGGAGGATCCCAAGCCTCAAGGGGTTGGTGGAGTCCCTTATGTT	1324
DB	1256	CCATCCCTTTCTCGGAGGATCCCAAGCCTCAAGGGGTTGGTGGAGTCCCTTATGTT	1315
QY	1325	CTCTCACACGCTACTTTGGGATGATTTGTCACACAGCTGTCTGCAGACACTCTTCAACAACCGA	1384
DB	1316	CTCTCACACGCTACTTTGGGATGATTTGTCACACAGCTGTCTGCAGACACTCTTCAACAACCGA	1375
QY	1385	GGAGGAGAGAGAAATTTCTATTAGAGGCTAGAAAAAATTTCTTGGGGCCGACGGGGAGC	1444
DB	1376	GGAGGAGAGAGAAATTTCTATTAGAGGCTAGAAAAAATTTCTTGGGGCCGACGGGGAGC	1435
QY	1445	CAGCGGTTGCAAAATGAGATTTGACATGGGATTTCCCTTAACTCGCCCGGTTGGGACTA	1504
DB	1436	CAGCGGTTGCAAAATGAGATTTGACATGGGATTTCCCTTGACTCGCCCGGTTGGGACTA	1495
QY	1505	CAACACGGCTGAAGGTAGGGAGAGCTTGAAAAATCTATCCCAAGGCTCTGGTGGCGGCTCT	1564
DB	1496	CAACACGGCTGAAGGTAGGGAGAGCTTGAAAAATCTATCCCAAGGCTCTGGTGGCGGCTCT	1555
QY	1565	CGGGGCGCTCAAGA CCGCCCACTAAATTTGGCTAAGGTAAAGAGAAAGTATGACAGGAGC	1624
DB	1556	CGGGGCGCTCAAGA CCGCCCACTAAATTTGGCTAAGGTAAAGAGAGTATGACAGGAGC	1615
QY	1625	GAAAGACCCCTCTGTTTCTTGAGAGGCTCTTGGAGGCTTTCAGGCGGTACACCCC	1684
DB	1616	GAAAGACCCCTCTGTTTCTTGAGAGGCTCTTGGAGGCTTTCAGGCGGTACACCCC	1675
QY	1685	TTTTGATCCACCTCAGAGGCGCCAAAAAGCCTCAGTGGCTTTTGGCCTTTATAGGACAGTC	1744
DB	1676	TTTTGATCCACCTCAGAGGCGCCAAAAAGCCTCAGTGGCTTTTGGCCTTTATAGGACAGTC	1735
QY	1745	AGCCTTGGATATTAGAAAAAGCTTTCAGAGCTGGAAGGGTTTACAGGAGCTGAGTTACG	1804
DB	1736	AGCCTTGGATATTAGAAAAAGCTTTCAGAGCTGGAAGGGTTTACAGGAGCTGAGTTACG	1795
QY	1805	TGATCTAGTGAAGGAGGACAGAAAGTATATTACAAAAGGGAGACAGAGAAAGGAA	1864
DB	1796	TGATCTAGTGAAGGAGGACAGAAAGTATATTACAAAAGGGAGACAGAGAAAGGAA	1855
QY	1865	ACAAAAGGAGAGAGAAAGAGAGGAAAGGAGGAAAGACGTAATAAATCGGCAAGAGAA	1924
DB	1856	ACAGAAGAAAGAAAGGAGAGAGAAAGGAGGAAAGACGTAATAAATCGGCAAGAGAA	1915
QY	1925	GAAATTTGACTAAGATCTTGGCTGCTAGTGGTTGAAGGAAAGAACATATACGAAAGAGAG	1984
DB	1916	GAAATTTGACTAAGATCTTGGCTGCTAGTGGTTGAAGGAAAGAACATATACGAAAGAGAG	1975
QY	1985	AGATTTTAGGAAAAATTTAGTTCAGGCCCTTACAGTTCAGGGAACTTGGGCAATAGGACCCC	2044
DB	1976	AGATTTTAGGAAAAATTTAGTTCAGGCCCTTACAGTTCAGGGAACTTGGGCAATAGGACCCC	2035
QY	2045	ACTCGACAAAGGACCAATGTGCTATTGTAAAGAAAGAGGACACTGGGCAAGGAACTGCC	2104
DB	2036	ACTCGACAAAGGACCAATGTGCTATTGTAAAGAAAGGACACTGGGCAAGGAACTGCC	2095

Qy 2105 CAAGAAGGAAACAAAGGACCAAGGATCTTAGCTCTAGTCTCTAGAGAGATAAAGATTAGGGAG 2164
Db 2096 CAAGAAGGAAACAAAGGACCGAAG-TCCTAGCTCTAGAGAGATAAAGATTAGGGAG 2154
Qy 2165 ACGGGTTTCGACCCCTCCCGAGCCAGGGTAACCTTTGAGGTGGAGGGGCAACCACT 2224
Db 2155 AC-GGGTTTCGACCCCTCCCGAGCCAGGGTAACCTTTGAGGTGGAGGGGCAACCACT 2213
Qy 2225 TGAGTTCTCTGTTGATACCGGAGCGAAACATTTCACTAGTCTACTACAGCCATTTAGGAAACT 2284
Db 2214 TGAGTTCTCTGTTGATACCGGAGCGGAGCAATTTAGTCTGCTACAAACATTTAGGAAACT 2273
Qy 2285 AAAAGATAAAAACTCTGGGTGATGGGTGCCACAGGGCAACAAACAGATATCCATGGACTAC 2344
Db 2274 AAAAGAAAAAAATCTCTGGGTGATGGGTGCCACAGGGCAACCGGAGTATCCATGGACTAC 2333
Qy 2345 CCGAAGAACAGTTGACTTTGGAGTTGGACGGGTAAACCACTCTGTTCTGGTTCATACCTGA 2404
Db 2334 CCGAAGAACCCGTTGACTTTGGAGTTGGACGGGTAAACCACTCTGTTCTGGTTCATCCCTGA 2393
Qy 2405 GTGCCCCAGCACCCCTCTTTAGGTAGAGACTTATTGACCAAGATGGGAGCACAATTTCTTT 2464
Db 2394 GTGCCCCAGTACCCCTCTTTAGGTAGAGACTTACTGACCAAGATGGGAGCTCAATTTCTTT 2453
Qy 2465 TGAACAAGGGAAACAGAGAGTGTCTGCAAAATAACAAACCTATCACTGTGTTGACCCCTCA 2524
Db 2454 TGAACNAGGAAGACCAAGAGTGTCTGTGAATAACAAACCCATCACTGTGTTGACCCCTCA 2513
Qy 2525 ATTAGATGACGAATATGACTATATCTCTCCCTAGTAAAGCCTGATCAAAATATACAAATT 2584
Db 2514 ATTAGATGATGAATATGACTATATCTCTCCCAAGTAAAGCCTGATCAAGATATACAGTC 2573
Qy 2585 CTGGTTGGAAACAGTTTCCCAAGCCTGGGAGAACCGCAGGATGGTTGGCAAGCA 2644
Db 2574 CTGGTTGGAGCAGTTTCCCAAGCCTGGGAGAACCGCAGGATGGTTGGCAAGCA 2633
Qy 2645 AGTTCCCCCAAGTTATTTCAACTGAAGGCCAGTGCACACAGTGTCACTGACAGACAGTA 2704
Db 2634 AGTTCCCCCAAGTTATTTCACTGAAGGCCAGTGTCTACACAGTATCAGTCAGACAGTA 2693
Qy 2705 CCCCTTGAGTAAAGAGCTCAAGAGGAATTCGGCCGCATGTCCAAAGATTAATCCAAACA 2764
Db 2694 CCCCTTGAGTAGAGAGCTCGAGAAGGAATTTGGCCGCATGTTCAAAGATTAATCCAAACA 2753
Qy 2765 GGGCATCTAGTTCTGTGCAATCTCTCCCTGGAATCTCCCTGCTACCGTTAGAAAGCC 2824
Db 2754 GGGCATCTAGTTCTGTGCAATCTCCCTTGGAAATCTCCCTGCTACCGTTAGAAAGCC 2813
Qy 2825 TGGGACTAATGACTATCGACAGTACAGGACTTGAGAGAGTCAATAAACGGGTGCAGGA 2884
Db 2814 TGGGACCAATGATTTATCGACAGTACAGGACTTGAGAGAGTCAATAAAGGGTGCAGGA 2873
Qy 2885 TATACACCACACAGTCCCGAACCCCTTATAACCTCTTTGTGCTCTCCACCCCAACGGAG 2944
Db 2874 CATACACCACAGTCCCGAACCCCTTATAACCTCTTGAGCGCCCTCCCGCTGAAAGGAA 2933
Qy 2945 CTGGTATACAGTATTTGAGTCTTAAGGATGCCTTTCTTCTGCTGAGATTTACACCCACTAG 3004
Db 2934 CTGGTATACAGTATTTGAGTCTTAAGGATGCCTTTCTTCTGCTGAGATTTACACCCACTAG 2993
Qy 3005 CCAACCACTTTTGGCTTTCGATGAGAGATCCAGGTACGGGAGAGAACCGGCGAGCTCAC 3064
Db 2994 CCAACCACTTTTGGCTTTCGATGAGAGATCCAGGTACGGGAGAGAACCGGCGAGCTCAC 3053
Qy 3065 CTGGACCCGACTGCCCCCAAGGGTTCAAGAACTCCCGGACCATCTTTGACGAAGCCCTACA 3124
Db 3054 CTGGACCCGACTGCCCCCAAGGGTTCAAGAACTCCCGGACCATCTTTGACGAAGCCCTACA 3113
Qy 3125 CAGAGACCTGGCCAACTTTAGGATCCAAACCCCTCAGGTGACCCCTCTCCAGTACGTGGA 3184
Db 3114 CAGGACCTGGCCAACTTTAGGATCCAAACCCCTCAGGTGACCCCTCTCCAGTACGTGGA 3173
Qy 3185 TGACCTGCTTTTGGCGGGAGCCACCAACAGGACTGTCTTAGAGGCACGAAGGCCTACT 3244

Db 3174 TGACCTGCTTTCTGGCGGGAGCCCAAAACAGGACTGCTTAGAAGGTACGAAGGCCTACT 3233
Qy 3245 GCTGGAAATTTCTGACCTTAGCTTACAGAGCCTCTGTCTAAGAGGCCACAGATTTTCAGGAG 3304
Db 3234 GCTGGAAATTTCTGACCTTAGCTTACAGAGCCTCTGTCTAAGAGGCCACAGATTTTCAGGAG 3293
Qy 3305 AGAGGTAACATATCTTGGGGTACATGTTTGGGACGGGACGGATGGCTGACGAGGACG 3364
Db 3294 AGAGGTAACATATCTTGGGGTACATGTTTGGGCGGGCGGACGGATGGCTGACGAGGACG 3353
Qy 3365 GAAGAAAACTGTAGTCCAGATACGGCCCCCAACCAAGCCAAACAAATAGAGAGATTTT 3424
Db 3354 GAAGAAAACTGTAGTCCAGATACGGCCCCCAACCAAGCCAAACAAATAGAGAGATTTT 3413
Qy 3425 GGGGACAGCTGGATTTTGCAGACTGTGGATCCCGGGGTTTTCGACCTTTAGCAGCCCCACT 3484
Db 3414 GGGGACAGCTGGATTTTGCAGACTGTGGATCCCGGGGTTTTCGACCTTTAGCAGCCCCACT 3473
Qy 3485 CTACCCGCTAACCAAGAAAAAGGGGAATTTCTCTTGGGCTCTTGAGCAACAGAAAGGATTT 3544
Db 3474 CTACCCGCTAACCAAGAAAAAGGGGAATTTCTCTTGGGCTCTTGAGCAACAGAAAGGATTT 3533
Qy 3545 TGATGCTATCAAAAGGCCCTCTGTGAGCGCACCTGCTCTGGCCCTCCCTGACGTAATACTAA 3604
Db 3534 TGATGCTATCAAAAGGCCCTCTGTGAGCGCACCTGCTCTGGCCCTCCCTGACGTAATACTAA 3593
Qy 3605 ACCCTTTACCTTTATGTGTGATGAGCTAAGGAGTAGCCCGGGAGTTTTTAACCCAAAC 3664
Db 3594 ACCCTTTACCTTTATGTGTGATGAGCTAAGGAGTAGCCCGAGGATTTTTTAACCCAAAC 3653
Qy 3665 CCTAGGACCATGAGAAAGACCTGTGCTTACCTGTCTCAAGAAAGCTCGATCTGTAGCCAG 3724
Db 3654 CCTAGGACCATGAGAAAGACCTGTGCTTACCTGTCTCAAGAAAGCTCGATCTGTAGCCAG 3713
Qy 3725 TGGTTGGCCCATATGCTGAAAGGCTATCGCAGCTGTGGCCATATCTGTCAAGGACGCTGA 3784
Db 3714 TGGTTGGCCCATATGCTGAAAGGCTATCGCAGCTGTGGCCATATCTGTCAAGGACGCTGA 3773
Qy 3785 CAAATTGACTTTGGGACAGAAATATACCTGTAATAGCCCCCCTGATTTGGAGAACATCGT 3844
Db 3774 CAAATTGACTTTGGGACAGAAATATACCTGTAATAGCCCCCCTGATTTGGAGAACATCGT 3833
Qy 3845 TCGGACGCCCCAGACCCGATGGATGACCAACGCCCGCATGACCCACTATCAAGACCTGCT 3904
Db 3834 TCGGACGCCCCAGACCCGATGGATGACCAACGCCCGCATGACCCACTATCAAGACCTGCT 3893
Qy 3905 TCTCACAGAGAGGTCACTGTTGCTTCCACAGCGCTCTCAACCCCTGCACTCTTTCTGCC 3964
Db 3894 TCTCACAGAGAGGTCACTTCTGCTCCACAGCGCTCTCAACCCCTGCACTCTTTCTGCC 3953
Qy 3965 TGAAGACCTGATGAAACCACTGACTCATGATGGCATCAACTATTGATGGAGAGCTGG 4024
Db 3954 TGAAGACCTGATGAAACCACTGACTCATGATGGCATCAACTATTGATGGAGAGCTGG 4013
Qy 4025 GGTCCGCAAGACCTTACAGACATACCGCTGACTGGAGAAAGTGTAACTGTTTCACTGA 4084
Db 4014 GGTCCGCAAGACCTTACAGACATACCGCTGACTGGAGAAAGTGTAACTGTTTCACTGA 4073
Qy 4085 CGGAAGCAGCTATGTGGTGGAAAGTAAAGGATGGCTGGGGCGCGGTGGTGGACGGAC 4144
Db 4074 CGGAAGCAGCTATGTGGTGGAAAGTAAAGGATGGCTGGGGCGCGGTGGTGGACGGAC 4133
Qy 4145 CCGCAGCATCTGGGCCAGAGCCTTCGCGGAAGGAACTTTAGACCAAAAGGCTGAGCTCAT 4204
Db 4134 CCGCAGCATCTGGGCCAGAGCCTTCGCGGAAGGAACTTTAGCGCAAAAGGCTGAGCTCAT 4193
Qy 4205 GGGCCCTCAACCAAGCTTTGGGCTGGCGGAGGGAATCCATAAATTTATACGGACAG 4264
Db 4194 GGGCCCTCAACCAAGCTTTGGGCTGGCGGAGGGAATCCATAAATTTATACGGACAG 4253
Qy 4265 CAGGTATGCTTTTTCGCACTGCACACGTACATGGGGCCATCTATATAACAAAGGGGTTGCT 4324

Db	4254	CAGGTATGCTTTGCGACTGCAACGTAACGCGGGCCATCTATATAAACAAGGGGTGCT	4313	QY	5405	ACTTGAGTGGGTGAGACAAACGAGCGTGGAGGCAACTCCGGGAGGCGCTACTCAGGAGGAGG	5464
QY	4325	TACCTCAGCAGGAGGGAATAAAGAACAAAGAGGAAATTTCTAAGCCTATTAGAGCCGT	4384	Db	5394	GCTCAGTGGGTGAGCGAGCGAGCGTGGAAAGCAGCTCCGGGAGGCGCTACTC---AGGAG	5450
Db	4314	TACCTCAGCAGGAGGGAATAAAGAACAAAGAGGAAATTTCTAAGCCTATTAGAGCCTT	4373	QY	5465	AGACTGTCAGATCCACATCGTTTCCAAAGTGGAGATTACAGTCTAGTTAGACGCCACCG	5524
QY	4385	ACATTTACAAAAAGGCTAGCTATTATATACATGCTCTGTGACATCAGAAAGCTTAAGATCT	4444	Db	5451	AGACTTGAAGTTCCACATCGCTTCCAAAGTTGGAGATTACAGTCTATGTTAGACGCCACCG	5510
Db	4374	ACATTTGCCAAAAGGCTAGCTATTATATACACTGTCTGTGACATCAGAAAGCCAAAGATCT	4433	QY	5525	TCACAGAAACCTTCGAGACTCGGTGGAAAGGCCCTTATCTCGTACTTTTTCACACACCAAC	5584
QY	4445	CATATCCAGGGAACAGATGCTGACCGGGTTGCCAAGCAGGACGCCAGGGTGTAA	4504	Db	5511	TCACAGAAACCTTCGAGACTCGGTGGAAAGGCCCTTATCTCGTACTTTTTCACACACCAAC	5570
Db	4434	CATATCTAGAGGAAACAGATGGCTGACCGGGTTGCCAAGCAGGACGCCAGGCTGTAA	4493	QY	5585	GGCTGTGAAAGTTCGAAGGAATCTCCACCTGTGATCCATGATCCACCTCCACGTTTAAACCGGCGCC	5644
QY	4505	CCTTCTGCCTTATAATAGAAATGCCAAAGCCCCAGAACCCAGACGACGTACACCCCTAGA	4564	Db	5571	GGCTGTGAAAGTTCGAAGGAATCTCCACCTGTGATCCATGATCCACCTCCACGTTTAAACCGGCGCC	5630
Db	4494	CCTTCTGCCTTATAATAGAAAGGCCAAAGCCCCAGAACCCAGACGACGTACACCCCTAGA	4553	QY	5645	ACCTCCCGATTCGGGGTGGAAAGCCGAAAGACTGAAATCCCTTAAAGCTTCGCGCTCCA	5704
QY	4565	AGACTGGCAAGATATAAAGATAGACCAAGTTCTCTGAGACTCCGGAAGGACCTGTCTA	4624	Db	5631	ACCTCCCGACTCGGGTGGAGAGCCGAAAGACTGAGAAATCCCTTAAAGCTTCGCGCTCCA	5690
Db	4554	AGACTGGCAAGATATAAAGATAGACCAAGTTCTCTGAGACTCCGGAAGGACCTGTCTA	4613	QY	5705	TCGCGTGGTTCCTTACTCTGTCAATAAACCTCTCAGACTAATGATGCGCATAGGAGACA	5764
QY	4625	TACCTCAGATGGAAGGAATCTGCCCCACAAAGAGGGTTAGATATGTCACACAGAT	4684	Db	5691	TCGCGTGGTTCCTTACTCTTACTCTAAACAATACTCCCGAGCCAGTAGTAAACGCTTATAGACA	5750
Db	4614	TACCTCATATGGGAAGGAATCTGCCCCACAAAGAGGGTTAGAAATATGTCCACAGAT	4673	QY	5765	GGCTGAACTCCCAATAAACCTTATCTCACTCGTGTAAATTACTGACTCCGGGACAGGTA	5824
QY	4685	ACATCGTCTAACCCACTAGGAATAAACAACCTGACAGCAGTTGGTCAGAACATCCCCCTTA	4744	Db	5751	GCTCGAAACCCCATAGACCTTTATCCCTTACCTGGCTGATTATTGACCCCTGATACGGGTG	5810
Db	4674	ACATCGTCTAACCCACTAGGAATAAACAACCTGACAGCAGTTGGTCAGAACATCCCCCTTA	4733	QY	5825	TTAATATCAACAACACTCAAGGGAGGCTCCTTTTAGGAACTGCTGGCTGATCTATACG	5884
QY	4745	TCATGTTCTGAGCTACCAAGAGTGTGACTCGGTGGTCAAAATGTTGTGCCCTGCCA	4804	Db	5811	TCACCTGTAATAGACTCGAGGTGTTGCTCCTAGAGGACCTGGTGGCTGAACTGCATT	5870
Db	4734	TCATGTTCTGAGCTACCAAGAGTGTGACTCGGTGGTCAAAATGTTGTGCCCTGCCA	4793	QY	5885	TTTGCTCTCAGACTCAGTATTTC---CTAGTCTCAGCTCACCCCCAGATATCCTCCATGCTC	5941
QY	4805	GCTGGTTAATGCTTAATCCTTCAGAAATGCTCCAGGGAAGAGACTAAGGGAGCCACCC	4864	Db	5871	TCCTGCTCGATGATTAAACCCGCTGTTAABAGCACACCTCCCAACCTAGTCCGTAGTT	5930
Db	4794	GCTGGTTAATGCTTAATCCTTCAGAAATGCTCCAGGGAAGAGACTAAGGGAGCCACCC	4853	QY	5942	ACGGATTTTATGTTGCCAGACCAACAAATAAATGGAATAAATTCGCGGAATCCCAGAG	6001
QY	4865	AGCGCTCACTGGGAAGTGGACTTCACTGAGGTAAAGCGGCTAAATACGGAACAATA	4924	Db	5931	ATGGGTCTTATGCTGCCCAGG---CACAGAGAAAGAGAAATACTGTGGGGTCTCGGG	5987
Db	4854	AGCGCTCACTGGGAAGTGGACTTCACTGAGGTAAAGCGGCTAAATACGGAACAATA	4913	QY	6002	ATTTCTTTGTAACAATGGAACCTGTAACTCTAATGATGGATATTCGGAATGSCCAA	6061
QY	4925	CCTATTGGTTTTGTAGACACCTTTTTCAGATGGGTAGAGGCTTATCTACTAAGAAAGA	4984	Db	5988	AATCTCTCTGTAGGAGATGGAGCTGCTCACCTCCAAACGATGGAGACTGGAATGSCCAA	6047
Db	4914	TCTATTGGTTTTGTAGACACCTTTTTCAGATGGGTAGAGGCTTATCTACTAAGAAAGA	4973	QY	6062	CCTCTCAGCAGATAGGGTAAAGTTTCTTATGTCAACACCTATACACCTCTCTGGAACAAT	6121
QY	4985	GACTTCAACCGTGGCTAAAAAATACCTGGAAGAAATTTTCCAGATTTTGGATACC	5044	Db	6048	TCCTCTCCAGACCGGGTAAATTTCTCCTTTGTCAA-----TTCGGGCCCGG	6095
Db	4974	GACTTCAACCGTGGCTAAGAAATACTGGAAGGAAATTTTTCAGATTTTGGATACC	5033	QY	6122	TTAATTTACCTGACCTGGATTAGAACTGGAAAGCCCCCAAGTGTCTCTCTCAGACCTTAGATT	6181
QY	5045	TAAGGTAATAGGCTCAGACAATGGTCCAGCTTTTGTGTCAGGTAAGTCAGGGACTGGC	5104	Db	6096	GCAAGTACAAAATGATGAAACTATATAAAGATAAGAGCTGCTCCCATCAGACTTAGATT	6155
Db	5034	TAAGGTAATAGGCTCAGACAATGGTCCAGCTTTTGTGTCAGGTAAGTCAGGGACTGGC	5093	QY	6182	ACCTAAAAATAAGTTTCACTGAGAAAGGAACAAAGAAATATCTTAAATGGTAAATG	6241
QY	5105	CAAGATATTGGGATGATTGGAAACTGCAATGTGCATACAGACCCCAAGCTCAGGACA	5164	Db	6156	ATCTAAAGATAAGTTTCACTGA--AAGGAAACAGGAAATATTTCAAAAGTGGATAATG	6213
Db	5094	CAAGATATTGGGATGATTGGAAACTGCAATGTGCATACAGACCCCAAGCTCAGGACA	5153	QY	6242	GTATGCTTTGGGGAATGGTATATTATGAGGCTCGGGTAAACAAACAGGCTCCATTCTTAA	6301
QY	5165	GGTAGAGAGATGAATAGAACCAATTAAGAGACCTTTACTAAATTGACCCGAGACTGG	5224	Db	6214	GTATGAGCTGGGAATAGTTTTTTTATATATGCGGG---GGAGCAGGGTCCACTTTAA	6269
Db	5154	GGTAGAGAGATGAATAGAACCAATTAAGAGACCTTTACTAAATTGACCCGAGACTGG	5213	QY	6302	CTATTCCGCTCAAAAATAAACACAGCTG---GAGCCTCAATGGCTATAGACCAAAATACGG	6358
QY	5225	CGTTAATGATTGATAGCTCTCTGCGCTTTGTGCTTTTGTAGGTTAGGAACACCCCTGG	5284	Db	6270	CCATTGCTTAGGATAGAGACGGGACAGAAACCCCTGTGGCAATGGGACCCGATAAAG	6329
Db	5214	CATTAAATGATTGATGCTCTCTGCGCTTTGTGCTTTTGTAGGTTAGGNAACACCCCTGG	5273	QY	6359	TCTTGACGGGTCAAGACCCCAACCAAGGACCCAGGACCACTCTCT-----	6405
QY	5285	ACAGTTTGGGCTGACCCCTTATGAATTAATCTACGGGGGACCCCCCTTGTGTAAGAT	5344	Db	6330	TACTGGCTGAAACAGGGGCCCCCGGCTGGAGCCACCGCATTAACCTTCCCGGTGCCCAAT	6389
Db	5274	ACAGTTTGGGCTGACCCCTTATGAATTAATCTACGGGGGACCCCCCTTGTGTAAGAT	5333	QY	6406	-----AACATAACTTCTGGATCAGACC	6427
QY	5345	TGCTTCTGATAGTGTGCTGCTGCTTTCCAGCCTTTCTCTAGGCTCAAGGC	5404	Db	6390	TAACCTCGCTGCGGCTGACATAACACAGCCGCTAGCAACAGTACCACTGGATTGATTC	6449
Db	5334	TGCTTCTGATAGTGTGCTGCTGCTTTCCAGCCTTTCTCTAGGCTCAAGGC	5393				

QY	6428	CCACTGAGCTTAACAGCA-----CGACTAAATGGGGCGAAACCTTTT	6477
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Db	6510	GTCCTCATCAGGGAGCTTTTCCAAAGCCATCAACTCCACCGACCTGATGCACTTCTTCTT	6569
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Db	6570	GTTTGGCTTGTCTATCTCTCAGGGCCCTCTTATTATGAGGGGATGGCTAAAGAAAGAAAT	6629
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Db	6750	TTTGTCTATAGTACTGTGGTTTATGACAGGCTCAGAAATCAGTATTAGTACCTGGTT	6809
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Db	6810	ATAACAGGTGGTGGGCAATGCACTACCTGGGTTAAACCCCTGTGTTCACCTCAGTCTTCA	6869
QY	6833	ACCAACTAAGATTTTTGCAATTTATGGTCCAAATGTTTCCCGAGTGTAATCATATCCCG	6892
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QY	6893	AAAAAGCAATCCTTGTGAATATGACTACAGAAATCATCGACAAAAGAGAGAACCCATAT	6952
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QY	6953	CTCTGACATTTGTGTGATGCTCGGACTTGGAGTGGCAGCAGGTGTAGGAACAGGAACAG	7012
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QY	7073	TAAACAGAGATCTCCAAGCCCTAGAAAAATCTGTGAGTAACCTGGAGGAATCCCTAACCT	7132
Db	7110	TGACAGAGATCTCCGAGCCTTAAAGAGTCTGTAGCAACCTAGAGAGTCCCTGACTT	7169
QY	7133	CCTTATCTGAAGTAGTCCCTACAGAAATAGAGGGTTAGATTTATTATTCTTAAAGAAG	7192
Db	7170	CTTTGTCTGAAGTGGTTCTACAGAAACCGAGGGGATTAGATCTGCTGTTTCTAAGAGAAG	7229
QY	7193	GAGGATTTATGTAGCCTTGAGAGAGAAATGCTGTTTTTATGTGGATCAATTCAGGGGCCA	7252
Db	7230	GTTGGTTATGTGCACCCCTTAAAGAGAAATGTTGCTCTTATGTAGATCACTCAGGAGCCA	7289
QY	7253	TCAGAGACTCATGAACAGCTTAGAGAAAGTTTGGAGAACCGTCGAAGGGGAAAGGAAA	7312
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QY	7313	CTACTCAAGGGTGGTTTTGAGGGATGGTTCAACAGGTCTCTTTTGGTTGGCTTACCCCTTT	7372
Db	7350	CTGACAGGGGTGGTTTTGAAGGATGGTTCAACAGGTCTCTCTTGGATGACCAACCTGCTTT	7409
QY	7373	CTGCTTTTAAAGGACCCCTTAATAGTCTCTCTCTGTTTACTCACAGTTGGGCCCATGATTA	7432
Db	7410	CTGCTCTGACGGGGCCCCCTAGTAGTCTGCTCTGTTACTTACAGTTGGGCCCTTGCTTAA	7469
QY	7433	TTAAACAAGTTAATTTGCCCTTCAATAGAGAACGAATAAGTGCAAGTCCAGATCATGGTACTTA	7492
Db	7470	TTAATAGGTTTGTTCCTTTGTTTAGAGAACGAAGTGAGTGCAAGTCCAGATCATGGTACTTA	7529
QY	7493	GACAAACAGTACCAAAGGCCGCTTAGC---AGGGAGAGTGGCCGCTAGCTCTACACAGTTCT	7549

Db	7530	GGCAACGATCCNAGGCCTTCTGAGCCAAGGAGAACTGACCTCTAGCCTTCCAGCTTCT	7589
Qy	7550	AAGATTAGAACTATTAAACAAGAGAGAAGTGGGGAAATGAAAGATGAAATAACAACTAA	7609
Db	7590	AAGATTAGAACTATTAAACAAGACAAGAAGTGGGGAAATGAAAGGATGAAATGCACCTAA	7649
Qy	7610	GCTAATGAGAAGCTTAAATTTGTTCTGAATTCAGAGTTGTTCCTTATAGGTAAAGAT	7669
Db	7650	CCCTCCAGAAACCCAGGAGTTAATAAAGCTCTAAATGCCCCCGAATTCAGACCCCTG	7709
Qy	7670	TAGTGTTTTTTGCTGTTTTTAAATATCCGGAAGTAAAAATAGGCCCTGAGTACATGCTCTTA	7729
Db	7710	CTGGCTGCCAGTAAATAGGTAGAAAGTCAACATTCCTATTTGTTCCAGGGCCTGCTATCCT	7769
Qy	7730	GGCATGAAACTTCTTGAACTATTTGAGATAACAAGAAAGGAGTTTCTTAACTGCTTGT	7789
Db	7770	GGCCT-AAGTAAGATACAGGAAATGAGTTGAC----TAATCGCTTATCTGGATTCTGTA	7824
Qy	7790	TTAGCTTCTGTAAAACTGGTTGCGCCATAAAGATGTTGAAATGTTGATACACATATCTTG	7849
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Qy	7850	GTGACAAATGTCCTCCCCCAACCCCGAAAATGCGCAATGTGTAACTCTTAAACAATTTA	7909
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Qy	7910	AATTAAATTGTCACCAAGAGCGGGCTCTCGAAGTTTAAATTTGACTGGT-----	7959
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Qy	7960	-----TTGTGATATTTTGAATGATTGGTTGTAAAGCGGGGCTTTGTTGTGAACCCCA	8014
Db	8005	CGGCTCTCGATATTTAAATGATTGGTTGTGACGACACAGGCTTTGTTGTGAACCCCA	8064
Qy	8015	TAAAGCTGTCGAGCTCCACACTCCGGGCGCGAGTCTCTACCCCTGCGTGGTGTACGA	8074
Db	8065	TAAAGCTGTCGCGATTCCGCACTCGGGGCGCGAGTCTCTACCCCTGCGTGGTGTACGA	8124
Qy	8075	CTGTGGCCCCAGCGCTTGGAAATAAAATTCCTCTTGTGTTTGCATCAAAAAA	8132
Db	8125	CTGTGGCCCCAGCGCTTGGAAATAAAATCTCTGCTGTTTGCATCAAAAAA	8182

RESIT.T 5

US-08-766-528-1
Sequence 1, Application US/08766528
Patent No. 6190861
GENERAL INFORMATION:
APPLICANT: Jay A. Fishman
TITLE OF INVENTION: MOLECULAR SEQUENCE OF SWINE RETROVIRUS
TITLE OF INVENTION: AND METHODS OF USE
NUMBER OF SEQUENCES: 74
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD, LLP
STREET: 60 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/766,528
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/572,645
FILING DATE: 14-DEC-1995
ATTORNEY/AGENT INFORMATION:
NAME: Louis Myers

/
/ REGISTRATION NUMBER: 35,965
/ REFERENCE/DOCKET NUMBER: MGP-038CP
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (617) 227-7400
/ TELEFAX: (617) 227-5941
/ INFORMATION FOR SEQ ID NO: 1:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 8060 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: cDNA
/ US-08-766-528-1

Query Match 67.1%; Score 5460; DB 3; Length 8060;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 5521; Conservative 0; Mismatches 10; Indels 5; Gaps 5;

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QY 4388 GGGAAACAAAGAAAG 4447
DB |||||

Qy 1921 AGAAGAAATTTGACTAAGATCTTGCTCGAGTGGTTGAAGGAAAGCAATACGGAAGAG 1980
Db 4448 AGAAGAAATTTGACTAAGATCTTGCTCGAGTGGTTGAAGGAAAGCAATACGGAAGAG 4507
Qy 1981 AGAGAGATTTTAGGAAATTTAGTTCAGGCTTAGACAGTCAAGGAACTCTGGCAATAGGA 2040
Db 4508 AGAGAGATTTTAGGAAATTTAGTTCAGGCTTAGACAGTCAAGGAACTCTGGCAATAGGA 4567
Qy 2041 CCCCACTCGAACGAGCAATGTGCATATTTGTAAGAAAGAGGACACTGGCAAGGAAT 2100
Db 4568 CCCCACTCGAACGAGCAATGTGCATATTTGTAAGAAAGAGGACACTGGCAAGGAAT 4627
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Db 4628 GCCCAAGAAAGGAAACAAAGGACCAAGGATCCTAGCTCTAGAAAGAGATAAGATTAGG 4687
Qy 2161 GGAGACGGGGTTGGGACCCCTCCCGAGCCAGGGTAACTTTGAAAGGTGGAGGGCAAC 2220
Db 4688 GGAGACGGGGTTGGGACCCCTCCCGAGCCAGGGTAACTTTGAAAGGTGGAGGGCAAC 4747
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Qy 2341 CTACCCGAAGAACAGTTGACTTTGGGAGTGGGACGGTAAACCACTCGTTTCTGTGTATAC 2400
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Qy 2401 CTGAGTGCAGACCCCTCTTAGTGTAGAGACTTATTGACCAAGTGGGAGCACAATTTT 2460
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Db 5046 TCCAAATTAGATGACGAATATCGACTATACTTCCCTTAGTAAAGCTTGATCAAAATATAC 5105
Qy 2581 AATTCTGTTGGAAACAGTTTCCCAAGCTGGGAGAAACCGCAGGATGGGTTGGCAA 2640
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Qy 2761 AACAGGGCATCCTAGTTCCTGTCCAATCTCCCTGGAATATCTCCCTGTCTACCGGTTAGAA 2820
Db 5286 AACAGGGCATCCTAGTTCCTGTCCAATCTCCCTGGAATATCTCCCTGTCTACCGGTTAGAA 5345
Qy 2821 AGCCTGGGACTAATGACTATCGACCAGTACAGGACTTCAGAGAGGTCAATAAAGGGTGC 2880
Db 5346 AGCCTGGGACTAATGACTATCGACCAGTACAGGACTTCAGAGAGGTCAATAAAGGGTGC 5405
Qy 2881 AGGATATACCCCAACAGTCCCGAACCTTATAACTCTTGTGTCTCTCCACCCCAAC 2940
Db 5406 AGGATATACCCCAACAGTCCCGAACCTTATAACTCTTGTGTCTCTCCACCCCAAC 5465
Qy 2941 GGAGCTGTGTATACAGTATTGGAATTTAAAGGATGCTTCTTCTGCTGTAGATTACACCCA 3000
Db 5466 GGAGCTGTGTATACAGTATTGGAATTTAAAGGATGCTTCTTCTGCTGTAGATTACACCCA 5525
Qy 3001 CTAGCCAAACCACTTTTTCCTTCGAATGGAGAGATCCAGGTACGGGAAAGACCCGGGACG 3060

Db 5526 CTAGCCAAACCACTTTTTCCTTCGAATGGAGAGATCCAGGTACGGGAAGAACCGGGACG 5585
Qy 3061 TCACCTTGGACCCGACTGCCCCCAAGGGTTCAAGAACTCCCCGACCATCTTTTGAAGAAAGCCC 3120
Db 5586 TCACCTTGGACCCGACTGCCCCCAAGGGTTCAAGAACTCCCCGACCATCTTTTGAAGAAAGCCC 5645
Qy 3121 TACACAGAGACCTTGGCCAACTTCAGGATCCAAACACCTTCAGGTGACCTCTCTCAGTACG 3180
Db 5646 TACACAGAGACCTTGGCCAACTTCAGGATCCAAACACCTTCAGGTGACCTCTCTCAGTACG 5705
Qy 3181 TGGATGACCTGCTTCTGGCGGAGCCACCAACAGAGACTGCTTAGAAGGACCAAGAGGAC 3240
Db 5706 TGGATGACCTGCTTCTGGCGGAGCCACCAACAGAGACTGCTTAGAAGGACCAAGAGGAC 5765
Qy 3241 TACTGCTTGGAAATTTGCTGACCTAGGCTACAGAGCTCTGCTTAAGAAAGGCCCCAGATTGCA 3300
Db 5766 TACTGCTTGGAAATTTGCTGACCTAGGCTACAGAGCTCTGCTTAAGAAAGGCCCCAGATTGCA 5825
Qy 3301 GGAGAGAGGTAAACATCTTGGGGTACAGTTTGGGGAACGGGACGCGATGGCTGACGAGG 3360
Db 5826 GGAGAGAGGTAAACATCTTGGGGTACAGTTTACGGGACGGGACGCGATGGCTGACGAGG 5885
Qy 3361 CACGGAAGAAACCTGTAGTCCAGATACGGGCCCAACACAGCCCAACAAATGAGAGAGT 3420
Db 5886 CACGGAAGAAACCTGTAGTCCAGATACGGGCCCAACACAGCCCAACAAATGAGAGAGT 5945
Qy 3421 TTTTGGGGACAGCTTGGATTTTGCAGACTGTGGATCCCGGGGTTTGGCAGCTTTAGCAGGCC 3480
Db 5946 TTTTGGGGACAGCTTGGATTTTGCAGACTGTGGATCCCGGGGTTTGGCAGCTTTAGCAGGCC 6005
Qy 3481 CACTCTACCCGCTAACCAAGAAAGGGGAAATTTCTCTGGGCTCTGAGACCAAGAGG 3540
Db 6006 CACTCTACCCGCTAACCAAGAAAGGGGAAATTTCTCTGGGCTCTGAGACCAAGAGG 6065
Qy 3541 CATTTGATGTATCAAAAAGSCCTGTGAGCGCACCTGTCTTGCCCTCTCCCTGACGTAA 3600
Db 6066 CATTTGATGTATCAAAAAGSCCTGTGAGCGCACCTGTCTTGCCCTCTCCCTGACGTAA 6125
Qy 3601 CTAACCCCTTTTACCCCTTTATGTGTGATGAGCCTTAAGGGAGTAGCCCGGGGAGTTTAAACCC 3660
Db 6126 CTAACCCCTTTTACCCCTTTATGTGTGATGAGCCTTAAGGGAGTAGCCCGGGGAGTTTAAACCC 6185
Qy 3661 AAAACCTTAGGACCAATGGAGAGACCTGTGCGCTACCTGTCTCAAGAAAGCTCGATCCTGTAG 6245
Db 6186 AAAACCTTAGGACCAATGGAGAGACCTGTGCGCTACCTGTCTCAAGAAAGCTCGATCCTGTAG 6245
Qy 3721 CCAGTGTGTGGCCCATATGCTGCTGAGGCTATCGCAGCTGTGGCCATCTGCTCAAGGAGC 3780
Db 6246 CCAGTGTGTGGCCCATATGCTGCTGAGGCTATCGCAGCTGTGGCCATCTGCTCAAGGAGC 6305
Qy 3781 CTGACAAATTGACTTTGGGAC- AGAATATTAATCTGTAATAGCCCCCATGCTTGGAGAAC 3839
Db 6306 CTGACAAATTGACTTTGGGACAGAAATAAATCTGTAATAGCCCCCATGCTTGGAGAAC 6365
Qy 3840 ATCGTTGGGACGCCACAGACCGATGGATGACCAACGCCCGCATGACCCACTATCAAAAGC 3899
Db 6366 ATCGTTGGGACGCCACAGACCGATGGATGACCAACGCCCGCATGACCCACTATCAAAAGC 6425
Qy 3900 CTGCTTCTCAGAGAGGGTCAAGTTCGCTCCACAGCGGCTCTCAACCCCTGCCACTCTT 3959
Db 6426 CTGCTTCTCAGAGAGGGTCAAGTTCGCTCCACCAACCGCTCTCAACCCCTGCCACTCTT 6485
Qy 3960 CTGCTTGAAGAGACTGATGAACCAAGTCTATGATGCTTCCCATCAACTTATGTTGAGGAG 4019
Db 6486 CTGCTTGAAGAGACTGATGAACCAAGTCTATGATGCTTCCCATCAACTTATGTTGAGGAG 6545
Qy 4020 ACTGGGGTCCCAAGAGCTTTACAGACATACCGCTGACTGGAGAGAGTCTAACCTGGTTC 4079
Db 6546 ACTGGGGTCCCAAGAGCTTTACAGACATACCGCTGACTGGAGAGAGTCTAACCTGGTTC 5605
Qy 4080 ACTGACGGAAGCAGCTATGTGTGTGAAGGATGGCTGGGGCGCGGTGTGGAC 4139

Db 6606 ACTGACGGAAGCAGCTATGTGTGGGAAGTAAGAGATGGCTGGGGCGGGTGTGGAC 6665
QY 4140 GGGACCCGACGATCTGGGCGACGACCTCGCCGGAAGAACTTTCAGCACAAAAGGCTGAG 4199
Db 6666 GGGACCCGACGATCTGGGCGACGACCTCGCCGGAAGAACTTTCAGCACAAAAGGCTGAG 6725
QY 4200 CTCATGGCCCTCAGCAAGCTTTTGGGCTGGGCGGAAGGAATTCATATAACATTTATAGC 4259
Db 6726 CTCATGGCCCTCAGCAAGCTTTTGGGCTGGGCGGAAGGAATTCATATAACATTTATAGC 6785
QY 4260 GACAGAGTATGCTTTTGGGCTGACACGTCACATGAGGCGCATCTATATAACAAAGGGG 4319
Db 6786 GACAGAGTATGCTTTTGGGCTGACACGTCACATGAGGCGCATCTATATAACAAAGGGG 6845
QY 4320 TTGCTTACCTCAGCAGGAGGGAATAAAGAAACAAAGAGGAATTCCTAAGCCCTATTAGAA 4379
Db 6846 TTGCTTACCTCAGCAGGAGGGAATAAAGAAACAAAGAGGAATTCCTAAGCCCTATTAGAA 6905
QY 4380 GCGGTACATTTACCAAAAAGGCTAGCTATATACATGCTCTGAGCATCAGAAAGCTAAA 4439
Db 6906 GCGGTACATTTACCAAAAAGGCTAGCTATATACATGCTCTGAGCATCAGAAAGCTAAA 6965
QY 4440 GATCTCATATCCAGAGAAACAGATGGCTGACCGGGTTGCCNAGCAGGACGCCAGGCT 4499
Db 6966 GATCTCATATCCAGAGGAACCAAGATGGCTGACCGGGTTGCCNAGCAGGACGCCAGGCT 7025
QY 4500 GTTAACTTCTGCTATATAGAAATGCCAAAGCCCGAGAACCCAGACGACAGTACACC 4559
Db 7026 GTTAACTTCTGCTATATAGAAATGCCAAAGCCCGAGAACCCAGACGACAGTACACC 7085
QY 4560 CTAGAGACTGGCAAGAGATAAAAAAGATAGACCACTTCTGAGACTCCGGAAGGGACC 4619
Db 7086 CTAGAGACTGGCAAGAGATAAAAAAGATAGACCA- TTCTCTGAGACTCCGGAAGGGACC 7144
QY 4620 TGTATACCTCAGATGGGAAGAAATCTGCGCCCAACAAAGAGGGTTAGAAATGTCCAA 4679
Db 7145 TGTATACCTCAGATGGGAAGAAATCTGCGCCCAACAAAGAGGGTTAGAAATGTCCAA 7204
QY 4680 C-AGATACATCGTCTAACCCACTAGGAACCTAGAACCTGACAGCTGGTCTAGAACATC 4738
Db 7205 CAAGATACATCGTCTAACCCACTAGGAACCTAGAACCTGACAGCTGGTCTAGAACATC 7264
QY 4739 CCTTATCATGTTCTCAGGCTACAGAGTGGCTGACTCGGTGGTCAAAATTTGTGTC 4798
Db 7265 CCTTATCATGTTCTCAGGCTACAGAGTGGCTGACTCGGTGGTCAAAATTTGTGTC 7324
QY 4799 CTGCCAGCTGGTTAAATGCTTAATCTTCCAGATGCTCTCAGGAAGAGACTAAGGGGAG 4858
Db 7325 CTGCCAGCTGGTTAAATGCTTAATCTTCCAGATGCTCTCAGGAAGAGACTAAGGGGAG 7384
QY 4859 CCACCCAGGCGCTCACTGGGAAGTGGACTTCACTGAGGTAAAGCCGGCTAAATACGAAA 4918
Db 7385 CCACCCAGGCGCTCACTGGGAAGTGGACTTCACTGAGGTAAAGCCGGCTAAATACGAAA 7444
QY 4919 CAAATACCTATTGGTTTTGTAGACACCTTTTCAGGATGGGTAGAGGCTTATCCTACTAA 4978
Db 7445 CAAATACCTATTGGTTTTGTAGACACCTTTTCAGGATGGGTAGAGGCTTATCCTACTAA 7504
QY 4979 GAAAGAGACTTCAACCGTGGTCTAAAAAATCTGGAAGAAATTTTTCCTAAGATTGG 5038
Db 7505 GAAAGAGACTTCAACCGTGGTCTAAAAAATCTGGAAGAAATTTTTCCTAAGATTGG 7564
QY 5039 AATACCTAAGTAAATAGGCTCAGACAAATGGTCCAGCTTTTGGTCCAGGTAAGTCAGGG 5098
Db 7565 AATACCTAAGTAAATAGGCTCAGACAAATGGTCCAGCTTTTGGTCCAGGTAAGTCAGGG 7624
QY 5099 ACTGGCAAGATATTGGGGATTGATTGGAACTGCAATTTGTCATACAGACCCCAAGCTC 5158
Db 7625 ACTGGCAAGATATTGGGGATTGATTGGAACTGCAATTTGTCATACAGACCCCAAGCTC 7684
QY 5159 AGGACAGGTAGAGAGATGATAGAACCATTAAGAGACCTTACTAAATGACCCGGA 5218
Db 7685 AGGACAGGTAGAGAGATGATAGAACCATTAAGAGAGACCTTACTAAATGACCCGGA 7744

QY 5219 GACTGCGTTAATGATGATAGTCTCTCGCCCTTTGTGCTTTTAGGGTTAGGAACAC 5278
Db 7745 GACTGCGTTAATGATGATGATAGTCTCTCGCCCTTTGTGCTTTTAGGGTTAGGAACAC 7804
QY 5279 CCCTGGACAGTTTGGGCTGACCCCTATGAATTAATCTCTACGGGGGACCCCCCATTTGGT 5338
Db 7805 CCCTGGACAGTTTGGGCTGACCCCTATGAATTAATCTCTACGGGGGACCCCCCATTTGGT 7864
QY 5339 AGAAATTTGCTTCTGTACATAGTGTGACCTGCTGCTTTTCCAGCCCTTTGTCTTAGGCT 5398
Db 7865 AGAAATTTGCTTCTGTACATAGTGTGCTGCTTTTCCAGCCCTTTGTCTTAGGCT 7924
QY 5399 CAAGGACCTTTGAGTGGTGAGACAACAGAGCTGGAGGCAACTCCGGGAGGCTTACTCAGG 5458
Db 7925 CAAGGACCTTTGAGTGGTGAGACAACAGAGCTGGAGGCAACTCCGGGAGGCTTACTCAGG 7984
QY 5459 AGAGGAGACTTTGAGATCCCATGCTTTCCAAAGTGGGAGATTACGTCTAGCTTAGACG 5518
Db 7985 AGAGGAGACTTTGAGATCCCATGCTTTCCAAAGTGGGAGATTACGTCTAGCTTAGACG 8044
QY 5519 CCACCGTGCAGGAAC 5534
Db 8045 CCACCGTGCAGGAAC 8060

RESULT 6

US-09-661-858-1
; Sequence 1, Application US/09661858
; Patent No. 669663
; GENERAL INFORMATION:
; APPLICANT: Jay A. Fishman
; TITLE OF INVENTION: MOLECULAR SEQUENCE OF SWINE RETROVIRUS
; AND METHODS OF USE
; NUMBER OF SEQUENCES: 74
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 60 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA: US/09/661,858
; FILING DATE: 14-Sep-2000
; PRIOR APPLICATION NUMBER:
; APPLICATION NUMBER: 08/766,528
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Louis Myers
; REGISTRATION NUMBER: 35,965
; REFERENCE/DOCKET NUMBER: MGP-038CP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)227-5941
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8060 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-661-858-1

Query Match 67.1%; Score 5460; DB 3; Length 8060;
Best Local Similarity 99.7%; Pred.No. 0;
Matches 5521; Conservative 0; Mismatches 10; Indels 5; Gaps 5;

Qy	1	GCCTGGTGTACGACTGTGGGCCCCAGCGCGCTTGGAATAAAAAATCCTTCTGCTGTTTGCA	60	1081	GAGCTCCGGCGGTGGAGGACCTCTCGAGGACTCGGAGCCGGAGGGCGCCACCCCGG	1140
Db	2528	GGTGTGTGTACGACTGTGGGCCCCAGCGCGCTTGGAATAAAAAATCCTTCTGCTGTTTGCA	2587	3608	GAGCTCCGGCGGTGGAGGACCTCTCGAGGACTCGGAGCCGGAGGGCGCCACCCCGG	3667
Qy	61	TCAAGACCGCTTCTCGTAGTGATTAAGGGAGTCGCTTTTCGAGGCTCGAGGTTCTT	120	1141	AGCGGACAGACGAGATCGGACATTACCGCTCGCAGGTACGGCCCTCCACACACCGGGG	1200
Db	2588	TCAAGACCGCTTCTCGTAGTGATTAAGGGAGTCGCTTTTCGAGGCTCGAGGTTCTT	2647	3668	AGCGGACAGACGAGATCGGACATTACCGCTCGCAGGTACGGCCCTCCACACACCGGGG	3727
Qy	121	TTTTCTGGTCTTACATTTGGGGGCTCGTCGGGATCTGTGCGGCCACCCCTAACACCG	180	1201	GCCAAATTCAGCCCTCCAGTATTGGCCCTTTCTTCTGAGATCTCTATAATTGGAAAA	1260
Db	2648	TTTTCTGGTCTTACATTTGGGGGCTCGTCGGGATCTGTGCGGCCACCCCTAACACCG	2707	3728	GCCAAATTCAGCCCTCCAGTATTGGCCCTTTCTTCTGAGATCTCTATAATTGGAAAA	3787
Qy	181	AGAACCGACTTGGAGGTAAGGATCCTCTTTTTTAACGTGTATGCAATGACCGGCCGC	240	1261	CTAACCAATCCCTTTCTCGAGGATCCCAACGCCCTCACGGGTTGGTGAGTCCCTTA	1320
Db	2708	AGAACCGACTTGGAGGTAAGGATCCTCTTTTTTAACGTGTATGCAATGACCGGCCGC	2767	3788	CTAACCAATCCCTTTCTCGAGGATCCCAACGCCCTCACGGGTTGGTGAGTCCCTTA	3847
Qy	241	GTCTCTGTCTGAGTGTCTGTTTTCAGTGTGCGGCTTTCGGTTTGGAGTGTCTCTC	300	1321	TGTTCTCTCACCGCTTACTTGGGATGATTGTCAACAGCTCTCGCAGACACTCTTTCACAA	1380
Db	2768	GTCTCTGTCTGAGTGTCTGTTTTCAGTGTGCGGCTTTCGGTTTGGAGTGTCTCTC	2827	3848	TGTTCTCTCACCGCTTACTTGGGATGATTGTCAACAGCTCTCGCAGACACTCTTTCACAA	3907
Qy	301	AGGCGTTAAGGCTGGGGACTGTGATCAGCAGACGTGTAGGAGGATCACAGGCTGCTG	360	1381	CCGAGGACGAGAGAGAAATCTATTAGAGCTAGAAAAATGTTCTCTGGGCGCGACGGC	1440
Db	2828	AGGCGTTAAGGCTGGGGACTGTGATCAGCAGACGTGTAGGAGGATCACAGGCTGCTG	3887	3908	CCGAGGACGAGAGAGAAATCTATTAGAGCTAGAAAAATGTTCTCTGGGCGCGACGGC	3967
Qy	361	CCCTGGGGACGCCCGGGAGCTGAGGAGAGCCAGGAGCGCTGGTGTCTCTTACTGTC	420	1441	GACCCACGCGGTTGCAAAATGAGATTGACATGGGATTTCCCTTAATCGCCCGGTTGGG	1500
Db	2888	CCCTGGGGAGCGCCCGGGAGGTGAGGAGCCAGGAGCGCTGGTGTCTCTTACTGTC	2947	3968	GACCCACGCGGTTGCAAAATGAGATTGACATGGGATTTCCCTTAATCGCCCGGTTGGG	4027
Qy	421	GGTCAGAGGACCGAATCTGTTGTGAAGCGAAAGCTTCCCTCCCGGACCGTCCGACT	480	1501	ACTACACACGCTGAAGGTAGGAGAGCTTGAATACTATCGCCAGGCTCTGTGTGGCGG	1560
Db	2948	GGTCAGAGGACCGAATCTGTTGTGAAGCGAAAGCTTCCCTCCCGGACCGTCCGACT	3007	4028	ACTACACACGCTGAAGGTAGGAGAGCTTGAATACTATCGCCAGGCTCTGTGTGGCGG	4087
Qy	481	CTTTTGCTGTGTGGAAGACGTGGAGCGGTACAGTGTGTCTGGATCTGTGTTCTG	540	1561	GTCTCCGGGGCGCTCAAGACGGCCCACTAATTTGGCTAAGAGAGTGAATGTCAGG	1620
Db	3008	CTTTTGCTGTGTGGAATACGTGGACGGTCAAGTGTGTCTGGATCTGTGTTCTG	3067	4088	GTCTCCGGGGCGCTCAAGACGGCCCACTAATTTGGCTAAGAGAGTGAATGTCAGG	4147
Qy	541	TTTTGTGTGTCTTGT	600	1621	GACCGAATGAACCCCTCTGTTTTCTTGGAGGCTCTTGGAAAGCTTTCAGGCGGTACA	1680
Db	3068	TTTTGTGTGTCTTGT	3127	4148	GACCGAATGAACCCCTCTGTTTTCTTGGAGGCTCTTGGAAAGCTTTCAGGCGGTACA	4207
Qy	601	CGACCCCTCTTAGTTTGACTCTCGACCAATGGACTGAAGTTAAATCCAGGCTCATATT	660	1681	CCCTTTTGTATCCACCTCAGAGGCCCAAAAGCTCAGTGCCTTTGGCCCTTATAGGAC	1740
Db	3128	CGACCCCTCTTAGTTTGACTCTCGACCAATGGACTGAAGTTAAATCCAGGCTCATATT	3187	4208	CCCTTTTGTATCCACCTCAGAGGCCCAAAAGCTCAGTGCCTTTGGCCCTTATAGGAC	4267
Qy	661	TGTCAAGTTTCAAGAGGACCTTGGCAGACTTCTGTGTCTCTGAAATGGCGGACAT	720	1741	AGTCAGGCTTGGATATTAGAAAGAGCTTTCAGAGACTGGAAGGGTTACAGGAGGCTGAGT	1800
Db	3188	TGTCAAGTTTCAAGAGGACCTTGGCAGACTTCTGTGTCTCTGAAATGGCGGACAT	3247	4268	AGTCAGGCTTGGATATTAGAAAGAGCTTTCAGAGACTGGAAGGGTTACAGGAGGCTGAGT	4327
Qy	721	TGATGTTGGATGGCCATCAGAGGGACCTTTAATCTGAGATTATCTGGCTGTTAAAG	780	1801	TACGTGATCTAGTGAAGGACGAGAAAGTATTATTACAAAGGGAGACAGAAAGAAA	1860
Db	3248	TGATGTTGGATGGCCATCAGAGGGACCTTTAATCTGAGATTATCTGGCTGTTAAAG	3307	4328	TACGTGATCTAGTGAAGGACGAGAAAGTATTATTACAAAGGGAGACAGAAAGAAA	4387
Qy	781	CAGTTATTATTTTCAGACTGGACCCGGCTCTCATCCCGATCAGAGGCCCTATATCTTACGT	840	1861	GGGAAACAAAGAAAAGAGAGAAAGAGAGAAAGGGAGAAAGAGTAAATAACCGCAAG	1920
Db	3308	CAATTTATTTTTCAGACTGGACCCGGCTCTCATCCCGATCAGAGGCCCTATATCTTACGT	3367	4388	GGGAAACAAAGAAAAGAGAGAAAGAGAGAAAGGGAGAAAGAGTAAATAACCGCAAG	4447
Qy	841	GGCAAGATTGTGACAGGATCTTCGCGCATGGGTTAAACCAATGGTGTAATAGCCAGAA	900	1921	AGAAAGATTTCCTACTAAGATCTTGGCTGAGTGGTTTGAAGGGAAAAACAATACGAAAGAG	1980
Db	3368	GGCAAGATTGTGACAGGATCTTCGCGCATGGGTTAAACCAATGGTGTAATAGCCAGAA	3427	4448	AGAAAGATTTCCTACTAAGATCTTGGCTGAGTGGTTTGAAGGGAAAAACAATACGAAAGAG	4507
Qy	901	AGCAGGTCCTCGAATTTCTGGCTCTTGGAGAGAAAACAAACACTCGGCTGAAAAGTCA	960	1981	AGAGAGATTTTAGGAAAAATTAGGTCAGGCCCTTAGACAGTCAAGGAACTCTGGGCAATAGGA	2040
Db	3428	AGCAGGTCCTCGAATTTCTGGCTCTTGGAGAGAAAACAAACACTCGGCTGAAAAGTCA	3487	4508	AGAGAGATTTTAGGAAAAATTAGGTCAGGCCCTTAGACAGTCAAGGAACTCTGGGCAATAGGA	4567
Qy	961	AGCCCTCTCTCATATCTACCCCGAGATTGAGGAGCCACCGGCTTGGCGGAAACCCCAAT	1020	2041	CCCACTCGACAGAACCAATGTGCATATTGTAAAGAGAGGACACTCTGGGCAAGGAACT	2100
Db	3488	AGCCCTCTCTCATATCTACCCCGAGATTGAGGAGCCACCGGCTTGGCGGAAACCCCAAT	3547	4568	CCCACTCGACAGAACCAATGTGCATATTGTAAAGAGAGGACACTCTGGGCAAGGAACT	4627
Qy	1021	CTGTTTCCCGCACCCCTTATCTGGCAGAGGTTGCCGAGGGGACCCCTTGGCCCTCTG	1080	2101	GCCCCAAGAGGGAAACAAAGGATCTTAGATCTCTAGAGAGATTAAGATTAGG	2160
Db	3548	CTGTTTCCCGCACCCCTTATCTGGCAGAGGTTGCCGAGGGGACCCCTTGGCCCTCTG	3607	4628	GCCCCAAGAGGGAAACAAAGGATCTTAGATCTCTAGAGAGATTAAGATTAGG	4687
				2161	GGAGACGGGTTTCGGACCCCTCTCCCGAGCCGAGGTTAACTTTTGAAGGTGGAGGGGCAAC	2220

Db	4688	 GGAGACGGGGTTGCGGACCCCTCCCGAGCCCGAGGGTAATCTTGAAGGTTGGAGGGGCAAC	5825	5766	TACTGCTGGAATTTGTTGACCTAGGCTACAGAGCCCTCTGCTAAGAAGGCCAGATTGTGCA	Qy
Qy	2221	CAGTTTCAGTTCTCTGGTTGATACCGGAGCGAAACATTCAGTGTCTACTACAGCCATTTAGGAA	3360	3301	GGAGAGAGGTAAACATATCTTGGGGTACAGTTTCGGGAACGGGACGCGATGGCTGACCGAGG	Db
Db	4748	CAGTTGAGTTCTCTGGTTGATACCGGAGCGAAACATTCAGTGTCTACTACAGCCATTTAGGAA	5885	5826	GGAGAGAGGTAAACATATCTTGGGGTACAGTTTCGGGAACGGGACGCGATGGCTGACCGAGG	Qy
Qy	2281	AACATAAAGATAAAAATCTCTGGGTGATGGGTGCCACAGGCGAAACAAACAGTAGTATCCATGGA	3420	3361	CACGGAAGAAAACCTGTAGTCCAGATACCGGCCCCCAACCAAGCCCAACAAATGAGAGACT	Db
Db	4808	AACATAAAGATAAAAATCTCTGGGTGATGGGTGCCACAGGCGAAACAAACAGTAGTATCCATGGA	5945	5886	CACGGAAGAAAACCTGTAGTCCAGATACCGGCCCCCAACCAAGCCCAACAAATGAGAGACT	Qy
Qy	2341	CTACCCGAAGACAGTTGACTTGGGAGTGGGACGGGTAAACCACTCGTTTCTGGTCAATAC	3480	3421	TTTTGGGGACAGCTGGATTTTTCAGACTGCTGTGATCCCGGGTTTTCGACACTTAGCAGCCCC	Db
Db	4867	CTACCCGAAG - ACAGTTGACTTGGGAGTGGGACGGGTAAACCACTCGTTTCTGGTCAATAC	6005	5946	TTTTGGGGACAGCTGGATTTTTCAGACTGCTGTGATCCCGGGTTTTCGACACTTAGCAGCCCC	Qy
Qy	2401	CTGAGTGGCCAGCACCCCTCTTAGGTAGAGACTTATTGACCAAGATGGGAGCACAATTT	3540	3481	CACCTCTACCCGCTAAACCAAGAAAAGGGGAATTTCTCTGGGCTCTCTGAGCACCAGAAAG	Db
Db	4926	CTGAGTGGCCAGCACCCCTCTTAGGTAGAGACTTATTGACCAAGATGGGAGCACAATTT	6065	6006	CACCTCTACCCGCTAAACCAAGAAAAGGGGAATTTCTCTGGGCTCTCTGAGCACCAGAAAG	Qy
Qy	2461	CTTTTGAACAAGGGAAACAGAGTGTCTGCAATTAACAAACCTATCACTGTGTTGACCC	3600	3541	CAATTTGATGCTATCAAAAAGGCCCTGTGAGCGACCTGCTCTGGCCCTCCCTGACGTAA	Db
Db	4986	CTTTTGAACAAGGGAAACAGAGTGTCTGCAATTAACAAACCTATCACTGTGTTGACCC	6125	6066	CAATTTGATGCTATCAAAAAGGCCCTGTGAGCGACCTGCTCTGGCCCTCCCTGACGTAA	Qy
Qy	2521	TCCAATTAGATGACGAATATCGACTATATCTCTCCCTAGTAAGACCTGATCAAAATATAC	3660	3601	CTAAACCCCTTTACCCCTTTTATGTGGATGAGCGTAAGGAGTAGCCCGGGAGTTTTAAACC	Db
Db	5046	TCCAATTAGATGACGAATATCGACTATATCTCTCCCTAGTAAGACCTGATCAAAATATAC	6185	6126	CTAAACCCCTTTACCCCTTTTATGTGGATGAGCGTAAGGAGTAGCCCGGGAGTTTTAAACC	Qy
Qy	2581	AAATCTGGTTGGAAACAGTTTCCCAAGCCTGGGCAGAAACCGCAGGAGTGGTTTGGCAA	3720	3661	AAACCCCTAGGACCATGGAGAGACCTGTGCGCCTACCTGTCAAAGAGCTCGATCCTGTAG	Db
Db	5106	AAATCTGGTTGGAAACAGTTTCCCAAGCCTGGGCAGAAACCGCAGGAGTGGTTTGGCAA	6245	6186	AAACCCCTAGGACCATGGAGAGACCTGTGCGCCTACCTGTCAAAGAGCTCGATCCTGTAG	Qy
Qy	2641	AGCAAGTTCCTCCACCAAGTTATTCAACTGAAGCCAGTGCACACCAAGTGTCACTGAGAC	3780	3721	CAAGTGGTTGGCCCATATATGCCCTGAAGGCTATCGAGCTGTGGCCATACCTGTCAAGGACG	Db
Db	5166	AGCAAGTTCCCCACCAAGTTATTCAACTGAAGCCAGTGCACACCAAGTGTCACTGAGAC	6305	6246	CAAGTGGTTGGCCCATATATGCCCTGAAGGCTATCGAGCTGTGGCCATACCTGTCAAGGACG	Qy
Qy	2701	AGTACCCCTTGAGTAAGAGCTCAAGAGGAATTCGGCGCGATGTCCAAAGATTATATCC	3839	3781	CTGACAAATTTGACTTTGGGAC - AGAATATAACTGTAAATAGCCCCCATGATGGAGAAC	Db
Qy	5226	AGTACCCCTTGAGTAAGAGCTCAAGAGGAATTCGGCGCGATGTCCAAAGATTATATCC	6365	6306	CTGACAAATTTGACTTTGGGACCAAGATAATACTGTAAATAGCCCCCATGATGGAGAAC	Qy
Qy	2761	ACAGGGCATCTAGTTCCCTGTCCTCAATCTCCCTGGAACTCTCCCTGCTACCGTTAGAA	3899	3840	ATCGTTTCGGCAGCCCCCAGACCGATGGATGACCAACGCCCGCATGATCAAAAGC	Db
Db	5286	ACAGGGCATCTAGTTCCCTGTCCTCAATCTCCCTGGAACTCTCCCTGCTACCGTTAGAA	6425	6366	ATCGTTTCGGCAGCCCCCAGACCGATGGATGACCAACGCCCGCATGATCAAAAGC	Qy
Qy	2821	AGCCTGGGACTAATGACTATCGACACAGTACAGGACTTGAGAGAGGTCAATAACGGGTGC	3959	3900	CTGCTTCTCAGAGAGGCTCAGTTTCGCTCCACAGCGCTCTCAACCTGCGCATCTTT	Db
Qy	5346	AGCCTGGGACTAATGACTATCGACACAGTACAGGACTTGAGAGAGGTCAATAACGGGTGC	6485	6426	CTGCTTCTCAGAGAGGCTCAGTTTCGCTCCACCAACCGCTCTCAACCTGCGCATCTTT	Qy
Qy	2881	AGGATATACCCCAACAGTCCCGAAACCTTTATAACCTCTTGTGTCTCTCCACCCCAAC	4019	3960	CTGCTTGAAGAGACTGATGAACCAAGTACTCATGATTGCCATCAACTATTGATTGAGGAG	Db
Qy	5406	AGGATATACCCCAACAGTCCCGAAACCTTTATAACCTCTTGTGTCTCTCCACCCCAAC	6545	6486	CTGCTTGAAGAGACTGATGAACCAAGTACTCATGATTGCCATCAACTATTGATTGAGGAG	Qy
Qy	2941	GGAGCTGGTATACAGTATTGGACTTAAGGATGCTTCTCTGCTGAGATTACACCCCA	4079	4020	ACTGGGGTCCGCAAGGACCTTACAGACATACCGCTGACTGGAGAGTGTCTAAGCTGTTTC	Db
Qy	5466	GGAGCTGGTATACAGTATTGGACTTAAGGATGCTTCTCTGCTGAGATTACACCCCA	6605	6546	ACTGGGGTCCGCAAGGACCTTACAGACATACCGCTGACTGGAGAGTGTCTAAGCTGTTTC	Qy
Qy	3001	CTAGCCAAACCACTTTTGGCTTCGAATGGAGAGTCCAGGTACGGGAAGAACCGGGCAGC	4139	4080	ACTGACGGAAGCAGCTATGTGTGGAAGGTAAAGAGATGGCTGGGGCGGGGTGGTGGAC	Db
Qy	5526	CTAGCCAAACCACTTTTGGCTTCGAATGGAGAGTCCAGGTACGGGAAGAACCGGGCAGC	6665	6606	ACTGACGGAAGCAGCTATGTGTGGAAGGTAAAGAGATGGCTGGGGCGGGGTGGTGGAC	Qy
Qy	3061	TCACCTGGACCCGACTGCCCCAAGGGTTCAAGAACTCCCGGACCATCTTTTGACGAAGCCC	4199	4140	GGGACCCGACCATCTGGGCCAGCAGCTGCCGGAAGGAATTTTCAGCACAAAAGGCTGAG	Db
Qy	5586	TCACCTGGACCCGACTGCCCCAAGGGTTCAAGAACTCCCGGACCATCTTTTGACGAAGCCC	6725	6666	GGGACCCGACCATCTGGGCCAGCAGCTGCCGGAAGGAATTTTCAGCACAAAAGGCTGAG	Qy
Qy	3121	TACACAGAGACCTGGCCAACTTCAGGATCCAAACCTCAGGTGACCTCTCCAGTACG	4259	4200	CTCATGGCCCTCAGCGAAGCTTTTGGCGGTGGCGGAGGGAATTTCCATAAATTTATACG	Db
Qy	5646	TACACAGAGACCTGGCCAACTTCAGGATCCAAACCTCAGGTGACCTCTCCAGTACG	4319	6726	CTCATGGCCCTCAGCGAAGCTTTTGGCGGTGGCGGAGGGAATTTCCATAAATTTATACG	Qy
Qy	3181	TGGATGACCTGCTTCTGGCGGAGCCACCAACAGGACTCTTTAGAGGACCAAGAGGCAC	6845	4260	GACAGAGGTATGCTTTGGGACTGACAGTATCATGGGGCCATCTATAAACAAGGGGG	Db
Qy	5706	TGGATGACCTGCTTCTGGCGGAGCCACCAACAGGACTCTTTAGAGGACCAAGAGGCAC	4379	6786	GACAGAGGTATGCTTTGGGACTGACAGTATCATGGGGCCATCTATAAACAAGGGGG	Qy
Qy	3241	TACTGCTGGAATTTGCTGACTTAGGCTACAGAGCTCTGCTAAGAGAGGCCAGATTGCA	6905	4320	TTGCTTACCTCAGCAGGGAGGGAATAAAGAAACAAAGAGGAAATTTCTAAGCCCTATTAGAA	Db
				6846	TTGCTTACCTCAGCAGGGAGGGAATAAAGAAACAAAGAGGGAATTTCTAAGCCCTATTAGAA	

QY 4380 GCCGTACATTTACCAAAAGGCTAGCTATTATATACACTGTCTCTGACATCAGAAAGCTAAA 4439
DB 6906 GCCGTACATTTACCAAAAGGCTAGCTATTATATACACTGTCTCTGACATCAGAAAGCTAAA 6965
QY 4440 GATCTCATATCCAGAGGAAACAGATGGCTGACCGGGTTGCCAAGAGGAGGCCAGGGT 4499
DB 6966 GATCTCATATCCAGAGGAAACAGATGGCTGACCGGGTTGCCAAGAGGAGGCCAGGGT 7025
QY 4500 GTTAACTCTTCCCTATTAATAGAAATGCCAAAGCCCAAGACCCAGACGACATACACC 4559
DB 7026 GTTAACTCTTCCCTATTAATAGAAATGCCAAAGCCCAAGACCCAGACGACATACACC 7085
QY 4560 CTAGAAGACTGGCAAGAGATAAAAGATAGACAGTTCTCTGAGACTCCGGAGGGAC 4619
DB 7086 CTAGAAGACTGGCAAGAGATAAAAGATAGACCA-TTCTCTGAGACTCCGGAGGGAC 7144
QY 4620 TGCTATACCTCAGATGGGAAGAAATCTGTGCCCAAAAGAGGGTTAGAAATATGTCAA 4679
DB 7145 TGCTATACCTCAGATGGGAAGAAATCTGTGCCCAAAAGAGGGTTAGAAATATGTCAA 7204
QY 4680 C-AGATACATCGTTACCCACCTAGGAATTAACACCTGACAGCTGAGTGTGCAACATC 4738
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QY 4739 CCCTTATCATGTTCTGAGGCTTACAGAGTGGCTGACTCGGTGCTCAAAATTTGTGCC 4798
DB 7265 CCCTTATCATGTTCTGAGGCTTACAGAGTGGCTGACTCGGTGCTCAAAATTTGTGCC 7324
QY 4799 CTGCCAGCTGGTTAATGCTAATCTCTCCAGAAATCCCTCCAGGGAAGAGACTAAGGGGAAG 4858
DB 7325 CTGCCAGCTGGTTAATGCTAATCTCTCCAGAAATCCCTCCAGGGAAGAGACTAAGGGGAAG 7384
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DB 7445 CAATACCTATTGCTTTTGTAGACACCTTTTCAAGGATGGTACAGGCTTATCTACTAA 7504
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DB 7565 AATACCTAAGTAATAGGTCAGACATATGGTCCAGCTTTTGTGCCAGAGTAAGTCAGG 7624
QY 5099 ACTGGCCAGATATTGGGATTTGTAATGGAATCTGTAATGTCATACAGACCCCAAGCTC 5158
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DB 7805 CCCTGGACAGTTTGGCTGACCCCTATGAATTAATCTACAGGGGACCCCTTATGGT 7864
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QY 5399 CAAGGCACCTCAGTGGGTGAGACCAACAGCGTGGAGGCAACTCCGGGAGGCGCTACTCAGG 5458
DB 7925 CAAGGCACCTCAGTGGGTGAGACCAACAGCGTGGAGGCAACTCCGGGAGGCGCTACTCAGG 7984

QY 5459 AGAGAGAGACTTGCAGATCCACATCGTTTCCAAAGTGGAGATTCAGTCTACGTTAGACG 5518
DB 7985 AGGAGGAGACTTGCAGATCCACATCGTTTCCAAAGTGGAGATTCAGTCTACGTTAGACG 8044
QY 5519 CCACCGTGCAGGAAC 5534
DB 8045 CCACCGTGCAGGAAC 8060
RESULT 7
US-08-766-528-2
; Sequence 2, Application US/08766528
; Patent No. 6190861
; GENERAL INFORMATION:
; APPLICANT: Jay A. Fishman
; TITLE OF INVENTION: MOLECULAR SEQUENCE OF SWINE RETROVIRUS
; TITLE OF INVENTION: AND METHODS OF USE
; NUMBER OF SEQUENCES: 74
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 60 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/766,528
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/572,645
; FILING DATE: 14-DEC-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Louis Myers
; REGISTRATION NUMBER: 35,965
; REFERENCE/DOCKET NUMBER: MGP-038CP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)227-5941
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7333 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
US-08-766-528-2

Query Match 61.1%; Score 4970.8; DB 3; Length 7333;
Best Local Similarity 79.4%; Pred. No. 0;
Matches 6531; Conservative 0; Mismatches 702; Indels 989; Gaps 15;
QY 1 GCCTGGGTACGACTGGGCCCCCAGAGCGCTTGGAAATAAAATCTCTTCTGCTTTTGA 60
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QY 61 TCAAGACCGCTTCTCGTGAGTGATTAAGGGGAGTCCGCTTTTCCGAGCCTCGAGG- 115
DB 69 TCAAGACCGCTTCTGTGTGAGTGATT-TGGGGTGTGCGCTCTTCGAGCCGAGGAGGG 127
QY 116 ----TTCTTTTGTGCTTCTTACATTTGGGGGCTGTCGCGGATCTGTGCGGGCCACCCC 171
DB 128 GATTGTTCTTTTACTGCGCTTTTCATTGTTGTCGTTGGCGGAAATCTTCGAGCCACCCC 187
QY 172 TAACACCCGAGAACCGACTTGGAGGTAAAGAGATCTCTTTTAACTGTATCATGTA 231
DB 188 TTACACCCGAGAACCGACTTGGAGGT-AAAGGGATCCCTTTTGAAC--ATATGTGTGTG 244
QY 232 CCGGCCGCGCTCTGTTCTGAGTGTCTGTTTTCAGTGGTGGCGGCTTTTCGGTTTGACG 291

245	Db	 TCGCGCGGCTCTCTGTTCTGAGTGTCTGTTTTCGGTGTATGCGGCTTTTCGGTTTGACG	304
292	Qy	TGTCCTCTCAGGCGGTAAAGGGCTGGGGAGCTGTGATCAGCAGAGCTGTCTAGGAGATCAC	351
305	Db	TGTCCTCTCAGACCGTAAAGACTGTGAGGACTGTGATCAGCAGACGTGTCTAGGAGATCAC	364
352	Qy	AGGCTGTGTCCTTCGGGGGACGCCCGGAGGTGTAGGAGAGCCAGGGACGCCTGTGTCT	411
365	Db	AGGCTGCCACCTTCGGGGAGCGCCCGGAGGTGGGAGAGCCAGGGACGCCTGTGTCT	424
412	Qy	CTTACTGTGCGTTCAGAGGACCGAAATTTCTGTCTGTCTGTGAGCGAAAGCTTCCCGCTCCGGCAC	471
425	Db	CCTACTGTGCGTTCAGAGGACCGAGATTTCTGTGTTGAAGCGAAAGCTTCCCGCTCCGGCGC	484
472	Qy	CGTCCGACTTTTTCGCTGTTGTGAGAGACGTGTGAGCGGGTCACTGTGTCTGTGATCTGT	531
485	Db	CGTCCGACTTTTTCGCTGTTGTGGAAGACCGGACCGGGTGTGTCTGTGATCTGT	544
532	Qy	TGCTTTCTGTTGTGTCTTGTCTGTGTGTCTTGTCTTACAGATTTTAAATATGGGAC	591
545	Db	TGCTTTCTGTTGTGTGTCTTGTCTTGTGTGTCTTGTCTTACAGATTTTAAATATGGGAC	604
592	Qy	AGACGGGTGACGACCCCTCTTAGTTTGAATCTCTCGACCATTTGACGTAAAGTTTAAATCCAGGG	651
605	Db	AGACAGTGTACTACCCCTTAGTTTGAATCTCTCGACCATTTGACGTAAAGTTTAAATCCAGGG	664
652	Qy	CTCATTAATTTGTCTGAGTTTGAAGAGGACCTTTGGCAGACTTTCTGTCTCTGAAT	711
665	Db	CTCATTAATTTGTCTGAGTTTGAAGAGGACCTTTGGCAGACTTTCTGTCTCTGAAT	724
712	Qy	GGCGCATTTCTGATTTGATGSCCATCAGAGGGACCTTTTAAATCTCAGATTTATCCTGG	771
725	Db	GGCGCATTTCTGATTTGATGSCCATCAGAGGGACCTTTTAAATCTCAGATTTATCCTGG	784
772	Qy	CTGTTAAGCAGTTATTTTTCAGACTTGCACCGGCTCTCATCCCGATCAGAGACCTTATA	831
785	Db	CTGTTAAGCAGTTATTTTTCAGACTTGCACCGGCTCTCATCCGATCAGAGACCTTATA	844
832	Qy	TCCTTACGTGGCAAGATTTGGCAGAGATCTCTCGGCATGGGTAAACCATGTGCTGAATA	891
845	Db	TCCTTACGTGGCAAGATTTGGCAGAGATCTCTCGGCATGGGTAAACCATGTGCTGAATA	904
892	Qy	AGCCAGAAAGACAGGTCCCGAATTTCTGGCTCTTGGAGAGAAAACAAACACTCGGCTG	951
905	Db	AACCAAGAAAGACAGGTCCCGAATTTCTGGCTCTTGGAGAGAAAACAAACACTCGGCTG	964
952	Qy	AAAAAGTCAAGCCCTCTCTCATATCTACCCCGAGATTTGAGGAGCCACCGCTTTGGCCG	1011
965	Db	AAAAAGTCAAGCCCTCTCTCATATCTACCCCGAGATTTGAGGAGCCACCGCTTTGGCCG	1024
1012	Qy	AACCCCAATCTGTTCCCGACACCCCTTATCTGCGACAGGGTCCCGGAGGGAGCCCTTGT	1071
1025	Db	AACCCCAATCTGTTCCCGACACCCCTTATCTGCGACAGGGTCCCGGAGGGAGCCCTTGT	1084
1072	Qy	CCCTCTCTGAGCTCCGGGGTGGAGGACCTCTCTGAGGACTCGGAGCCGAGGGGCG	1131
1085	Db	CCCTCTCTGAGCTCCGGGGTGGAGGACCTCTCTGAGGACTCGGAGCCGAGGGGCG	1144
1132	Qy	CCACCCCGAGCGGACAGACAGATCGGACATTAACCGTCCGCGACGTACGGCCCTCCCA	1191
1145	Db	CCACCCCGAGCGGACAGACAGATCGGACATTAACCGTCCGCGACGTACGGCCCTCCCA	1204
1192	Qy	CACGGGGGCGCAATTGACGCCCTCAAGTATTTGGCCCTTTTCTCTGTGAGATCTTATA	1251
1205	Db	TGCGAGGGGGCAATTGACGCCCTCAAGTATTTGGCCCTTTTCTCTGTGAGATCTTATA	1264
1252	Qy	ATTGGAATCTAACCATCCCTTTCTCGGAGATCCCGCAACCGCTCAGGGGTTGGTG	1311
1265	Db	ATTGGAATCTAACCATCCCTTTCTCGGAGATCCCGCAACCGCTCAGGGGTTGGTG	1324
1312	Qy	AGTCCCTTATGTTCTCTCACACGCTTCTTGGGATGATTTGTCAACAGCTGTCTGCAGAC	1371

Qy	2452	CACAAATTTCTTTTGAACAAGGAAACCCAGAGTGTCTGCAAAATAACAAACCTTACACTG	2511	Qy	3532	ACCAGAAGGCAATTTGATGTATCAAAAAGCCCTGTGTAGCGCACCTGTCTTGCCCTCC	3591
Db	2465	CTCAATTTCTTTTGAACAAGGAAACCCAGAGTGTCTGCAAAATAACAAACCTTACACTG	2524	Db	3517	-----	3516
Qy	2512	TGTTGACCTCCAAATTAGATGAGCAATATCGAATATCTCTCCCTTAGTAAAGCTGATC	2571	Qy	3592	CTGACGTAACTAAACCTTTTACCCTTTATGTGTGATGAGCGTAGAGGAGTAGCCCGGAG	3651
Db	2525	TGTTGACCTCCAAATTAGATGAGCAATATCGAATATCTCTCCCTTAGTAAAGCTGATC	2584	Db	3517	-----	3516
Qy	2572	AAATATACAAATTTCTGTTGGAACAGTTTCCCAAGCTGGGCAAGAACCGCAGGATGG	2631	Qy	3652	TTTTAAACCCAAACCTTAGGACCATGAGAGAACCTGTGCGCTACCTGTCAAGAAGTGG	3711
Db	2585	AAATATACAAATTTCTGTTGGAACAGTTTCCCAAGCTGGGCAAGAACCGCAGGATGG	2644	Db	3517	-----	3516
Qy	2632	GTTTGGCAAGCAAGTTTCCCAAGCTGGGCAAGAACCGCAGGATGG	2691	Qy	3712	ATCCTGTAGCAAGTGTGTGGCCCATATGCTGAAGGCTATCGCAGCTGTGGCCATCTGG	3771
Db	2645	GTTTGGCAAGCAAGTTTCCCAAGCTGGGCAAGAACCGCAGGATGG	2704	Db	3517	-----	3516
Qy	2692	CAGTCAGACAGTACCTTGAAGTAAAGCAAGTCAAGAGGAAATTCGGCCGCGATGTCAAA	2751	Qy	3772	TCAAGGACGCTGACAAATTTGACTTTGGGACAGAAATAAATGTATAATAGCCCCCATGCAT	3831
Db	2705	CAGTCAGACAGTACCTTGAAGTAAAGCAAGTCAAGAGGAAATTCGGCCGCGATGTCAAA	2764	Db	3517	-----	3516
Qy	2752	GATTAATCCAAACAGGGCATCTAGTTCCTGTCGAATCTCCCTGGAATCTCCCTGCTAC	2811	Qy	3832	TGGAGAACATCGTTTCGGCAGCCCCCAGACCGGATGGATGACCAACCGCCGATGACCCACT	3891
Db	2765	GATTAATCCAAACAGGGCATCTAGTTCCTGTCGAATCTCCCTGGAATCTCCCTGCTAC	2824	Db	3517	-----	3516
Qy	2812	GGTTAGAAAGCTGGGACTAATGACTATCGACAGTACAGGACTTCGAGAGAGGTCAATA	2871	Qy	3892	ATCAAAGCTGCTTCTCACAGAGGGGTCAAGTTTCGCTCCACACGCGCTCTCAACCTG	3951
Db	2825	GGTTAGAAAGCTGGGACTAATGACTATCGACAGTACAGGACTTCGAGAGAGGTCAATA	2884	Db	3517	-----	3516
Qy	2872	AAAGGGTGCAGGACATACACCAACAGTCCGAAACCTTTAACTCTTTGTGCTCTCC	2931	Qy	3952	CCACTCTTCTGCTGAAGAGACTGATGAACCAAGTGACTCATGATTGCCATCACTATTGA	4011
Db	2885	AAAGGGTGCAGGACATACACCAACAGTCCGAAACCTTTAACTCTTTGTGCTCTCC	2944	Db	3517	-----	3516
Qy	2932	CACCCCAACGGAGCTGGTATACAGTATTTGAATTAAGGATGCTCTTCTGCTGAGAT	2991	Qy	4012	TTGAGGAGACTGGGGTCCGCAAGGACCTTACAGACATACCGCTGCTGAGAGAGTGTAA	4071
Db	2945	CGCCTGAACGGAACTGGTATACAGTATTTGAATTAAGGATGCTCTTCTGCTGAGAT	3004	Db	3517	-----	3516
Qy	2992	TACACCCCACTAGCAACCACTTTTTCGCTTCGAAATGAGAGATCCAGGTACGGGAAGAA	3051	Qy	4072	CCTGGTTCACTGACGGAAGCAGCTATGTGTGGAAGGTAAAGAGATGGCTGGGGGGCGG	4131
Db	3005	TACACCCCACTAGCAACCACTTTTTCGCTTCGAAATGAGAGATCCAGGTACGGGAAGAA	3064	Db	3517	-----	3516
Qy	3052	CCGGGACGCTCACCTGGACCCGACTGCCCCAAGGTTTCAAGAACTCCCCGACCATCTTTG	3111	Qy	4132	TGGTGGAGGGGACCCGCAACGATCTGGGCCAGCAGCTGCCGGAAGGAATTTTCAGCACAA	4191
Db	3065	CCGGGACGCTCACCTGGACCCGACTGCCCCAAGGTTTCAAGAACTCCCCGACCATCTTTG	3124	Db	3517	-----	3516
Qy	3112	ACGAAGCCCTACACAGAGACTGGCCAACTTCAGATTCACACCTCAGGTGACCTCC	3171	Qy	4192	AGGCTGAGCTCATGGCCCTCACGCAAGCTTTTGGCTGGCCGAAAGGAAATCCATAACA	4251
Db	3125	ACGAAGCCCTACACAGAGACTGGCCAACTTCAGATTCACACCTCAGGTGACCTCC	3184	Db	3517	-----	3516
Qy	3172	TCCAGTACGTGGATGACCTGCTTGGCGGAGCCACCAACAGGACTGCTTTAGAGGCA	3231	Qy	4252	TTTATACGGAACAGCAGGTATGCTTTTGGCACTGCACAGTACATGGGGCCATCTATAAAC	4311
Db	3185	TCCAGTACGTGGATGACCTGCTTGGCGGAGCCACCAACAGGACTGCTTTAGAGGTA	3244	Db	3517	-----	3516
Qy	3232	CGAAGGCACTACTGCTGGAATTTGTCTGACCTAGGCTACAGAGCTCTGCTAAGAGGCC	3291	Qy	4312	AAAGGGGTTGCTTTACCTCAGCAGGAGGGAATAAAGAACAAAGAGGAAATTTCTAAGCC	4371
Db	3245	CGAAGGCACTACTGCTGGAATTTGTCTGACCTAGGCTACAGAGCTCTGCTAAGAGGCC	3304	Db	3517	AAAGGGGTTGCTTTACCTCAGCAGGAGGGAATAAAGAACAAAGAGGAAATTTCTAAGCC	3576
Qy	3292	AGATTTCAGAGAGAGGTAAATATATTTGGGGTACAGTTTCGGGGAACGGGAGGATGGC	3351	Qy	4372	TATTAGAAGCCGTACATTTTACCAAAAAGGCTAGCTATTATATACACTGTCTTGACATCAGA	4431
Db	3305	AGATTTCAGAGAGAGGTAAATATATTTGGGGTACAGTTTCGGGGAACGGGAGGATGGC	3364	Db	3577	TATTAGAAGCCGTACATTTTCCAAAAGGCTAGCTATTATATACACTGTCTTGACATCAGA	3636
Qy	3352	TGACGGGCAACGGAAGAACTGTGTCAGATACCGGCCCAACCAACAGCCCAACAA	3411	Qy	4432	AAGCTAAAGATCTCATATCCAGAGGAAACAGATGGGTGACCGGGTTGCCAAGCAGGAG	4491
Db	3365	TGACGGGCAACGGAAGAACTGTGTCAGATACCGGCCCAACCAACAGCCCAACAA	3424	Db	3637	AAGCCAAAGATCTCATATCTAGAGGGAACAGATGGGTGACCGGGTTGCCAAGCAGGAG	3696
Qy	3412	TGAGAGGTTTGGGGACAGCTGGATTTTGGAGACTGTGATCCCGGGGTTTGGGACCT	3471	Qy	4492	CCCAAGGTTTAACTCTTCTGCTTATATAGAAATGCCCAAGCCCCCAGAACCCGACGAC	4551
Db	3425	TGAGAGGTTTGGGGACAGCTGGATTTTGGAGACTGTGATCCCGGGGTTTGGGACCT	3484	Db	3697	CCCAAGGTTTAACTCTTCTGCTTATATAGAAACGCCCAAGCCCCCAGAACCCGACGAC	3756
Qy	3472	TAGCAGCCCACTCTTACCCGCTAAACCAAGAAAGGGGAAATTTCTCTGGGCTCTGAGC	3531	Qy	4552	AGTACACCTTAGAGACTTGGCAAGAGATATAAAGATAGACAGTCTCTCTGAGACTCCGG	4611
Db	3485	TAGCAGCCCACTCTTACCCGCTAAACCAAGAA-----	3516	Db	3757	AGTACACCTTAGAGACTTGGCAAGAGATATAAAGATAGACAGTCTCTCTGAGACTCCGG	3816
				Qy	4612	AAGGGACCTGTCTATACCTCAGATGGGAAGGAAATCTCTGCCCAACAAAGAGGGTTAGAT	4671

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Db 3937 GAACATCCCTTTATCATGTTCTGAGGCTACCAAGAGTGGCTGATCGGTGGTCAACATTT 3996
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Db 4117 ACGGAACAAATATCTATTGGTTTTTTGTAGACACCTTTTTCAGGATGGGTAGAGGCTTATC 4176
Qy 4972 CTACTAAGAAAGAGACTTCAACCGTGGTGGCTTAAAGAAATATCTGGAAGAAATTTTTCGA 5031
Db 4177 CTACTAAGAAAGAGACTTCAACCGTGGTGGCTTAAAGAAATATCTGGAAGAAATTTTTCGA 4236
Qy 5032 GATTTGGAAATACCTAAGGTAAATAGGCTCAGACAAATGCTCCAGCTTTTGTGCCAGGTAA 5091
Db 4237 GATTTGGAAATACCTAAGGTAAATAGGCTCAGACAAATGCTCCAGCTTTTGTGCCAGGTAA 4296
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Db 4297 GTCAGGAGCTGGCCAAAGATATTGGGGATTGATTTGGAAATCTGCAATGTGCATACAGACCCC 4356
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Db 4417 CCAAGAGACTGGCAATTAATGATTTGATGATGCTCTCGTCCCTTTTGTGCTTTTGTAGGTTA 4476
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Db 4537 CGTTGGCAGAAATTGCTTTGCAATAGTCTGATGCTGCTTTTCCAGCCTTTGTTCT 4596
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Db 4597 CTAGGCTCAGGCACCTTGAGTGGGTGAGCAACGAGCGTGGAGCACTCCGGGAGGCCT 4656
Qy 5452 ACTCAGAGAGAGAGACTTCCAGATCCCATCGTTTCCAAGTGGGAGATTCAGTCTACG 5511
Db 4657 ACTC---AGAGAGACTTCCAAGTTCACATCGCTTCCAAGTGGGAGATTCAGTCTATG 4713
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Db 4714 TTAGAGCCCAACCGTGAGGAAACCTCGAGACTCGGTAGAAAGGACCTTATCTCGTACTTT 4773
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Db 4805 -----AATCCCTTA 4814
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Db 4815 AGCTTGCCCTCCATCGCGTGGTTCTTACTCTGTCAATAAATCTCTCAAGTTAATGTTAAA 4874
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Qy 5983 CATTTGGGAAATCCAGAGATTTCTTTGTAAACATGGAACGTGTGTAACTCTAATGAT 6042
Db 5115 TATTTGGAAATCCTCAGGATTTCTTTTGCNAAGCAATGAGCTGCATAACTTCTAATGAT 5174
Qy 6043 GGATATTGGAATGGCCAACTCTCAGCAGGATAGGTTAAGTTTCTTATGTCAACACC 6102
Db 5175 GGAATTTGGAATGGCCAGTCTCTCAGCAAGACAGATGAATTTCTCTTTTGTAAACAT 5234
Qy 6103 TATACAGCTCTGGCAATTTTAAATTAACCTGACCTCGGATTAGAACCTGGAAGCCCAAG--- 6159
Db 5235 CCTACCAGTTATAATCAATTTAATATTGSCCATGGGAGATGGAAGATTGGCAACAGCGG 5294
Qy 6160 -----TGCTCTCTTCAGACCTAGATTACCTA 6186
Db 5295 GTCAAAAAAGATGTACGAAATAAGCAATAAGCTGTCTCATCTCGTTAGACCTAGATTACTTA 5354
Qy 6187 AAAATAAGTTTCACTGAGAAAGAAACAAAGAAATATCTCTAAAATGGGTAAATGCTATG 6246
Db 5355 AAAATAAGTTTCACTGAAAGAAAGAAACAAAGAAATATTTCAAAAGTGGGTAAATGCTATA 5414
Qy 6247 TCTTTGGGGAATGGTATATTATGAGGCTCGGGTAAACAAACAGGCTCCATTTCTTAACTATT 6306
Db 5415 TCTTTGGGGAATAGTGTACTATGAGGCTCTGGGAGAAAGAAAGGATCTGTCTTCTGACTATT 5474
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QY 7429 ATTATTAACAAGTTAATGCTTCTTCAATAGAGAACGAATAAGTGAGTGCAGTCAATCATGTA 7488
DB 6615 TTAATTAATAGGTTTGTGCTTCTGTTAGAGAACGAGTGAGTGCAGTCCAGATCATGTA 6674
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DB 6675 CTTAGGCAACAGTACCAAGCCGCTTAGCAGCCAGGAGAACTGACCTCTAGCCTTCCCGAG 6734
QY 7546 TTCTAAGATTGAACCTATTAACAAGAGAGAGTGGGAATGAAAGGATGAAATATACAC 7605
DB 6735 TTCTAAGATTGAACCTATTAACAAGAGAGTGGGAATGAAAGGATGAAATATGCAAC 6794
QY 7606 CTAAGCTAATGAGAGCTTAAATGTTCTGTAATTCAGAGTGTGTTCTTATAGGTAA 7665
DB 6795 CTAACCCCTCCAGAACCCAGGAAGTAAATAAAGCTCTAAATGCCCCCGAATTCAGAC 6854
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DB 6970 TGTAAAACTGACTGGCACCATAGAAAGATTGATTACACATTCAGACGCCCTAGTGACCTAT 7029

QY 7846 CTTGGTGACAAATGTTCTCCCCCAACCCGAAACATGCGCAATGTGTAACTCTAAACAA 7905
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DB 7090 TTTAAATTAATGTTGTCACGAGCGGCTCTCGAATTTTAAATGATTTGTTCCATGG 7149
QY 7960 -----TTGTGATATTTTGAATGATTTGTTTGTAAAGCGCGGCTTTGTTGTGAAC 8010
DB 7150 AGCGCGGCTCTCGATATTTTAAATGATTTGTTGTGACGACAGGCTTTGTTGTGAAC 7209
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QY 8131 AA 8132
DB 7330 AA 7331

RESULT 8
US-09-661-858-2
; Sequence 2, Application US/09661858
; Patent No. 669663
; GENERAL INFORMATION:
; APPLICANT: Jay A. Fishman
; TITLE OF INVENTION: MOLECULAR SEQUENCE OF SWINE RETROVIRUS
; AND METHODS OF USE
; NUMBER OF SEQUENCES: 74
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 60 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/661,858
; FILING DATE: 14-Sep-2000
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/766,528
; FILING DATE: <unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Louis Myers
; REGISTRATION NUMBER: 35,965
; REFERENCE/DOCKET NUMBER: MGP-038CP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)227-5941
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7333 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-661-858-2

Query Match 61.1%; Score 4970.8; DB 3; Length 7333;
Best Local Similarity 79.4%; Pred. No. 0;
Matches 6531; Conservative 0; Mismatches 702; Indels 989; Gaps 15;

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Db																							68	
Qy	61	TC	AA	GAC	CG	CTT	CT	CG	TAG	TG	ATTA	AGG	GGAG	TCCG	CTTTT	CCG	AG	CT	TG	AGG	---	115		
Db																								
Qy	69	TC	AA	GAC	CG	CTT	CT	TG	TG	AG	TG	AT	TG	GG	GGT	CG	T	TC	CG	AG	CG	CG	127	
Db																								
Qy	116	---	TT	CT	TTT	TG	CT	GT	T	TAC	ATTT	TGG	GGG	CT	CG	T	CCG	GGAT	CT	GT	CG	CG	171	
Db																								
Qy	128	GA	TT	GT	T	CT	TT	T	ACT	TG	CG	CTT	CA	TT	TG	TG	CG	T	GG	CG	GG	AA	187	
Db																								
Qy	172	TA	AC	CC	G	AG	AA	CC	G	ACT	TG	GA	GGT	AAAA	AG	AT	CT	CT	TTT	TA	AC	GT	231	
Db																								
Qy	188	TT	AC	CC	G	AG	AA	CC	G	ACT	TG	GA	GGT	---	AA	GG	GA	T	CC	CT	T	GG	244	
Db																								
Qy	232	CC	GG	CC	GG	CT	CT	CT	GT	T	CT	GT	AG	TG	T	CT	GT	TTT	C	AG	TG	GG	291	
Db																								
Qy	245	TC	GG	CC	GG	CG	T	CT	GT	T	CT	T	AG	TG	T	CT	GT	T	TC	GG	TG	AT	304	
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Qy	292	TG	T	CT	CT	C	AG	G	CCG	T	TA	AG	GC	T	G	GG	GA	CT	GT	GA	T	AG	351	
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Qy	305	TG	T	CT	CT	C	AG	CC	T	TA	AG	CA	CT	GG	AG	A	CT	GT	GA	T	AG	GA	364	
Db																								
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Qy	365	AG	GT	CC	CA	CC	CT	TG	GG	GG	AG	CG	CC	CG	GG	AG	CT	AG	GA	GC	CG	CT	424	
Db																								
Qy	412	CT	T	ACT	GT	CG																		

1085	Db	 CCCTCTTGAGCTCCGGTGGAGGGACCTGCTGCCGGACCTCGAGCCGGAGAGCGC	1144
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1145	Db	CCACCCGGAGCGGACAGACGATCCGATATTACCGCTGCGCACCTATGCGCCCTCCCA	1204
1192	Qy	CACCGGGGGCCAAATTGCAGCCCTCAGATATTGGGCCCTTTCTCTGCAGATCTCTATA	1251
1205	Db	TGCAGGGGGCCAAATTGCAGCCCTCAGATATTGGGCCCTTTCTCTGCAGATCTCTATA	1264
1252	Qy	ATTGGAAAATAACCATCCCCCTTTCTCGAGGATCCCAACGCTCACGGGGTGGTGG	1311
1265	Db	ATTGGAAAATAACCATCCCCCTTTCTCGAGGATCCCAACGCTCACGGGGTGGTGG	1324
1312	Qy	AGTCCCTTATGTTCTCTCACCGCTACTTGGGATGATGTCAACAGCTGCTCGACACAC	1371
1325	Db	AGTCCCTTATGTTCTCTCACCGCTACTTGGGATGATGTCAACAGCTGCTCGACACAC	1384
1372	Qy	TCTTCAACCCGAGGAGCGAGAGAAATTCATTAGAGGCTAGAAAATATGTTCTCTGGGG	1431
1385	Db	TCTTCAACCCGAGGAGCGAGAGAAATTCATTAGAGGCTAGAAAATATGTTCTCTGGGG	1444
1432	Qy	CCGACGGGCGACCAACGCGGTTGCAAAATGAGATTGCATGGGATTTCCCTTAACTCGCC	1491
1445	Db	CCGACGGGCGACCAACGCGAGTTGCAAAATGAGATTGCATGGGATTTCCCTTAACTCGCC	1504
1492	Qy	CCGTTTGGGACTACAACCGGCTGAAGGTAGGAGAGCTTGAAAATCTATCGCCAGGCTC	1551
1505	Db	CCGTTTGGGACTACAACCGCTGAAGGTAGGAGAGCTTGAAAATCTATCGCCAGGCTC	1564
1552	Qy	TGTTGGCGGTCCTCCGGGGCCCTCAAGACGGCCCACTAATTTGGCTAAGGTAAAGAAAG	1611
1565	Db	TGTTGGCGGTCCTCCGGGGCCCTCAAGACGGCCCACTAATTTGGCTAAGGTAAAGAAAG	1624
1612	Qy	TGATGACGGACCGAATGAACCCCTCTGTGTTTTCTTGAGAGGCTCTTGGAAAGCCTTCA	1671
1625	Db	TGATGACGGACCGAATGAACCCCTCTGTGTTTTCTTGAGAGGCTCTTGGAAAGCCTTCA	1684
1672	Qy	GGCGGTACCCCTTTTGATCCCACTCAGAGGCCCAAAAAGCCTCAGTGGCTTTGGCCT	1731
1685	Db	GGCGGTACCCCTTTTGATCCCACTCAGAGGCCCAAAAAGCCTCAGTGGCCTTTGGCCT	1744
1732	Qy	TTATAGSACAGTCAGCCTTGGATATTAGAAGAAGCTTCAGAGCTGGAAGGTTTACAGG	1791
1745	Db	TCATTTGGCAGTCGGCTCTGGAATACAGGAAGAACTTCAGAGCTGGAAGGTTTACAGG	1804
1792	Qy	AGCTGATGTTACGTGATCTAGTGAAGGAGCGAGAAAGTATATTACAAAGGGAGACAG	1851
1805	Db	AGCTGATGTTACGTGATCTAGTGAAGGAGCGAGAAAGTATATTACAAAGGGAGACAG	1864
1852	Qy	AAGAAGAAAGGGAACAAAGAAAAGAGAGAAAGAGAGAAAGGAGAAAGGAAAGACGTAAATA	1911
1865	Db	AAGAAGAAAGGGAACAAAGAAAAGAGAGAAAGAGAGAAAGGAGAAAGGAAAGACGTAAATA	1924
1912	Qy	AACGGCAAGAGAGAAATTTGACTAAGATCTTGGCTGAGTGGTTGAAGGAAAGCAATA	1971
1925	Db	GACGGCAAGAGAAAGATTTGACTAAGATCTTGGCGCAGTGGTTGAAGGAAAGCAATA	1984
1972	Qy	CGGAAAGAGAGAGATTTTAGGAAATTAGGTCAGGCCCTAGACAGTCAAGGAACTGG	2031
1985	Db	GGGAGAGAGAGAGATTTTAGGAAATTAGGTCAGGCCCTAGACAGTCAAGGAACTGG	2044
2032	Qy	GCAATAGCACCCACTCGACAAAGACCAATGTCATATCTGAAAGAAAGGACACTGGG	2091
2045	Db	GCAATAGCACCCACTCGACAAAGACCAATGTCATATCTGAAAGAAAGGACACTGGG	2104
2092	Qy	CAAGGAATCGCCCCAAGAGGGAAAACAAAGGACCAAGGATCTTAGCTCTAGAAAGATA	2151
2105	Db	CAAGGAATCGCCCCAAGAGGGAAAACAAAGGACCAAGGATCTTAGCTCTAGAAAGATA	2164
2152	Qy	AAGATTAGGGAGACGGGGTTCCGACCCCTCCCCGAGCCGAGGTAACTTTGAGGTGG	2211

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Db 2225 AGGGCAACAGTTGAGTTCCTGGTTCATACCGAGCGGAGCATTCAGTGTCTACTACAC 2284
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Db 2525 TGTTGACCTCCAAATTAGATGATGAATATCGACTATATCTCTCCCAAGTAAAGCTGATC 2584
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Db 2585 AAGATATACAGTCTCGTGTGGAGAGTTTCCCAAGCTGGCGGAGAAACCGCAGGATGG 2644
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Qy 7069 ATTGTACAGAAATCTCCAAGCCCTAGAAAATCTGTCAGTAACCTGGAGGATCCCTA 7128
Db 6255 ATTGTACAGAAATCTCCAAGCCCTAGAAAATCTGTCAGTAACCTGGAGGATCCCTA 6314
Qy 7129 ACCTCCTTATCTGAAGTAGTCTCAGAAATAGAGAGGTTAGATTTATTTCTAAAA 7188
Db 6315 ACCTCCTTATCTGAAGTAGTCTCAGAAATAGAGAGGTTAGATTTATTTCTAAAA 6374
Qy 7189 GAAGGAGGATTTATGTAGCTTGAAGGAGGAATGCTGTTTTATGTGGATCAATCAGGG 7248
Db 6375 GAAGGAGGTTATGTAGCTTGAAGGAGGAATGCTGTTTTATGTAGATCACTCAGGA 6434
Qy 7249 GCCATCAGAGACTCCATGAAACAAGTTAGAGAAAGTTGGAGAGCGTTCGAGGGAAG 7308
Db 6435 GCCATCAGAGACTCCATGAAACAAGTTAGAGAAAGTTGGAGAGCGTTCGAGGGAAG 6494
Qy 7309 GAAACTACTCAAGGGTGTGGAGGATGTTCAACAGGTCTCTTGTGGTCCCTACCTA 7368
Db 6495 GAGGCTGACAGGGGTGTTTGAAGGATGTTTCAACAGGTCTCTTGTGGATCACCCTG 6554
Qy 7369 CTTTCTGCTTTAAACAGGACCTTAAATAGTCTCTCTCTCTCTCTCTCTCTCTCTCT 7428
Db 6555 CTTTCTGCTCTGACGGGGCCCTAGTAGTCTCTCTCTCTCTCTCTCTCTCTCTCT 6614
Qy 7429 ATTATTAACAAGTTAATTCCTTCAATAGAGACGAATTAAGTCCAGATCATGGA 7488
Db 6615 TTAATTAATAGTTTGTGCTTTGTTTGAAGGATGTTTCAACAGGTCTCTTGTGGATCATGGA 6674
Qy 7489 CTTAGACAAAGTACCAAGCCCTCTAGC---AGGAGAGTGGCCGCTAGCTTACAG 7545
Db 6675 CTTAGGCAACAGTACCAAGGCTTCTGAGCCCAAGGAGAACTGACCTCTAGCCTTCCAG 6734
Qy 7546 TTTCAAGATTAGAACTATTAACAAGAGAGAGTGGGGAATGAAGAGGATGAATAACAAC 7605
Db 6735 TTTCAAGATTAGAACTATTAACAAGAGAGAGTGGGGAATGAAGAGGATGAATAACAAC 6794

Qy 7606 CTAAGCTAATGAGAAGCTTTAAATTTCTGAAATCCAGAGTTTGTTCCTTATAGGTAAA 7665
Db 6795 CTAACCTCCAGAACCCAGGAAGTTTAAATAAAGCTCTAAATGCCCCGAAATCCAGAC 6854
Qy 7666 AGATTAGGTTTTTTGCTGTTTTAAATATGCGGAAGTAAATAGGCGCTGAGTACATGC 7725
Db 6855 CTTGCTGGCTGCGAGTAAATAGGTAGAGGTCACTCTCTATTTTCCAGGGCTGCTA 6914
Qy 7726 TCTAGCATGAAACTTCTTGAACATATTTGAGATAACAAGAAAGGAGTTTCTTAATCTGC 7785
Db 6915 TCTGCGCT-AAGTAAGATAACAGGAATGAGTTGAC----TAATCGCTTATCTGGATTC 6969
Qy 7786 TTTGTTTGTGTTTCTGTAAGTCTGTTGGCCATAAAGATGTTGAAATGTTGATACATAT 7845
Db 6970 TGTAAACCTGACTGGCACCACATAGAGAAATGATTACACATTGACAGCCCTAGTGACCTAT 7029
Qy 7846 CTTGGTGAACAATGCTCTCCCAACCCGCAATGCGCAATGTGTAACTCTTAAACAA 7905
Db 7030 CTTAACTGCAATCTGCTCACTCTGCCAGGAGCCACGAGATCGGACCTCCCGAGCTAT 7089
Qy 7906 TTTAAATTAATTCGTCACGAGCGGGCTCTCGAAGTTTAAATTTGAACTGGT----- 7959
Db 7090 TTTAAATTAATTCGTCACGAGCGGGCTCTCGAATTTTAAATTTGAAATGATTTGTTCCATGG 7149
Qy 7960 -----TTGTGATATTTTGAATGATTTGTTTGTAAAGCGCGGCTTTGTTGTAAC 8010
Db 7150 AGCGGGCTCTCGATATTTTAAATGATTTGTTGACGACAGGCTTTGTTGTAAC 7209
Qy 8011 CCATAAAGCTGTCGAGCTCCACACTCGGGGCGGAGTCTCTACCCCTCGGTGTGT 8070
Db 7210 CCATAAAGCTGTCGAGTTCGCACTCGGGGCGGAGTCTCTACCCCTCGGTGTGT 7269
Qy 8071 ACAGCTGCGGCGGCGGCTTGGAAATAAATCTCTGTTGATCAAAAAA 8130
Db 7270 ACAGCTGCGGCGGCGGCTTGGAAATAAATCTCTGTTGATCAAAAAA 7329
Qy 8131 AA 8132
Db 7330 AA 7331

RESULT 9

US-09-171-553B-1
; Sequence 1, Application US/09171553B
; Patent No. 6756227
; GENERAL INFORMATION:
; APPLICANT: GALBRAITH, DANIEL N.
; APPLICANT: HAWORTH, CHRISTINE
; APPLICANT: LEES, GILLIAN M.
; APPLICANT: SMITH, KENNETH T.
; TITLE OF INVENTION: PORCINE RETROVIRUS
; FILE REFERENCE: CFV-5.01
; CURRENT APPLICATION NUMBER: US/09/171.553B
; PRIOR FILING DATE: 1999-02-08
; PRIOR FILING DATE: 1997-04-18
; PRIOR FILING DATE: 1997-04-18
; PRIOR FILING DATE: 1997-02-10
; PRIOR FILING DATE: 1996-04-19
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 1
; LENGTH: 3320
; TYPE: DNA
; ORGANISM: Porcine retrovirus
US-09-171-553B-1

Query Match 35.8%; Score 2915.2; DB 3; Length 3320;
Best Local Similarity 94.3%; Pred. No. 0;
Matches 3051; Conservative 0; Mismatches 173; Indels 12; Gaps 2;

QY	2970	GATGCTTCTTCTGCTGAGATTACACCCCACTAGCCAAACCACTTTTTCCTTCGAATGG	3029		Db	1102	CGCGTGACTGGGAAAGTGTCTAACTGGTTCACTGACGGAAGCAGTATGTGTGGAAAGT	1161	
Db	22	GATGCTTCTTCTGCTGAGATTACACCCCACTAGCCAAACCACTTTTTCCTTCGAATGG	81		QY	4110	AAGAGATGGCTGGGCGCGCGTGTGGACGGGACCGCACCATCTTGGGCCAGACGACCTG	4169	
QY	3030	AGAGATCCAGGTACGGGAAGAACCGGGGAGCTCACCTGACCGGACTGCCCCAAGGGTTC	3089		Db	1162	AAGAGATGGCTGGGCGCGGAGTGTGGACGGGACCGCACCATCTTGGGCCAGACGACCTG	1221	
Db	82	AGAGATCCAGGTACGGGAAGAACCGGGGAGCTCACCTGACCGGACTGCCCCAAGGGTTC	141		QY	4170	CCGGAAGGAACCTTACGACAAAGGCTGAGCTCATGGCCCTCACGCAAGCTTTTGGCGCTG	4229	
QY	3090	AAAGAACTCCCGACCACTTTTGACGAAGCCCTACACAGAGACTGCGCAACTTTCAGGATC	3149		Db	1222	CCGGAAGGAACCTTACGACAAAGGCTGAGCTCATGGCCCTCACGCAAGCTTTTGGCGCTG	1281	
Db	142	AAGAACTCCCGACCACTTTTGACGAAGCCCTACACAGGACTGCGCAACTTTCAGGATC	201		QY	4230	GCCGAAGGGAATCCATAAACATTTATACGGAACAGAGTATGCTTTGGGACTGCACAC	4289	
QY	3150	CAACACCTCAGGTGACCTCTCCAGTACGTGGATGACTGCTTCTGCGGGAGCCACC	3209		Db	1282	GCCGAAGGGAATCCATAAACATTTATACGGAACAGAGTATGCTTTGCGACTGCACAC	1341	
Db	202	CAACACCTCAGGTGACCTCTCCAGTACGTGGATGACTGCTTCTGCGGGAGCCACC	261		QY	4290	GTACATGGGGCCCATCTATAAACAAAGGGGTTGCTTACCTCAGCAGGAGGGAATAAAG	4349	
QY	3210	AAACAGGACTGCTTGAAGGACGAAGGCACTACTGCTGGAATTTGCTGACCTAGCTAC	3269		Db	1342	GTACACGGGGCCCATCTATAAACAAAGGGGTTGCTTACCTCAGCAGGAGGGAATAAAG	1401	
Db	262	AAACAGGACTGCTTGAAGGTAAGGAGCACTACTGCTGGAATTTGCTGACCTAGGCTAC	321		QY	4350	AAACAAAGAGGAATTTCTAAGCCCTATTAGAAGCCGTACATTTTACCAAAAAAGGCTAGCTAT	4409	
QY	3270	AGAGCCTCTGCTAAGAGGCCAGATTTTGACGAGAGAGTAAACATCTTTGGGGTACAGT	3329		Db	1402	AAACAAAGAGGAATTTCTAAGCCCTATTAGAAGCCCTTACATTTTGCCAAAAAGGCTAGCTAT	1461	
Db	322	AGAGCCTCTGCTAAGAGGCCAGATTTTGACGAGAGAGGTAAACATCTTTGGGGTACAGT	381		QY	4410	ATACACTGCTTGGGACATCAGAAAGCTAAAGATCTCATATCCAGAGGAACAGATGGCT	4469	
QY	3330	TTGCGGGAGCGGCAGCGATGGCTGACGAGGCAACGGAAGAAACCTGTAGTCCAGATACCG	3389		Db	1462	ATACACTGCTTGGGACATCAGAAAGCCAAAGATCTCATATCTAGAGGGAACAGATGGCT	1521	
Db	382	TTGCGGGAGCGGCAGCGATGGCTGACGAGGCAACGGAAGAAACCTGTAGTCCAGATACCG	441		QY	4470	GACCGGTTGCCAAGCAGCAGCCAGGGTGTAACTTCTGCTTATATAGAAATGCCCC	4529	
QY	3390	GCCCAACACACGCCAAAACAAATGAGAGAGTTTTGGGGACAGCTGGATTTTGCAGACTG	3449		Db	1522	GACCGGTTGCCAAGCAGCAGCCAGGGCTGTAACTTCTGCTTATATAGAAATGCCCC	1581	
Db	442	GCCCAACACACGCCAAAACAAATGAGAGAGTTTTGGGGACAGCTGGATTTTGCAGACTG	501		QY	4530	AAAGCCCAAGAACCCAGACGACAGTACACCTTAGAAGACTGGCAAGAGATAAAAAAGATA	4589	
QY	3450	TGATCCCGGGTTTCGACCTTAGCAGCCCACTCTACCCGCTAACCAAGAAAGGS	3509		Db	1582	AAAGCCCAAGAACCCAGACGACAGTACACCTTAGAAGACTGGCAAGAGATAAAAAAGATA	1641	
Db	502	TGATCCCGGGTTTCGACCTTAGCAGCCCACTCTACCCGCTAACCAAGAAAGGS	561		QY	4590	GACCACTTCTTGAGACTCCGGAAGGACCTGCTATACCTCAGATGGGAAGGAATTCCTG	4649	
QY	3510	GAATTCCTCTGGGCTCTGAGCACCAAGAGCAATTTGATGCTATCAAAAAGGCCCTGCTG	3569		Db	1642	GACCACTTCTTGAGACTCCGGAAGGACCTGCTATACCTCATATGGGAAGGAATTCCTG	1701	
Db	562	GGATTCCTCTGGGCTCTGAGCACCAAGAGCAATTTGATGCTATCAAAAAGGCCCTGCTG	621		QY	4650	CCCAACAAAGAGGGTTAGAAATATGTCCAACAGATACATCGTCTAACCCACCTAGGAAC	4709	
QY	3570	AGCGCACTGCTGCGCCCTCTGACGTAACCTTAAACCTTTTACCTTTATGTTGGATGAG	3629		Db	1702	CCCAACAAAGAGGGTTAGAAATATGTCCAACAGATACATCGTCTAACCCACCTTAGGAAC	1761	
Db	622	AGCGCACTGCTGCGCCCTCTGACGTAACCTTAAACCTTTTACCTTTTATGTTGGATGAG	681		QY	4710	AAACACCTCAGCAGTTGGTCAGAAACATCCCTTATCATGTTCTGAGGCTACACAGAGTG	4769	
QY	3630	CGTAAGGAGTAGCCGGGAGTTTAAACCAACCTTAGGACCACTAGGAGAGACCTGTC	3689		Db	1762	AAACACCTCAGCAGTTGGTCAGAAACATCCCTTATCATGTTCTGAGGCTACACAGAGTG	1821	
Db	682	CGTAAGGAGTAGCCGGGAGTTTAAACCAACCTTAGGACCACTAGGAGAGACCTGTT	741		QY	4770	GCTGACTCGGTGGTCAAAACATTTGTTGCTGCGAGCTGGTTAACTCTAATCTCTCCAGA	4829	
QY	3690	GCCTACTGTCAAAGAGCTCGATCCTGTAGCCAGTGGTTGGCCCATATGCTTGAAGGCT	3749		Db	1822	GCTGACTCGGTGGTCAAAACATTTGTTGCTGCGCTGCCAGCTGGTTAATCTCTCCAGA	1881	
Db	742	GCCTACTGTCAAAGAGCTTGATCCTGTAGCCAGTGGTTGGCCCGTATGTCTGAAGGCT	801		QY	4830	ATGCTCCAGGGAAGAGACTAAGGGGAAGCCACCCAGGCGCTCAGTGGGAAGTGGACTTC	4889	
QY	3750	ATCGAGCTGTGCCCATATGTTCAAGGACGCTGACAAATTTGACTTTGGGACAGAAATATA	3809		Db	1882	ATACCTCCAGGAAGAGACTAAGGGGAAGCCACCCAGGCGCTCAGTGGGAAGTGGACTTC	1941	
Db	802	ATCGAGCTGTGCCCATATGTTCAAGGACGCTGACAAATTTGACTTTTGGGACAGAAATATA	861		QY	4890	ACTGAGTTAAAGCCGCTTAAATACGGAACAAATACCTATTGTTTTTGTAGACACTTT	4949	
QY	3810	ACTGTAATAGCCCCCATGATTTGGAGACATCGTTGCGGACCCCGCCAGACCGATGGATG	3869		Db	1942	ACTGAGTTAAAGCCGCTTAAATACGGAACAAATATCTATTGTTTTTGTAGACACTTT	2001	
Db	862	ACTGTAATAGCCCCCATGATTTGGAGAACATCGTTGCGGACCCCGCCAGACCGATGGATG	921		QY	4950	TCAGGATGGGTAGAGCTTATCCTACTAAGAAAGAGACTTCAACCGTGGTGGCTAAAAAA	5009	
QY	3870	ACCAAGCCCGCATGACCCACTATCAAGACCTGCTTCTCAGAGAGGGTTCAGTTTCGCT	3929		Db	2002	TCAGGATGGGTAGAGCTTATCCTACTAAGAAAGAGACTTCAACCGTGGTGGCTAAGAAA	2061	
Db	922	ACCAAGCCCGCATGACCCACTATCAAGACCTGCTTCTCAGAGAGGGTTCAGTTTCGCT	981		QY	5010	ATACCTGGAAGAAATTTTCCAAAGATTTGGAATACCTTAAGGTAAAGGGTCAGACAATGGT	5069	
QY	3930	CCACAGCCGCTCTCAACCCCTGCCACTCTTCTGCTGGAAGAGACTGATGAACCAAGTACT	3989		Db	2062	ATACCTGGAAGAAATTTTCCAAAGATTTGGAATACCTTAAGGTAAAGGGTCAGACAATGGT	2121	
Db	982	CCACAGCCGCTCTCAACCCCTGCCACTCTTCTGCTGGAAGAGACTGATGAACCAAGTACT	1041		QY	5070	CCAGCTTTTGTGTCAGGTAAGTCAAGGACTGGCCAAAGATATTTGGGGATTTGATTGGAAA	5129	
QY	3990	CATGATTCATCAACTATTTGATTTGAGGACTGGGGTCGGAAGACCTTACAGACATA	4049		Db	2122	CCAGCTTTTGTGTCAGGTAAGTCAAGGACTGGCCAAAGATATTTGGGGATTTGATTGGAAA	2181	
Db	1042	CATGATTCATCAACTATTTGATTTGAGGAGACTGGGGTCGGAAGACCTTACAGACATA	1101		QY	5130	CTGCTATTTGCTATACAGACCCCAAGCTCAGGACAGGTAGAGAGGATGAATAGAACATTT	5189	
QY	4050	CCGCTGACTGGAGAGTGTCTAACTGTTTCACTGACGGAAGCAGCTATGTGTTGGAAGT	4109						

Db	2182	CTGCATTGTGCATACAGACACCCAAAGCTCAGGACAGGTAGAGAGGATGAATAGAACCAATT	2241
Qy	5190	AAAGAGACCTTACTTAATTTGACCGGAGACTGGCGTTAATGATTGATAGTCTCTCCTG	5249
Db	2242	AAAGAGACCTTACTTAATTTGACCGGAGACTGGCGTTAATGATTGATAGTCTCTCCTG	2301
Qy	5250	CCCTTTGTGCTTTTATAGGTTAGGAAACACCCCTGGACAGTTTGGGCTTGACCCCTATGAA	5309
Db	2302	CCCTTTGTGCTTTTATAGGTTAGGAAACACCCCTGGACAGTTTGGGCTTGACCCCTATGAA	2361
Qy	5310	TTACTCTACGGGGAGACCCCTTCTAGCTCAAGGCACTTCTAGTGGGTGAGACCAACGAGCG	5369
Db	2362	TTGCTCTACGGGGAGACCCCTTCTAGCTCAAGGCACTTCTAGTGGGTGAGACCAACGAGCG	2421
Qy	5370	CTGCTTTCCAGCCCTTTGCTCTAGCTCAAGGCACTTCTAGTGGGTGAGACCAACGAGCG	5429
Db	2422	CTGCTTTCCAGCCCTTTGCTCTAGCTCAAGGCACTTCTAGTGGGTGAGACCAACGAGCG	2481
Qy	5430	TGAGAGCAACTCCGGGAGGCTTACTCAGGAGGAGGACTTGCAGATCCCAATCGTTTC	5489
Db	2482	TGAGAGCACTCCGGGAGGCTTACTCAGGAGGAGGACTTGCAGATCCCAATCGTTTC	2538
Qy	5490	CAAGTGGAGATTCAAGTCTAGTTAGAGCCACCGTGCAGAAACCTCGAGACTCGGTGG	5549
Db	2539	CAAGTGGAGATTCAAGTCTAGTTAGAGCCACCGTGCAGAAACCTCGAGACTCGGTGG	2598
Qy	5550	AAGGGCCCTTATCTCGTACTTTTACACACCAACCGGCTGGAAGTCGAAGGAATCTCC	5609
Db	2599	AAGGGACCTTATCTCGTACTTTTACACACCAACCGGCTGGAAGTCGAAGGAATCTCC	2658
Qy	5610	ACCTGGATCCATGATCCAGCTTAAACCGGCGCCACTCCCGGATTCGGGGTGAAGGCC	5669
Db	2659	ACCTGGATCCATGATCCAGCTTAAACCGGCGCCACTCCCGGATTCGGGGTGAAGGCC	2718
Qy	5670	GAAGAAGACTGAAATCCCTTAAAGCTTGCCTCCATCGCGGTTCCTTACTCTGCTCAAT	5729
Db	2719	GAAGAAGACTGAAATCCCTTAAAGCTTGCCTCCATCGCGGTTCCTTACTCTGCTCAAT	2778
Qy	5730	AACCTCTCAGACTAATGATGCGATAGGACAGCTGAACTCCCATTAACCTTATC	5789
Db	2779	AACCTCTCAGACTAATGATGCGATAGGACAGCTGAACTCCCATTAACCTTATC	2838
Qy	5790	TCTCACCTGGTAAATCTGACTCCGACAGGTATTAAATCAACACACTCAAGGGGA	5849
Db	2839	TCTCACCTGGTAAATCTGACTCCGACAGGTATTAAATCAACACACTCAAGGGGA	2898
Qy	5850	GGCTCTTTTAGGAACCTGGTGGCTGATCTATAGCTTTGCTCAGATCAGTTATTCCTAG	5909
Db	2899	GGCTCTTTTAGGAACCTGGTGGCTGATCTATAGCTTTGCTCAGATCAGTTATTCCTAG	2958
Qy	5910	TCT-----GACCTCACCCCGAGATATCCTCGATCTCAGGATTTTATGTTGCCC	5960
Db	2959	TCTCAATGACCGAGGCAACACCCCGAGATATCCTCGATCTCAGGATTTTATGTTGCCC	3018
Qy	5961	AGGACCAACCAATTAATGGAACAATTCGGGAATCCAGAGATTTCTTTCTAAACAATG	6020
Db	3019	AGGACCAACCAATTAATGGAACAATTCGGGAATTCCTCAGGATTTCTTTCTAAACAATG	3078
Qy	6021	GAACTGTGTAACCTCTAATGATGATATTGGAATGGCCAACTCTCAGCAGGATAGGGT	6080
Db	3079	GAGCTGCATTAATCTAATGATGGAATTTGGAATGGCCAGTCTCTCAGCAAGACAGAT	3138
Qy	6081	AAGTTTCTTATGTCACCACTATACAGCTCTGGACAAATTTAATTAACCTGAT	6140
Db	3139	AAGTTTCTTATGTCACCACTATACAGCTCTGGACAAATTTAATTAACCTGAT	3198
Qy	6141	TAGAACTGGAACCCCAAGTCTCTCTTACAGACCTAGATTACCTTAAATAAGTT	6196
Db	3199	ATGGAAGATTGGCAACACCGGGTACAAAAGATGTACGAATAAGCAATAAGCT	3254
RESULT 10			
US-09-075-272-1			

;	Sequence 1, Application US/09075272		
;	Patent No. 6136598		
;	GENERAL INFORMATION:		
;	APPLICANT: MILLER, A. DUSTY		
;	APPLICANT: WOLGAMOT, GREG		
;	APPLICANT: BONHAM, LYNN		
;	TITLE OF INVENTION: MUS DUNNI ENDOGENOUS RETROVIRAL		
;	TITLE OF INVENTION: PACKAGING CELL LINES		
;	NUMBER OF SEQUENCES: 11		
;	CORRESPONDENCE ADDRESS:		
;	ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP		
;	STREET: Two Embarcadero Center, 8th Floor		
;	CITY: San Francisco		
;	STATE: California		
;	COUNTRY: U.S.A.		
;	ZIP: 94111		
;	COMPUTER READABLE FORM:		
;	MEDIUM TYPE: Floppy disk		
;	COMPUTER: IBM PC compatible		
;	OPERATING SYSTEM: PC-DOS/MS-DOS		
;	SOFTWARE: Patent In Release #1.0, Version #1.25		
;	CURRENT APPLICATION DATA:		
;	APPLICATION NUMBER: US/09/075,272		
;	FILING DATE: 08-MAY-1998		
;	CLASSIFICATION:		
;	PRIOR APPLICATION DATA:		
;	APPLICATION NUMBER: US 60/046,140		
;	FILING DATE: 09-MAY-1997		
;	ATTORNEY/AGENT INFORMATION:		
;	NAME: Poor, Brian W.		
;	REGISTRATION NUMBER: 32,928		
;	REFERENCE/DOCKET NUMBER: 14538A-003710		
;	TELECOMMUNICATION INFORMATION:		
;	TELEPHONE: (206) 467-9600		
;	TELEFAX: (415) 576-0300		
;	INFORMATION FOR SEQ ID NO: 1:		
;	SEQUENCE CHARACTERISTICS:		
;	LENGTH: 8655 base pairs		
;	TYPE: nucleic acid		
;	STRANDEDNESS: single		
;	TOPOLOGY: linear		
;	MOLECULE TYPE: cdna		
;	US-09-075-272-1		
Query Match 27.5%; Score 2237; DB 3; Length 8655;			
Best Local Similarity 60.5%; Pred. No. 0;			
Matches 4377; Conservative 0; Mismatches 2575; Indels 285; Gaps 31;			
Qy	461	CCCTCCGCGACCGTCCGACTCTTTTGCTGCTTGTGGAAGACGTGGAGCGGTACGTTG 520	
Db	601	CCGACCCCATCCATCTGAATCTTTTAAGTTGTCTGTCGACGCGAAGTCGCCCGCGTT 660	
Qy	521	TCGTGGATC-TGTTGGTTTCTGTTTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 579	
Db	661	TTGTTTCTTTTCTCTCAGTCTCGTGTCCGCTCTTGTGTGTGTGTGTGTGTGTGTGTGT 716	
Qy	580	TTAATATGGGACAGACCGTGTGACCCCTCTTGTGTTGTTGTTGTTGTTGTTGTTGTTG 639	
Db	717	TAGAAATGGGACAAATCTGTCTCCACTCCCTTTCTAACTCCCTGGAGATTGGAGGAGG 776	
Qy	640	TTAATATCCAGGCTCATAAATTTGTCAAGTTTCAAGTTTAAAGAGGACCTTTGGCAGACTTCT 699	
Db	777	TAAAAATCAGACACACAAATCAGTCAGTGGAGGTTAGAAAGGCCCATGGCAAACTTTT 836	
Qy	700	GTGTCTCTGAATGCCGACATTCGATGTGTGATGGCCATCAGAGGGGACCTTTAATCTGT 759	
Db	837	CGCGCTCCGAGTGGCAACGTTTGGAGTGGGCTGGCCACCGGAGGGTGTCTTTGACTTGT 896	
Qy	760	AGATTATCTGGCTGTTAAAGCACTTATTTTTCAGCTGGACCCGGCTCTCATCCCGATC 819	
Db	897	CACGTATGCCCGCTCAGCGCAATTTGTTTTTCAG---GAAGAAGGGGGTCAACCTGATC 953	
Qy	820	AGGAGCCCTATATCTTACGTGGCAAGATTTGGCAGAGGATCTCTCCGCCCATGGTTAAAC 879	

Db	954	AGATCCCTTACATTTGAGCTGCGAGAGTCTCGTCCAGTTCCACCTTCGTGGGTCAAGC	1013	Db	2029	AGAACTAGAGGACGGGAAAATAGCGGAGATCCCGTCAAGAGAGAAATTTGAGTAAGAT	2088
Qy	880	CATGG---CTGATAAGCAAGAAAGACAGGTCCCGGAATTTCTGGCTCTTTGAGAGAAA	936	Qy	1940	CTTGGCTGCGAGTGGTTGAAGGGAAAAGCAATACGAAAAGAGAGAGAGATTTTGGAAAAAT	1999
Db	1014	CCTGGACCCCAATCTCTTGAATACTGACCGTTCGAGTTGCCAGTCCGATGCAGCTGAGA	1073	Db	2089	TCGTGCCGCGAGT-----TATTAATGATAGGCAGTTCAGAAAAAAGGCAGAACAGGATT	2139
Qy	937	ACAAACACTCGGCTGGAAGTCAAGCCCTCTCTCATATCTACCCCGAGATTGAGGAGC	996	Qy	2000	TAGTTCAGGCCCTTAGACAGTCAAGGAACTTGGGCAATAGGACCCCACTCGACAAGGACCA	2059
Db	1074	AATCTGGTCCGTGAGCACCCCAAGATTTATCCAGAGATTGACGACCTCCTCTGGATGG	1133	Db	2140	CCTGGGCAACAGGGCAGTGAACCCGCCAGGTGGCGAAGAGCGCGCTGGAAGAAAGACCA	2199
Qy	997	CACCGCTTGGCGGAACCCCAATCTGTTCCCAACCCCTTATCTGGCACAGGGTGGCG	1056	Qy	2060	ATGTCATATTTCTAAAGAAAGAGGACACTGGGCAAGAGAACTGCCCAAGAGGAAACAA	2119
Db	1134	ACTCCCAACTCC---CCCTTACCCCTGCGCCAGCAGCCACTGCGAGCGCCCACTG	1190	Db	2200	ATGCGCTTTTGCAGAAAGAAAGGACACTGGGCTAAGACTGCTTAAAGAAAGAGGCA	2259
Qy	1057	CGAGGGGACCTTTGCCCCCTCTGGAGCTCGCGGCTGGAGGACCTGCTGCAAGGACTC	1116	Qy	2120	AGGACCAAGGATCTAGCTCTAGAGAAAGATAAAGATTAGGGGAGACGGGGTTCGACCC	2179
Db	1191	TGGACGCCCTGACCCGGAACCAAGCAAGCGGGCTCAGGGACCGCGGAGGACTC	1250	Db	2260	A-----TTCAAGGTCCTGACCTAGAACGATTAGGGAAGTCGGGGCTCAGACCC	2310
Qy	1117	GGAGCCGAGGGGCGCACCCCGGAGCGGACAGACAGATCGCGCATTTACCGCTCGCA	1176	Qy	2180	CCTCCCGAGCCGAGGTTAACTTTGAAGGTGAGGGGCAACCCAGTTGAGTTCTTGTTGA	2239
Db	1251	GGAGCCGCGGGTTCGGAGCCC--TGAGAGGAAGGGGGCCAGATTCCACAGTTGCTT	1308	Db	2311	CCTCCCTGAGCCTAGGGTAACTTTCTGTGTGAGGGGACTCCCGTTAAATTTCTTGATAGA	2370
Qy	1177	CGTACGGCCCTCCCAACACCGGGGGGCCAATTTGAGCCCTC-----CA	1219	Qy	2240	TACCGGAGCAAACTTCACTGCTACTACAGCCATTAGGAAACTAAAGATAAAATAATC	2299
Db	1309	GCCCCCTTAGAGCTCATGTGGAGGGCCAAACGCCAGGACCTAATGATCTCATCTTTTACA	1368	Db	2371	TACTGGAGCAGAGCATTTGGTACTCACAGCCCTCTGGGCAACTAGGCTCTTAAAGGAC	2430
Qy	1220	GTATTCGCTTTCTTCTGAGATCTCTATTAATTCGAAACTTAACCATCCCTTTCTC	1279	Qy	2300	CTGGGTGATGGGTGCGCACAGGGCAACACAGTATCCATGGACTACCCGGAAGACAGTTGA	2359
Db	1369	GTACTGGCTTTTCTTCTCTGATTTATATAATTCGAAACTTAACCATCCCTCCCTTCTC	1428	Db	2431	CATAGTGGTTGGAGCACTTGGGAGTAACTTTTACCCCTGGACCAACCAAGAGCCTTACA	2490
Qy	1280	GGAGGATCCCAACGCTCACCGGGTGTGGAGTCCCTTATGTTCTCTCACAGCCTAC	1339	Qy	2360	CTTGGGAGTGGGACGGGTAAACCACTCGTTTCTGTGTCATACCTGAGTGCACGACCCCT	2419
Db	1429	AGAAACCCCTCTGGGCTTACTGGGCTCTTGAATCACTTATGTTCTCTCATCAGCCAC	1488	Db	2491	GATAGATAAAACATGTGTGACCCACTTTTCTGTGTGATACCTGAGTGTCTGCTCCCT	2550
Qy	1340	TTGGGATGATTTCAACAGTGTCTGACAGACATCTTTCAACAACGAGGAGGAGAGAT	1399	Qy	2420	CTTAGTAGAGACTTATTGACCAAGATGGAGCAAAATTTCTTTTGAACAAGGGAACCC	2479
Db	1489	TTGGGATGATTTGTGACAGCTTTTTCAGGTTCTCTTTTACCACAGAGAAAGGAAAGAT	1548	Db	2551	TCGTGGACGTGATCTGTTTAAACAAACTAAAGGCTCAAGTTCAATTTACTTCAAGAGTCC	2610
Qy	1400	TCTATTAGAGGTAGAAAAATCTCTCTGGGCGGACGGGCGACCCACGCGTTGCAAAA	1459	Qy	2480	AGAACTGTCTGCAAAATAACAAACCTTATCACTGTGTGTGACCCCTCCAATTAGATGACGAATA	2539
Db	1549	CTGTATGGAGGCAAGAAAAACGTTCTAGAGAGGACGGCACACCCACTGCTCTCCCTAA	1608	Db	2611	ACAAGTAGCTGGGAAAAAGCCCCCTTGTCTTGTCTCCTCAGCACGGAAGAGATA	2670
Qy	1460	TGAGATTGACATGGGATTTTCCCTTAACTCGCCCCGGTTGGGACTACAAACGCTGAAG	1519	Qy	2540	TCGACTATATCTCTCCCTTAGTAAAGCTGATCAAAATATACAAATTTCTGTGTGGAAACAGTT	2599
Db	1609	CCTCGTGGACGAGCTTCCCTTTGAACCGCCCCCACTGGGACTACAACTCGGGAAG	1668	Db	2671	CGGTTGCTATGAAGAGCAACCCAAAGGTGCAGCCCCCTTTAGA--CTGGGTAACTCGCTT	2727
Qy	1520	TAGGAGAGCTTGAAAATCTATCGCAGGCTCTGGTGGCGGGTCTCGGGGGCGCTCAAG	1579	Qy	2600	TCGCCAAGCTCGGCGAGAAACCGCAGGATGGGTTTGGCAAGAGAGTTTCCCCCAAGT	2659
Db	1669	TAGGGACGCTCTTGTCTTACCGTGGACTCTGTGGCAGGTCTCAGAGGAGCGGCAAG	1728	Db	2728	CCCCAATGTCTGGCGGAAACAAGCAGGATGGGTTGGCTTAAACAAGTGCCTCCAGTCGT	2787
Qy	1580	ACGGCCCACTAATTTGGCTAAGGTAGAGAGTGTGCGAGGACCGAATGAACCCCTC	1639	Qy	2660	TATTCAACTGAAGGCGCAGTGCACACAGTGTCACTCAGTCAAGACGTACCCCTTGAGTAAAGA	2719
Db	1729	ACGGCCCACTAATTTGGCTAAGGTAGAGAGTGTGCGAGGACCGAATGAACCCCTC	1788	Db	2788	GGTAGACTTTAAGCTGTGCTACCCCACTCTCAGTAAGACAATACCCCATGAGCAAGGA	2847
Qy	1640	TGTTTTTCTTGAGAGCTCTTGAAGCTTTCAGCGGTACACCCCTTTTGTATCCCACTC	1699	Qy	2720	AGCTAAGAAAGAAATTCGGCCCGCATGTCCAAAGATTAATCCAAACAGGGCATCTAGTTCC	2779
Db	1789	AGTCTTTCTGGAGCTTTATGAGGGGTATAGGAGTACACCCCTTTCGATCCCTCGTC	1848	Db	2848	AGCTAAGGAGGCGATCCGACCTCATATTCCGAGGCTGTAGACCAAGGAATTTAGTGGC	2907
Qy	1700	AGAGGCCCAAAAAGCTCTAGTGGCTTTGGCTTTATAGGACAGTCAAGCTTTGATATTAG	1759	Qy	2780	TGTCCAATCTCCCTGGAATACCTCCCTGCTACCGGTTAGAAAGCTTGGGACTAATGACTA	2839
Db	1849	AGAGGACAGAAAGCGCTGTAGCCATGGCTTCAITTTGGCCAGTCTGCTCCCGATATAA	1908	Db	2908	CTGTCACTCCCCCTGGAACACTCCACTTTTGGCAGTACGAAGCCGAGGACCAATGATTA	2967
Qy	1760	AAGAGACTTCAGAGCTGGAAGGTTACAGGAGGTGAGTTACGTGATCTAGTGAAGGA	1819	Qy	2840	TCGACCACTACAGGACTTTGAGAGAGGTCAATAAAGCGGTGCGAGGATATACCCCAACAGT	2899
Db	1909	GAAAAAGCTACAGAGCTGGAGGGCTTCCAAAGATTATACGCTCCAAAGATTAGTGAAGGA	1968	Db	2968	TCGCCCGGTACAAGACTCCGGGAAGTTAATAAAGGGTCTTGGACATTCACCCCTACAGT	3027
Qy	1820	GGCAGAGAAAGTATATTACAAAAAGGAGACAGAAAGAAAGGGAACAAAGAAAGAGAG	1879	Qy	2900	CCGGAACCCCTTATAACCTCTTGTGTGCTCTCCCAACCCCAACGAGGTGTGTATACAGTATT	2959
Db	1969	AGCAGAGAGGTTTATACAAAGAGAGAAACAGAAAGAAAGAGAGGACGAGAGAGAAAGAA	2028	Db	3028	CCGGAACCCGTACAACCTTACTAAGCTCTCTCCACCCGAGAGAACCTGTGTATACGGTCT	3087
Qy	1880	AGAAAGAGAGAAAGGAGGAAAGACGTAAATAAACCGCAAGAGAGAAATTTGATAGAT	1939	Qy	2960	GGACTTAAAGGATGCTTCTTCTGCTGAGATTACACCCCACTAGCAACCACTTTTTC	3019
				Db	3088	GGATTTAAAGATGCTTCTTTTGGCTGTGCAACCCCAAGAGTCAACTTCTGTTTGC	3147

Db	5278	TAGAACATTAAAGGAGACCTTGACTAAATTTGGCCATCGAGACCGCGGGGAAAGACTGGGT	5337	Db	6355	CTCTTAAAAATTACAGCCCCCAGGACCATGCAAAAGGTAAATACTTGCACACCCCTACTCA	6414
Qy	5240	AGCTCTCCCTGCTTGTCTTTTAAAGGTAGGACACCCCTGGACAGTTTGGGCTGAC	5299	Qy	6191	TAAAGTTTCACTGAGAAAGGAAAAATATCTTAAATGGGTAAATGGTATGTCTT	6250
Db	5338	GGCTCTCTCCCTTGGCGTCTTCCGAGCCCGGAAACACCCCGGACGTTTGGGCTCAC	5397	Db	6415	TAAATTTCACTGAGAAAGGAAACAAG--CTCGCTGAGTTGGCTTAAAGGAAATAGGT	6471
Qy	5300	CCCTATGAATTAATCTCTACGGGGGACCCGCCCATTTGGTAGAAATTG-----CTTCTGT	5353	Qy	6251	GGGGAATGGTATATTATGAGGCTCGGGTAAACAACGAGGCTCCATTCTTAATATTTCGCC	6310
Db	5398	TCTTTTGAAGTCTGTATGGGGACCTCCCCCTTTAATAAAGATGGTGGACATTTGT	5457	Db	6472	GGGTTGGCGAGTATAT---ATTCCAATAAGAGACCCCTGGGTTTATCTTTACGATTTAGAC	6528
Qy	5354	ACATAGTGTGACGTCTGCTTTCCAGCGCTTTTGTCTTAGGCTCAAGGCACTTGAGTG	5413	Qy	6311	TCAAAATAAACAGCTGGAGCTCCAAATGGCTATAGGCCAAATACGGTCTTTGACGGGTC	6370
Db	5458	TCCCGATTCAAGCTCTGCTTACCTCTCTTTGCTTATTCAATTTAAAGGCCCTGAAAGT	5517	Db	6529	TGACAGTAAAGACCTGG---CAGTAAACATCCATAGGACCCCAAGGGTCTTTACGGAAC	6585
Qy	5414	GGTGACACACGAGCTGGAGGCACTCCGGGAGGCTTACTCAGGAGGAGGACATTGCA	5473	Qy	6371	AAAGACCCCCCA-----ACCAAGGACACGAGCACCTCTCTTAACATAACTTT	6415
Db	5518	AATTAGGACCCAAATTTGGGACACAGCTAAAGACGGGCTACACCCAGGACCAACCGCAG-	5576	Db	6586	AGGCCCCCCAGTTGSCACGGGCTCCCCGAGAGTCCCGAGCTCCAGCGCTCCACCACTT	6645
Qy	5474	GATCCACATCGTTTCCAAAGTGGGAGATTCAAGTCTACGTTAGACGCCACCGTGCAAGAAA	5533	Qy	6416	CTGSAATCAGACCCCACTGAGTCTAAACGACGACGATCAAAATGGGGGCAAAA-----	6465
Db	5577	--TACCCACGAGTTCAGGTGGGACCAAGTCTTGGTCAGACGACATCGAACCGGTAG	5634	Db	6646	CACGGCCCTACACAGTAGGACCTCATTTAGAGACAACTTAGCCTCCCCACCACTCCTAG	6705
Qy	5534	CTTCGAGACTCGGTGGAAGGCCCTTATCTCGTACTTTTGAACACCAACCGCTGTGAA	5593	Qy	6466	-----CTTTTACGCTCATCCAGGAGCTTTTCAAGCTCTTAACTCCACCA	6511
Db	5635	CCTTGAACACAGGTGGAAGGACCTATTATTAGTGTACTAAACAACCTCTTACGGCAGTGA	5694	Db	6706	ATACAGAAAACCGTCTGGTCACTAGTTTCAGGAGGACCTTTTATGTTTAAATAGGACTA	6765
Qy	5594	AGTCGAAGGAACTCCACCTGGATCCATGCATCCACGTTTAAACCGCGGCC-----	5644	Qy	6512	CTCCAGAGGCTACCTCTTCTTGTGCTATGCTTAGCTTCGGGGCCCACTTACTATGAAG	6571
Db	5695	AGTTGACGGGATTCCTCTCGGATCCACGCTTCACACGTTCAAGAGGGGCCCAAGTCAAGA	5754	Db	6766	ATCTCTAATATGACTCAATCATGTTGGTATGCTATGCCTCTAAACCCCTTATATGAAG	6825
Qy	5645	-----ACCTCCCGATTCGGGGTGGAAAGCCGAAAGACTGAAATATCCCTTAAAGCTTCG	5698	Qy	6572	GAATGGCTAGAGAGGGAAATTCATGTGACAAAAGAACATAGAGACCAATGACATGGG	6631
Db	5755	TGAAGAAAACCCACGAAGACNACTGGGCTGTGAGGCCACTGATACCTCTTAAAGCTTCG	5814	Db	6826	GAATGGCTCAGACTAGAACTTACAATATTACTTCAGATCATTTTC---TCAATGCTCTTGGG	6882
Qy	5699	CTTCCATCGCGTGGTTCTCTTACTCTGTCAATAACC-----	5733	Qy	6632	GATCCCAAAATTAAGCTTACCTTACTGAGGTTTCTGGAAAAGGCACCTGCATAGGAAAGS	6691
Db	5815	CTTGGCTCGCAGGAGCCCTCCATCACCTGAGACTAGGAAACCAACACCTCATGCGC	5874	Db	6883	GAGAGAACAGGAAGTTGACTCTGACAGCAGTTTCAGGAAATGGGCTTTGTTTAGGTTCAGG	6942
Qy	5734	---TCTCAGACTAATGGTATGCCATAGGACAGCCTGA-----ACTC	5774	Qy	6692	TTTCCCCCATCCCAACACACTTTTGTAAACACACTGAAAGCCTTTAATCAAACTCTGAGA	6751
Db	5875	CAGTTCAACAGCTCTGGGAAGTCTTAATGAAAAGGGAGACGTTGTATGGGTAGCCACTG	5934	Db	6943	TGCCCCCAGATAAATGGCACCTCTGTACACAGACTCAAAATATCCGACCTAACAAAGGTG	7002
Qy	5775	CCATAAACCTTATCTCTACCTCGTTAAATTAAGTCTCGGCACAGGATTAATATCAA	5834	Qy	6752	GTCAATATCTGTGTA CTGGTTATGACAGGTGTGGGCATGTAACTACTGATTAACCCCTT	6811
Db	5935	CAGTCCATCCCCCTTGGACTTGTGTGGCTGATCTCACCTGACATCTGTAATATAGCAG	5994	Db	7003	GTCAATATCTAGTGCTCCCATAGACACAGTATGGGCTTGCATAACAGGTCTCACTCCTT	7062
Qy	5835	CAACACTCAAGGGAGGCTCTTTTAGGAACCTGGTGGCCTGATCTATAGCTTTGCTCAG	5894	Qy	6812	GTGTTTCCACTTGGTTTGTAAACCAACTAAAGATTTTGTGCATTTATGGTCCAAATTTGTC	6871
Db	5995	CAGGATCTCCCAATTTGGGACCTTCCCGATCATACTGACTTGAATAACCCACCTCTGAAC	6054	Db	7063	GTATATCTATGTCTGTTTTCAAATAGCTCCAAAGATTTCTGTATTTTAGTTAGCTTATTC	7122
Qy	5895	ATCAGTTATCTTAGTC-----TGACCTCACCCCCAG	5926	Qy	6872	CCGAGTGTATTACTATATCCGAAAAGCAATCTTGATGAATATGACTACAGAAATCATC	6931
Db	6055	AAAAGTGTGTCCCAAAACGGGGTAGGAAGCACTACTGATGTTTCGGGGCAGTTCTATCGAG	6114	Db	7123	CTAGACTCTGTATCATGATGATAGCTCATTTCTAGACAAATTTGAACATCG---GGTCC	7179
Qy	5927	ATATCTCCATGCTCAGGATTTTATGTTTGGCCAGGACCAACCAATTAATGGA-----	5980	Qy	6932	GACAAAGAGAGAACCCATATCTCTGACACTGCTGTGTGTGATGCTCGGACTTGGAGTG---G	6988
Db	6115	CTAATCTTAGGGCTGCACAGTTTATGTTTGGCTTGTGCTGCTGAGGTCAGAAAGGAACTGC	6174	Db	7180	GCTGGAAGAGAGAACCCATTACTTAAACGTTAGCAGTGTCTTTTAGGATTTGGGAGTGGCCG	7239
Qy	5981	---AACATTCCGGAATCCAGAGATTTCTTTTGTAAACAATGGAACCTGTAACTCTA	6037	Qy	6989	CACGAGTGTAGAACAGGACAGCTGCCCTGTCACGGGACCAACAGCAGCAGCTAGAAACAG	7048
Db	6175	AACAAGAAATGAGAGGGCATCAGACTCTTTTGGGTAAATGGACATGTGAACCAACAG	6234	Db	7240	CAGCTGGGTAGGTACTGGAAACCGTGGCTTAAATCCAGACCCCCCGATCTTTGA-----	7294
Qy	6038	ATGATGATATTGGAA-----ATGGCCAACTCTCAGCAG	6072	Qy	7049	GACTTAGTAACCTTACATCGAATTTGTAAACAGAAAGATCTCCAAGAGCTTAGAAAAATCTGTCA	7108
Db	6235	GGGAAGCCTACTGGAAGCCTTCCGCTGATTTGGACCTGATCACGGTAAACGTTAGTG	6294	Db	7295	-----GGAATTCGTACAGCTATGATGATCTCAGAGCTATAGAACACTCTATAA	7347
Qy	6073	GATAGGTAAGTTTCTTATGTCAACACCTATACAGCTCTGGACAAATTAATTAACCTG	6132	Qy	7109	GTAACTGAGGAATCCCTAAACCTCTTATCTGGAAGTAGTCTCTAAGATAGAGAGGT	7168
Db	6295	GTTATGATAGCCAAACCAAGGAGAGAAACCCATACAAATACCTAGATTCTGGGTGTG	6354	Db	7348	CCAAACTAGAGAAATCTTTAACTTCTCTGCTGAGGTAGTACTGCAAAATAGAGAGGAT	7407
Qy	6133	ACCTGGATTAAGAACTGGAAGCCCAA--GTGCTCTCTTCAGACCTTAGATTACCTAAAAA	6190	Qy	7169	TAGATTTATTTCTTAAAGAGGAGGATTAATGCTAGCTTTGAAGGAGGAATGCTGTT	7228
				Db	7408	TAGATTGTATTCTTTAAAGAGGAGGACTTTGTCTCTCTCAAGAGGAATGTTGTT	7467

QY 7229 TTTATGTGGATCATTTAGGGGCCCATCAGAGCTCCATGAACAGCTTAGAGAAAGTTGG 7288
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RESULT 11
US-09-315-127-4
; Sequence 4, Application US/09315127
; Patent No. 6448390
; GENERAL INFORMATION:
; APPLICANT: The University of Tennessee, c/o Richard Cox
; TITLE OF INVENTION: Stable Envelope Proteins for Retroviral, Viral and
; TITLE OF INVENTION: Liposome Vectors and Use in Gene and Drug Therapy
; FILE REFERENCE: 44137-5023, U. of Tennessee
; CURRENT APPLICATION NUMBER: US/09/315.127
; CURRENT FILING DATE: 1999-05-20
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 8088
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: SEQ. ID NO. 3,
; OTHER INFORMATION: retroviral vector
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (5552)..(7552)
US-09-315-127-4

Query Match 26.8%; Score 2176; DB 3; Length 8088;
Best Local Similarity 59.0%; Pred. No. 0;
Matches 4361; Conservative 0; Mismatches 2765; Indels 266; Gaps 26;

QY 329 AGCAGAGCTGTAGGAGATCAGAGCTGCTGCCCTGGGGACGCCCGGAGGTGAGGA 388
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QY 389 GAGCAGGAGAGCGCTGGTGTCTCTACTGTGCTGAGGAGAGCCGAATCTGTGCTGAA 448
Db 446 GGACCAGGAGAGCGCTGGTGGACCCC- - - - -TGGTAAACGGGTC- - - - -GTTGTACCCGAT 497
QY 449 GCGAAGCTTCCCTCCCGACCGCTCCGACTCTTTTGTGCTGTGTAAGACGTGGAC 508
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QY 509 GGGTCAGCTGTCTCGATCTGTGGTTCTGTGTTTGTGTGTTGTGTTGTGTTGTGTTGT 568
Db 558 CGTCTCTGTTCTTTTGTGTTG- - - - -TTCTGGAAGCCCTCTGTCTCAGAGTCTTCT 614
QY 569 TGTCTACAGTTTAAATATAGGAGACAGCGGTGACGACCCCTCTAGTTGACTCTCGACA 628
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QY 629 TTGGACTAGTTAAATCCAGGCTCATTAATTTGCTCAGTTTAAAGAGGGACCTTG 688

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QY 809 TCATCCGATCAGAGAGCCCTATATCTCTGCTGCAAGATTTGGCAGAGGATCTCTCGCC 868
Db 852 ACATCCGAGCAAGTTCCATATATCTGCTGATAGGAGACCTCGCCAGAGATCCCCAC 911
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FEATURE:		NAME/KEY: misc feature		LOCATION: 1..8535		OTHER INFORMATION: /standard_name= "GalV SEATO Genome"	
Query Match		26.8%; Score 2176; DB 3; Length 8535;		Best Local Similarity		59.0%; Pred. No. 0;	
Matches 4361; Conservative		0; Mismatches 2765; Indels 266; Gaps		26;			
US-08-716-351A-1							
Qy	329	AGCAGCGTCTAGGAGATACAGGCTGTGCGCTGGGGAGCCCGGGAGGTGAGGA	388	1283	GGATCCCAACGCCTCACCGGGTGTGGAGTCCCTTATGTCTCTCACAGCCTACTTG	1342	
Db	756	AACAGCGTGTTCGGGCTCACCGCTGTGTAATCCAGGAGAGCGTCCAGGATCAGGGGA	815	1702	AAACCCAGCAGGTCTCACCGGGCTCCTGTAGTCTCTTATGTCTTCCCATCAGCCACTTG	1761	
Qy	389	GAGCAGGAGCGCTGTGTCTCTACTCTCGGTGAGAGACGGAATCTGTGTGAA	448	1343	GGATGATTGTCAACAGCTGTGCAGACATCTTTCACAAACCGAGGAGCGAGAGAATCT	1402	
Db	816	GGACCAGGAGCGCTGTGTGACCCC-----TCGGTAACGGGTC-----GTTGTGACCCGATT	867	1762	GGACGATTGCCAACAGCTCTACAGATTCTTTTCAACACTGAGGAACGGGAAGAATCT	1821	
Qy	449	GGAAAGCTTCCCGCTCCGGACCGTCCGACTCTTTTGGCTGTGTGGAAGACGTGGAC	508	1403	ATTAGAGGCTAGAAAAATGTTCTCGGGCCGACGGCGACCCACCGCGTGTGCAAAATGA	1462	
Db	868	TCATCGCCCGTGTGTAAGCGGCTCTGAATCTGATCTCTCTCTCGGTGCGCTCGCG	927	1822	CTTGGAGGCCGCAAAAATGTCTTGGGAGCATGGGGCCCTTACACAGCTCGAAGACCT	1881	
Qy	509	GGGTACGTGTCTGATCTGTGTGTTCTGTGTTGTGTGTCTTTGTGTGTGTCT	568	1463	GATTGACATGGGATTTCCCTTAACTCCTCCCGGTGTGGACTACAAACACGCTGAAAGTAG	1522	
Db	928	CCGTCTCTGTGTTCTTTTGTGTTG---TTTCTGAAAAGCTCTGTGTACAGTCTTTCT	984	1882	CATTATGAGGCTTCCCTCAATCGACTCTCTGGAATTAACAACACAGCCGCGAGTAG	1941	
Qy	569	TGTTACAGTTTAAATGAGACAGCGGTGACGACCCCTTGTAGTTGTGACTCTCGACCA	628	1523	GGAGAGTTGAAATCTATCGCAGGCTCTGTGTGGCGGTCTCGGGGGCGCTCAAGACG	1582	
Db	985	CTCCCAATCATCAATATGGACAAGATAATTCTACCCCTATCTCCCTCACTCTAAATCA	1044	1942	GGAGCGTCTTCTGTCTACCGCGGACTCTAGTGGCAGGTCTCAAAAGGGGCGAGCTCGCG	2001	
Qy	629	TTGAGCTGAAGTTAAATCAAGGCTCATATTTCTCAGTTTAAAGAGGACCTTG	688	1583	GCCCACTAATTTGGCTAAGTAAGAGAGTGTGTCAGGGACCGAATGAACCCCTCTCTGT	1642	
Db	1045	CTGGAGAGATGTGAAACAGGGCTCACATCTATCTCGTGAATCAAAAGGGAATG	1104	2002	TCCTACCAATTTGGCTAAGTAAGAGAGTCTTTCAGGGACCGGAGAACCCCTTCGGT	2061	
Qy	689	GCAGACTTCTGTCTCTGAATGCGCGACATTCGATTTGTGATGCGCATCAGAGGGAC	748	1643	TTTTCTTGAGAGCTCTTGGAAAGCTTTCAGCGGTACACCCCTTTTGTATCCCACTCAGA	1702	
Db	1105	GCAGACTTCTGTCTCTCGAGTGGCCACATCTCGGCTGGGGTGGCCACCGGAGGGAAC	1164	2062	TTTTCTTAGAACCTGTATGGAGGCTATAGAGATACACTCCGTTTGTATCCCTCTCTGA	2121	
Qy	749	CTTTAATCTGAGATTATCTCGCTGTAAAGCAGTTATTTTTCAGACTGGACCCGCTC	808	1703	GGCCCCAAAAGCTCTAGTGGCTTTTGGCTTTATAGACAGTCTAGCTTGTGATATTAGAAA	1762	
Db	1165	TTTTAATCTCTCTCTGATTTTTCAGTTTAAAGATTTGTCTTTTCAG---GAGAACGGGG	1221	2122	GGGACAAACAGCTGCGCTCGCATGGCTTTTATCGGACAGTCTAGCCCGCATATCAAGAA	2181	
Qy	809	TCATCCCGATCAGGAGCCCTATATCTTACGTGCAAGATTGTCAGAGGATCTCTCGCC	868	1763	GAAGCTTCAGAGCTCGAAGGTTTACAGGAGGCTGAGTTTACGTGATCTAGTGAAGGAGGC	1822	
Db	1222	ACATCCCGACCAAGTTCATATATCTGTGTATGCGAGACCTCCCCAGAAATCCCCACCC	1281	2182	AAAGTTACAGAGCTAGAGGGCTTCCAGGACTTTCCTTAAAGATTTAGTAAAGAGGC	2241	
Qy	869	ATGGTTTAAACATGAGTGAATAAGCAAGAACCCAGGTCCCGAAATTTCTGCTCTTGG	928	1823	AGAAAGATATATTAACAAAAGGGAGACAGAAAGAAAGAAAGGAAACAAAGAAAGAGAGA	1882	
Db	1282	ATGGGTGCCAGCTCCGCCAAGTCTGTTGTCTCTGATACCCGAAGACAGTTGCGGG	1341	2242	AGAAAGGTGTACCATTAAGAGAGAGACAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGGA	2301	
Qy	929	AGAGAAACAAACACTCGGCTGAAAGATCAAGCCCTCTCTCATATCTACCCCGAGAT	988	1883	AAGAGAGAAAGGAGGAGAAAGAGCTAATAAACCGCAAGAGAGAAATTTGACTAGATCTT	1942	
Db	1342	GAGGCCATCAGCTCTCTCCGACCCCTATCTACCCGCAACAGACGACTTACTCTCTCT	1401	2302	GGCAGAAAGAAAGGAGAGCGCGCATAGCGCGAAGAAAGAAAGAAAGAAAGTGTGACTAAATTTCT	2361	
Qy	989	TGAGAGCCACCGCTTGGCGGAAACCCCAATCTTTTCCCAACCC---CTTATCTGGC	1045	1943	GGCTGAGTGGTTGAAGGGAACCAATACGGAAGAGAGAGAGATTTTAGGAAATTTAG	2002	
Db	1402	CTCTGAACCCACGCCCCGCTATCTCGGCGGCACTGCAACCCCTCTGGCCCCCTCAGC	1461	2362	GGCCGCACTAGTAAGTAGAAGAGGCTCCACAGGTAGGCACAGGGAAACCTTGACCAACCA	2421	
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Qy	1106	TGCAGGACTCGAG---CCGAGGGGCGCCACCCCGAGCGGACAGACAGATCTCGGAC	1162	2063	TGCATATTTGAAAGAAAGAGACACTCGGCAAGAACTGCCCC---AAGAGGGGAAACAA	2119	
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RESULT 13

US-09-111-085-3

; Sequence 3, Application US/09111085

; Patent No. 6100034

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; GENERAL INFORMATION:
; APPLICANT: Stoye, Jonathan P
; APPLICANT: Weiss, Robin A
; TITLE OF INVENTION: Detection of retroviral subtypes based upon envelope
; TITLE OF INVENTION: specific sequences
; FILE REFERENCE: 4238/75168
; CURRENT APPLICATION NUMBER: US/09/111,085
; CURRENT FILING DATE: 1998-07-07
; EARLIER APPLICATION NUMBER: GB 9710154.7
; EARLIER FILING DATE: 1997-05-16
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 3482
; TYPE: DNA
; ORGANISM: Porcine retrovirus
; US-09-111-085-3
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Query Match 24.8%; Score 2016.4; DB 3; Length 3482;
Best Local Similarity 76.3%; Pred. No. 0;
Matches 2670; Conservative 0; Mismatches 716; Indels 114; Gaps 11;
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Db 426 TTGTGCATACAGACCCCAAGCTCAGGACAGGTTAGAGAGATGAATAGAACCAATTAAAGA 485
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RESULT 14

US-08-258-420-13/c
; Sequence 13, Application US/08258420
; Patent No. 5710037
; GENERAL INFORMATION:
; APPLICANT: Nienhuis, Arthur W.
; APPLICANT: Vanin, Elio F.
; TITLE OF INVENTION: No. 5710037el Retroviral Envelope and LTR and Retroviral Vector
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Carella, Byrne, Bain, Gilfillan, Cecchi, Stewart & Olstein
; STREET: 6 Becker Farm Road
; CITY: Roseland
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07068
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch diskette
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/258,420
; FILING DATE: 10-JUN-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Olstein, Elliot M.
; REGISTRATION NUMBER: 24, 025
; REFERENCE/DOCKET NUMBER: 271010-208
; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 201-994-1700
; TELEFAX: 201-994-1744
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8202 bases
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: genomic DNA
; FEATURE:
; NAME/KEY: viral genome
; US-08-258-420-13

Query Match 21.3%; Score 1728.6; DB 2; Length 8202;
Best Local Similarity 56.0%; Pred. No. 0;
Matches 3966; Conservative 0; Mismatches 2919; Indels 196; Gaps 29;

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QY 4219 TGCAGAAATGGACGCCCTTGTACCTCTACCAAAACGGGAGCTCTGTTTAAATGGGG 4160
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QY 3524 TCCTGAGCACCAAGAGGATTTGATGCTTATCAAAAGGCCCTCTGAGCGCACTGCTCT 3583

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Dd	4099	GGGGTTGCCAGATTGACTAAGCCCTTTGAACCTCTTTGTGCGAGAGAAGCGGCTACGC	4040
Qy	3644	CCGGGAGTTTTAAACCCAAACCTTAGGACCATCGAGAAAGACTGTGCGCTACCTGTCAAA	3703
Dd	4039	CAAAAGCGTCTTAACGCAAAAGCTGGGACCTTGGCGTGGCGGCTGCGCTACCTGTCTAA	3980
Qy	3704	GAAGCTCGATCTGTAGCCAGTGGTTGGCCCATATGCCTGAAGGCTATCGCAGCTGGC	3763
Dd	3979	AAAGCTAGACCCAGTGGCAGCTGGCTGGCCCGCCCTGCTACGGATGGTGGCAGCCATGC	3920
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Dd	3919	AGTTCTGACAAAGATGTGGCAAGCTCACTATGGGACAGCCGTTGGTCATTCTGGCCCC	3860
Qy	3824	CCATGCAATTGGAGAAACATCGTTGGGAGCCCCCAGACCCGATGATGACCAACGCCCGCAT	3883
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Dd	2002	AGCATCAGGACCGACATGGAAGTCCAGCGTTCTCAAAACCCCTTAAGATAGATTAAAC	1943

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2180 CATCTTGGTCCAGGGGSCAACAGAAAGATGCACAAATGACTAAACCGCGGACAG 2239
2356 TTGACTTGGGAGTGGGAGGTAAACCACTGCTTTCTGGTCTATACCTAGTGCCAGCAC 2415
2240 TTAACCTAGGCAAGGAATGGTGACACACTCTCTTGGTGGTACCTGAATGTCCGTACC 2299
2416 CCCTCTTAGGTAGAGACTTATTGACCAAGATGGGAGCACAAT--TTCTTTTCAACAG 2472
2300 CCCTTCTGGGGGAGATCTCTAACCAACTCGGAGCTCAGATCCACTTCTCCGAGGAG 2359
2473 GGAACACAGAGTGTCTGCAATTAACAAACCTATCACTGTGTGACCCCTCCAATTAGATG 2532
2360 GGGCCCAAGTGTAGACCGAGATGGCCCAACCCATCAAAATTTTGACTGTGTCTGCAAG 2419
2533 ACGAATATCGACTATATCTCTCCCTAGTAAGACCTGATCAAAATATACAAATCTGGTTGG 2592
2420 ATGAACACCGGCTTTTGACATCCCGGTCAACACAGCCTCCCT--GATGTCTGGTTAC 2476
2593 AACAGTTTCCCAAGCTGGGCGAAGAACCGCAGGATGGTTTGGCAAGCAAGTCCCC 2652
2477 AAGATTTTCCCAAGCTGGGCGAAGAACCGGAGGACTTGGGCGGCGCAAGTGTCAAGCCC 2536
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2597 GCCTAGAAGCTCATATGGGCAATTCGGCAACACATTTCAAAATTTCTAGAACTTGGAGTTT 2656
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2657 TCGACACTTGTCTGCTCAACCTCGAATACTCTCTTCTGCCAGTAAAGGCTGGTACCC 2716
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2893 CAACAGTCCGAACCTTTAATACCTCTTGTGTCTCTCCACCCCAACCGAGCTGGTATA 2952
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2953 CAGTATCGACTTAAGAGATGCTTCTCTGCTGAGATTTACACCCCACTAGCCACAC 3012
2837 CCGTACTGGACTTAAAGATGCTTCTTTTGTATACCTCTGCGCCGCCCAAGCGAGAAC 2896
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2957 GACTTCCCAAGGGTTCAAAACTCTCCCACTCTCTCGATGAGCTCTCCACAGGAGCC 3016
3133 TGGCCAACTTCAGGATCAACACCTCAGGTGACCTCTCTCAGTACGTGATGATCTGCG 3192
3017 TCACCGACTTCGGGACCCAGCATCCAGAAAGTGACCTCTGCTCCAGTATGTAGATGACCTCC 3076
3193 TTCTGGGGGACCCCAACAGGACTCTTAGAAGGACCGAGGCACTACTGTCTGGAAT 3252
3077 TCTTGGCGGCCCCCAAGAAAGCTCGACGAAGGTACTAGGCACTTACTTCCAGGAAC 3136
3253 TGCTGACTAGCTACAGAGCTCTGTGTAAGAGCCCAAGCTTTGACAGGAGAGGTAA 3312
3137 TAGGTGAGAAAGATACCGGGCATCTGCCAAGAGGCAAAATTTGTGACCAAGGTAA 3196
3313 CATACTTGGGTACAGTTTGGGGACCGGACCGGATGCTGACGAGGCAACGGAAGAAA 3372
3197 CTTACTTGGGTACATCTAGTGGGGAAGAAAGGTGGCTCAACCCCTGGGGCATAGAGA 3256
3373 CTGTAGTCCAGATACCGGCCCCCAACAGGCCCAAAATGAGAGAGTTTGGGGACAG 3432

3257 CTGTGGCTCGCATTCACCCCGGGAATCCCAGAGAGGTGCGTGAATTTCTTGGGAATG 3316
3433 CTGGAATTTGCAGACTGTGGATCCCGGGGTTTGGCACTTTAGCAGCCCCCACTCTACCCGC 3492
3317 CTGGTCTGTGCTGTGGATACCCCGTTTGTGAAATTTGGCCGCCCCCTTTACGCAC 3376
3493 TAAACCAAGAAAAGGGGAATTTCTCTGGGCTCTCTGAGACCAAGAGGCAATTTGATGCTA 3552
3377 TCACCAAGGAAGAGCACCCCTTTACCTGGCAGACAGAGCATCAATTTGGCTTTTGGGCAC 3436
3553 TCAAAAAGGCCCTGTGAGCGCACCTGTCTGGCCCTCCCTGACGTAACCTAAACCCCTTTA 3612
3437 TAAAAAAGGCATCTTGTCTGCCCCAGCCCTTGGGTTACCGGACACCTCAAAGGCCCTTTA 3496
3613 CCCTTTATGTGGATGACGTAAGGGAGTAGCCCGGGAGTTTAAACCCAAACCCCTAGGAC 3672
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3673 CATGGAAGAAGCTGTCTGCTGCTGCTCAAGAGCTCGATCTCTGTAGCCAGTGGTTGGC 3732
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3910 CAGAGAGGTCACTTTCGCTCCACAGCGCTCTCAACCTGCGCACTCTTCTGCTGAGAG 3969
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3970 AGACTGATGACCACTGACTCATGATTTGCCATCAACTATTGATTTGAGGAGACTGGGGTCC 4029
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4090 GCAGCTATGTGGTGAAGGTAAAGGATGCTGGGGCGGCTGGTGGAGCGGACCCGCA 4149
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4390 TACCAAAAGGCTAGCTATTATATACATCTCTCGACATCAGAAAGCTTAAGATCTCATAT 4449
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4450 CCAGAGGAACCCAGATGCTGACCGGGTTGCCAAGCAGGCGAGCCCGGCTG-----TTA 4503

4337	Db	CAGTAGGAAACAGACAGCGCTGACCGAGTGGCCGAGCGGCAATGCGCGGAAGTACTCGA	4399
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4397	Db	CCCTAGCCACAGAACCCTGACAAACACGACGACACATACTATTGAACATACATTATACCTCCG	4456
4564	Qy	AAGACTCGCAAGAGATAAAAAAGATAGACACGATTTCTCTGAGACTCCCGAAGGAGCACTGCT	4623
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4624	Qy	ATACCTCAGATGGGAAGGAAATCTCTGCCCCACAAAGAGGGTTAGATATGTTCCACAGA	4683
4514	Db	GGGAAAAAGAGGGGAAAATAGTCTCTCCCAAAAGGAAGCCCTGGCAATGATCCAGCAGA	4573
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4574	Db	TGCATGCTGGACACACATTGGGTAAATCGAAGCTTAAATTTGTTAAATGAAAAAATCTGACT	4633
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4634	Db	TTCTAAATCCCAAGGCAAGTACACTCATAGACGAAGTGACATCTGCCTGTAAAGTCTGTCT	4693
4804	Qy	AGCTGGTTAATGCTAAATCCTTCCAGATGCTCCAGGGAAGAGACTAAGGGGAAGCCACC	4863
4694	Db	AGCAGGTAAACGCTGGGGCTACCCGAGTGGCCAGCAGGGAACCGGACTCGTGGTAAACGCC	4753
4864	Qy	CAGCGCTCACTGGGAAGTGACATTCACCTAGAGTAAAGCCGGCTAAATACGGAACAAAT	4923
4754	Db	CGGAGTCTATTGGGAANAATAGCTTCACCTGAAGTAAACCTTCATGCTGGGTATTAAGT	4813
4924	Qy	ACCTATTGGTTTGTATAGACACCTTTTCAGGATGGGTAGAGGCTTATCTCTACTAAGAAAG	4983
4814	Db	ACTTACTAGTGTGTGTAGATACCTTTTCAGGATGGGTAGAAGCCTTTCCACCACCGGCAAG	4873
4984	Qy	AGACTTCAAACGCTGGTGGCTTAAAAAATACTGGAAGAAAAATTTTCCAAAGATTTGGAAATAC	5043
4874	Db	AAACGGCACACATAGTAGCCAAAGAAAGATCCTTAGAAGAAATCTTTCTCTAGATTTGGACTTC	4933
5044	Qy	CTAAGGTAATAGGCTCAGACAAATGCTCCAGCTTTTGTGCCCAGGTAAAGTCAGGACTGG	5103
4934	Db	CCAAGGTAATTGGGTGAGACAAACGGGCGGCGCTTCGTTTCCCAGGTAAAGTCAGGGGCTAG	4993
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4994	Db	CCAGGATACTGGGGATTAAATTGGAAAATGCAATTGCTTATAGACCCCAAGGCTCAGGAC	5053
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5054	Db	AGGTAGAGAGAATGAATAGAACAAATAAAAGAGACCCCTTACTTAAATTGACCTTAGAGACTG	5113
5224	Qy	CGGTTAATGATTGATAGCTCTCCTGCGCTTTGTGCTTTTATAGGTTAGGAACACCCCTG	5283
5114	Db	GCTTAAAGATTTGAGACGCGCTCTATCTCTAGCTCTATTAAAGACCCGGAATACGCGCTA	5173
5284	Qy	GACAGTTTGGGCTGACCCCTTATGAATTACTCTACGGGGGACCCCCCCTATGGTAGAAA	5343
5174	Db	ACCGCTTTGGGCTCACTCCATATGAATCCTCTATGAGGACCTCCCCC--TTTGTCAACC	5232
5344	Qy	TTGCTTCTGTATCATAGTGTCTGACGTGTGCTTTTCCAGGCTTTGTTCTCTAGGCTCAAGG	5403
5233	Db	TTACTTAACTCCTTTTCTCCCTCAAATTCATAAGACTGACCTTACAGGGCCC--GGCTAAAG	5290
5404	Qy	CACTTGAGTGGGTGAGACAAACGAGCGGTGGAGGCAACTCCGGGAGGCTCTACTCAGGAGGAG	5463
5291	Db	GACTACAAGCAGTAGTACGCCCCAAATCTGGGCGCCCTTTGGCAGAACTGTAC--CGGCCAG	5347
5464	Qy	GAGACTTTCAGATCCCATCGTTTCAAAGTGGAGAGTTCAGTCTACGTTAGAGCCCAACC	5523
5348	Db	GACATTGCGACACGACCAACCCCTTCAGGTGGGGGACTCCGTCTATGTTAGACGACACC	5407
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5408	Db	GTTCTCAGGGACTCGAGCTCTCGGTGGAAAGAGACCTCATTTGTTCTCTGACCAACCCA	5467

GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: February 5, 2006, 05:34:21 ; Search time 3825 Seconds
(without alignments)
17580.806 Million cell updates/sec

Title: US-10-723-552-3

Perfect score: 8132

Sequence: 1 GCGTGGGTACGACTGTGGG.....CTGTTTGCATCAAAAAAAA 8132

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA Main:*

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- 10: /cgn2_6/ptodata/1/pubpna/US11_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	8132	100.0	8132	8	US-10-723-552-3
2	6931.2	85.2	8916	6	US-10-113-664A-139
3	6931.2	85.2	8918	7	US-10-471-220-1
4	6915.6	85.0	8919	6	US-10-113-664A-138
5	6832.4	84.0	8918	7	US-10-471-220-3
6	6343.4	78.0	8764	6	US-10-113-664A-137
7	6319	77.7	8763	7	US-10-471-220-2
8	6288.8	77.3	8840	8	US-10-471-220-4
9	5460	67.1	8060	8	US-10-723-552-1
10	4970.8	61.1	7333	8	US-10-723-552-2
11	2237	27.5	8655	5	US-10-175-523-85
12	2237	27.5	8655	10	US-11-099-266-85
13	2167.8	26.7	185548	5	US-10-175-523-62
14	2167.8	26.7	185548	10	US-11-099-266-62
15	2113.2	26.0	215980	3	US-09-972-546-16
16	2113.2	26.0	215980	8	US-10-735-256-16
17	1910.8	23.5	1923	7	US-10-441-949-31
18	1910.8	23.5	1923	7	US-10-441-949-33
19	1910.8	23.5	1923	7	US-10-441-949-39
20	1910.8	23.5	1923	7	US-10-441-949-41
21	1774.4	21.8	11364	7	US-10-677-558-11
22	1765	21.7	8889	7	US-10-677-558-4
23	1765	21.7	11394	7	US-10-677-558-5

24	1722	21.2	2034	7	US-10-441-949-35
25	1722	21.2	2034	7	US-10-441-949-37
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30	1657.8	20.4	8323	3	US-09-970-597-2
31	1648.8	20.3	2000	3	US-09-851-859A-25
32	1648.8	20.3	2000	3	US-09-851-859A-30
33	1640.2	20.2	8332	3	US-09-006-298-1
34	1475.6	18.1	2040	6	US-10-113-664A-4
35	1403	17.3	1986	7	US-10-441-949-15
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38	1382.2	17.0	1986	7	US-10-441-949-17
39	1369	16.8	153740	7	US-10-322-696-85
40	1335.6	16.4	2034	7	US-10-441-949-11
41	1318	16.2	2034	7	US-10-441-949-13
42	1219.6	15.0	3604	7	US-10-284-839-4
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44	1041.2	12.8	2030	6	US-10-113-664A-5
45	1035	12.7	1923	7	US-10-441-949-61

ALIGNMENTS

RESULT 1
US-10-723-552-3
; Sequence 3, Application US/10723552 ✓
; Publication No. US20040185435A1
; GENERAL INFORMATION:
; APPLICANT: Jay A. Fishman
; TITLE OF INVENTION: MOLECULAR SEQUENCE OF SWINE RETROVIRUS
; NUMBER OF SEQUENCES: 74
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 60 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE: 26-Nov-2003
; PRIORITY DATA:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/661,858
; FILING DATE: 14-Sep-2000
; APPLICATION NUMBER: 08/766,528
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Louis Myers
; REGISTRATION NUMBER: 35,965
; REFERENCE/DOCKET NUMBER: MGP-038CP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)227-5941
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8132 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-10-723-552-3

Query Match		100.0%;	Score 8132;	DB 8;	Length 8132;		
Best Local Similarity		100.0%;	Pred. No. 0;				
Matches 8132; Conservative		0;	Mismatches	0;	Indels	0;	Gaps
		0;					
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QY	241	GTCTCTGTTCTGAGTGTCTGTTTTCAGTGTGGCGCTTTTCGGTTTGCAGCTGTCTCTC	300				
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QY	361	CCCTGGGGACGCCCGGGAGGTGAGGAGCCAGGAGCGCTGGTGTCTCTACTGTC	420				
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Db	1021	CTGTCCCCCAACCCCTTATCTGGCACAGGGTGC	1080	QY	1081	GAGCTCCGCGGTGGAGGACCTGTGCGAGGACTCGGAGCCGAGGGCGCCACCCCGG	1140
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Db	1201	GCCAAATTGAGCCCTCCAGTATTTGGCCCTTTCTTCTGAGATCTCTAATTTGAAAA	1260	QY	1261	CTAAACCATCCCTTCTCGAGGATCCCAACGCTCACGGGTTGGTGGAGTCCCTTA	1320
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QY	1321	TGTTCTCTCACAGCCTACTTGGGATGATTTGTCAACAGCTGTCTGACAGACACTCTTCAAA	1380	QY	1321	TGTTCTCTCACAGCCTACTTGGGATGATTTGTCAACAGCTGTCTGACAGACACTCTTCAAA	1380
Db	1321	TGTTCTCTCACAGCCTACTTGGGATGATTTGTCAACAGCTGTCTGACAGACACTCTTCAAA	1380	QY	1381	CGAGGAGCAGAGAGAAATTTCTATTAGAGCTAGAAAAAATGTTCTTGGGGCCGACGGGC	1440
Db	1381	CGAGGAGCAGAGAGAAATTTCTATTAGAGCTAGAAAAAATGTTCTTGGGGCCGACGGGC	1440	QY	1381	CGAGGAGCAGAGAGAAATTTCTATTAGAGCTAGAAAAAATGTTCTTGGGGCCGACGGGC	1440
QY	1441	GACCCACGCGTTCGAAATGAGATTTGACATGGATTTCCCTTAACTCGCCAGGCTCTCGTGGCGG	1500	QY	1441	GACCCACGCGTTCGAAATGAGATTTGACATGGATTTCCCTTAACTCGCCAGGCTCTCGTGGCGG	1500
Db	1441	GACCCACGCGTTCGAAATGAGATTTGACATGGATTTCCCTTAACTCGCCAGGCTCTCGTGGCGG	1500	QY	1501	ACTCAACACGCGTGAAGGTAGGAGGCTTGAATAATCTATCGCCAGGCTCTCGTGGCGG	1560
QY	1501	ACTCAACACGCGTGAAGGTAGGAGGCTTGAATAATCTATCGCCAGGCTCTCGTGGCGG	1560	Db	1501	ACTCAACACGCGTGAAGGTAGGAGGCTTGAATAATCTATCGCCAGGCTCTCGTGGCGG	1560
QY	1561	GTCTCCGGGGCGCTCAAGCGGCCCACTAAATTTGGCTTAAGTAAGAGATGATGCAGG	1620	QY	1561	GTCTCCGGGGCGCTCAAGCGGCCCACTAAATTTGGCTTAAGTAAGAGATGATGCAGG	1620
Db	1561	GTCTCCGGGGCGCTCAAGCGGCCCACTAAATTTGGCTTAAGTAAGAGATGATGCAGG	1620	QY	1621	GACCGAATCAACCCCTCTGTTTTTCTTGAGAGGCTCTTGGAAGCTTTCAGGCGGTACA	1680
QY	1621	GACCGAATCAACCCCTCTGTTTTTCTTGAGAGGCTCTTGGAAGCTTTCAGGCGGTACA	1680	Db	1621	GACCGAATCAACCCCTCTGTTTTTCTTGAGAGGCTCTTGGAAGCTTTCAGGCGGTACA	1680
QY	1681	CCCCCTTTGATCCACCTCAGAGGCCCAAAAAGCTCAGTGGCTTTGGCTTTTATAGGAC	1740	QY	1681	CCCCCTTTGATCCACCTCAGAGGCCCAAAAAGCTCAGTGGCTTTGGCTTTTATAGGAC	1740
Db	1681	CCCCCTTTGATCCACCTCAGAGGCCCAAAAAGCTCAGTGGCTTTGGCTTTTATAGGAC	1740	QY	1741	AGTCAGCCTTGGATATTAGAAAGAGCTTCAGAGACTGGAAGGTTTACAGGAGCCTGAGT	1800
QY	1741	AGTCAGCCTTGGATATTAGAAAGAGCTTCAGAGACTGGAAGGTTTACAGGAGCCTGAGT	1800	Db	1741	AGTCAGCCTTGGATATTAGAAAGAGCTTCAGAGACTGGAAGGTTTACAGGAGCCTGAGT	1800
QY	1801	TACGTGATCTAGTGAAGGAGGACAGAAAGTATTATCAAAAAGGGAGACAGAAAGAAA	1860	QY	1801	TACGTGATCTAGTGAAGGAGGACAGAAAGTATTATCAAAAAGGGAGACAGAAAGAAA	1860
Db	1801	TACGTGATCTAGTGAAGGAGGACAGAAAGTATTATCAAAAAGGGAGACAGAAAGAAA	1860	QY	1861	GGGAAACAAAGAAAAGAGAGAGAAAGGAGGAAAGACGCTAATAAACGCCAAG	1920
QY	1861	GGGAAACAAAGAAAAGAGAGAGAAAGGAGGAAAGACGCTAATAAACGCCAAG	1920	Db	1861	GGGAAACAAAGAAAAGAGAGAGAAAGGAGGAAAGACGCTAATAAACGCCAAG	1920
QY	1921	AGAAGATTTGACTAAGATCTTGGCTGCAAGTGTGAAGGAAAAGCAATACGGAAGAG	1980	QY	1921	AGAAGATTTGACTAAGATCTTGGCTGCAAGTGTGAAGGAAAAGCAATACGGAAGAG	1980
Db	1921	AGAAGATTTGACTAAGATCTTGGCTGCAAGTGTGAAGGAAAAGCAATACGGAAGAG	1980	QY	1981	AGAGAGATTTTAGGAAAATTTAGGTCAAGGCTTACAGTCAAGGAACTTGGGCAATAGGA	2040
QY	1981	AGAGAGATTTTAGGAAAATTTAGGTCAAGGCTTACAGTCAAGGAACTTGGGCAATAGGA	2040	Db	1981	AGAGAGATTTTAGGAAAATTTAGGTCAAGGCTTACAGTCAAGGAACTTGGGCAATAGGA	2040
QY	2041	CCCCCTCCAGCAGGACCAATTTGTCATATTGTAAGAAAAGAGACACTGGCGCAAGAACT	2100	QY	2041	CCCCCTCCAGCAGGACCAATTTGTCATATTGTAAGAAAAGAGACACTGGCGCAAGAACT	2100
Db	2041	CCCCCTCCAGCAGGACCAATTTGTCATATTGTAAGAAAAGAGACACTGGCGCAAGAACT	2100	QY	2101	GGCCCAAGAGGAAAACAAAGGACCAAGGATCTAGATCTTAGAAGAAATAAGATTAGG	2160
QY	2101	GGCCCAAGAGGAAAACAAAGGACCAAGGATCTAGATCTTAGAAGAAATAAGATTAGG	2160				

Db	2101	GCCCCAAGAGGGAAACAAAGGACCAAGGATCCTAGCTCTAGAGAAGATAAAGATTAGG	2160
Qy	2161	GGAGACGGGGTTGGGACCCCTCCCGCAGCCAGGGTAACTTTGAAAGCTGGAGGGCAAC	2220
Db	2161	GGAGACGGGGTTGGGACCCCTCCCGCAGCCAGGGTAACTTTGAAAGCTGGAGGGCAAC	2220
Qy	2221	CAGTTGAGTTCTCGTTTGATACCGGAGCGAAACATTCAGTGTCTACTACAGCCATTAGGAA	2280
Db	2221	CAGTTGAGTTCTCGTTTGATACCGGAGCGAAACATTCAGTGTCTACTACAGCCATTAGGAA	2280
Qy	2281	AACATAAAGATATAAATAATCTCGGTGATGGGTGCCACAGGGCAACAAAGTATCCATGGA	2340
Db	2281	AACATAAAGATATAAATAATCTCGGTGATGGGTGCCACAGGGCAACAAAGTATCCATGGA	2340
Qy	2341	CTACCCGAAGAACAGTTGACTTTGGAGTGGAGCGGTAAACCCACTCTTCTGTGTCATAC	2400
Db	2341	CTACCCGAAGAACAGTTGACTTTGGAGTGGAGCGGTAAACCCACTCTTCTGTGTCATAC	2400
Qy	2401	CTGAGTGCACAGACCCCTCTTAGGTAGAGACTTATTGACCAAGATGGGAGCAAAATTTT	2460
Db	2401	CTGAGTGCACAGACCCCTCTTAGGTAGAGACTTATTGACCAAGATGGGAGCAAAATTTT	2460
Qy	2461	CTTTTGAACAGGGAAACCAAGAGTGTGCAAAATAACAAACCTATCACTGTGTTGACCC	2520
Db	2461	CTTTTGAACAGGGAAACCAAGAGTGTGCAAAATAACAAACCTATCACTGTGTTGACCC	2520
Qy	2521	TCGAATTAGATGACGAATATCGACTATCTCTCCCTAGTAAAGCCTGATCAAAATATAC	2580
Db	2521	TCCGAATTAGATGACGAATATCGACTATCTCTCCCTAGTAAAGCCTGATCAAAATATAC	2580
Qy	2581	AAATTCGTGGTGAACAGTTTCCCAAGCTGGGAGAAACCGCAGGAGTGGTTTGGCAA	2640
Db	2581	AAATTCGTGGTGAACAGTTTCCCAAGCTGGGAGAAACCGCAGGAGTGGTTTGGCAA	2640
Qy	2641	AGCAAGTTTCCCAAGCTTATCAACTGAAGGCCAGTGGCCACACCACTGTCAGTCAGAC	2700
Db	2641	AGCAAGTTTCCCAAGCTTATCAACTGAAGGCCAGTGGCCACACCACTGTCAGTCAGAC	2700
Qy	2701	AGTACCCCTTGAGTAAAGAGCTCAAGAGGAATTCGGCCGCATGTCCAAAGATTATTC	2760
Db	2701	AGTACCCCTTGAGTAAAGAGCTCAAGAGGAATTCGGCCGCATGTCCAAAGATTATTC	2760
Qy	2761	AACAGGGCATCTAGTTCTCTGTCGAATCTCCCTGGAATCTCCCTGCTACCGGTTAGAA	2820
Db	2761	AACAGGGCATCTAGTTCTCTGTCGAATCTCCCTGGAATCTCCCTGCTACCGGTTAGAA	2820
Qy	2821	AGCCTGGAGCTAAATGACTATCGACCACTACAGGACTTCAGAGAGGTCAATAAACGGGTGC	2880
Db	2821	AGCCTGGAGCTAAATGACTATCGACCACTACAGGACTTCAGAGAGGTCAATAAACGGGTGC	2880
Qy	2881	AGGATATACCCCAACAGTCCGGAACCTTATACCTCTTGTGTGCTCTCCCAACCCCAAC	2940
Db	2881	AGGATATACCCCAACAGTCCGGAACCTTATACCTCTTGTGTGCTCTCCCAACCCCAAC	2940
Qy	2941	GGAGCTGTATACAGTATGACTTAAAGAGTAAAGGATGCTTCTGCTGAGATTACACCCCA	3000
Db	2941	GGAGCTGTATACAGTATGACTTAAAGAGTAAAGGATGCTTCTGCTGAGATTACACCCCA	3000
Qy	3001	CTAGCCAAACCACTTTTGGCTTCGAAATGGAGAGATCCAGGTACGGGAAAGAACCGGGCAGC	3060
Db	3001	CTAGCCAAACCACTTTTGGCTTCGAAATGGAGAGATCCAGGTACGGGAAAGAACCGGGCAGC	3060
Qy	3061	TCACCTGAGACCGGACTGCCCAAGGGTTCAAGAACTCCCGGACCACTTTTGAACGAGGCC	3120
Db	3061	TCACCTGAGACCGGACTGCCCAAGGGTTCAAGAACTCCCGGACCACTTTTGAACGAGGCC	3120
Qy	3121	TACACAGAGACTGCGCAACTTCAGGATCCACACCTCAGGTGACCTCTCCAGTACG	3180
Db	3121	TACACAGAGACTGCGCAACTTCAGGATCCACACCTCAGGTGACCTCTCCAGTACG	3180
Qy	3181	TGGATGACTGCTCTGGGGAGGCCACCAACAGGACTGCTTTAGAGGACGAGAGGCAC	3240
Db	3181	TGGATGACTGCTCTGGGGAGGCCACCAACAGGACTGCTTTAGAGGACGAGAGGCAC	3240
Qy	3241	TACTGCTGGAAATTTCTGACCTAGGCTACAGAGCTCTGCTAAAGAGGCCAGATTGCA	3300
Db	3241	TACTGCTGGAAATTTCTGACCTAGGCTACAGAGCTCTGCTAAAGAGGCCAGATTGCA	3300
Qy	3301	GGAGAGAGGTAAACATCTTGGGGTACAGTTTGGGGACGGGCAGCGATGGCTGACGGAGG	3360
Db	3301	GGAGAGAGGTAAACATCTTGGGGTACAGTTTGGGGACGGGCAGCGATGGCTGACGGAGG	3360
Qy	3361	CACGGAAGAAAACCTGTAGTCCAGATACCGGCCCAACACACAGCCCAACAAATGAGAGAGT	3420
Db	3361	CACGGAAGAAAACCTGTAGTCCAGATACCGGCCCAACACACAGCCCAACAAATGAGAGAGT	3420
Qy	3421	TTTTTGGGGACAGCTGGATTTTGCAGACTGTGGATCCCGGGTTCGCACTTTAGCAGCCC	3480
Db	3421	TTTTTGGGGACAGCTGGATTTTGCAGACTGTGGATCCCGGGTTCGCACTTTAGCAGCCC	3480
Qy	3481	CACCTACCCGCTAAACCAAGAAAAGGGGAAATTTCTCTGGGCTCTTGAGCACCAGAGG	3540
Db	3481	CACCTACCCGCTAAACCAAGAAAAGGGGAAATTTCTCTGGGCTCTTGAGCACCAGAGG	3540
Qy	3541	CATTTGATGCTATCAAAAAGGCCCTGCTGAGCGCACCTGCTCTGGCCCTCCCTGACGCTAA	3600
Db	3541	CATTTGATGCTATCAAAAAGGCCCTGCTGAGCGCACCTGCTCTGGCCCTCCCTGACGCTAA	3600
Qy	3601	CTAAACCCCTTTTACCCCTTTTATGTGGATGAGCGTAAAGGAGTAGCCCGGGAGTTTTAAACC	3660
Db	3601	CTAAACCCCTTTTACCCCTTTTATGTGGATGAGCGTAAAGGAGTAGCCCGGGAGTTTTAAACC	3660
Qy	3661	AAACCCCTAGGACCAATGAGAGAACCTGTGCGCTACCTGTCAAGAAAGCTCGATCTGTAG	3720
Db	3661	AAACCCCTAGGACCAATGAGAGAACCTGTGCGCTACCTGTCAAGAAAGCTCGATCTGTAG	3720
Qy	3721	CCAGTGTGGCCCATATGCTGAAGGCTATCGCAGCTGTGGCCCATCTGCTCAAGGACG	3780
Db	3721	CCAGTGTGGCCCATATGCTGAAGGCTATCGCAGCTGTGGCCCATCTGCTCAAGGACG	3780
Qy	3781	CTGACAAATTTGACTTTGGGACAGAAATATACTGTAATAGCCCCCATCATTTGGAGAAAC	3840
Db	3781	CTGACAAATTTGACTTTGGGACAGAAATATACTGTAATAGCCCCCATCATTTGGAGAAAC	3840
Qy	3841	TCGTTTCGGCAGCCCCCAGACCGATGGATGACAAACCGCCCGCATGACCCACTATCAAAGCC	3900
Db	3841	TCGTTTCGGCAGCCCCCAGACCGATGGATGACAAACCGCCCGCATGACCCACTATCAAAGCC	3900
Qy	3901	TGCTTCTCACAGAGAGGTGACGTTCCCTCCACAGCGCTCTCAACCTGCTCACTCTTC	3960
Db	3901	TGCTTCTCACAGAGAGGTGACGTTCCCTCCACAGCGCTCTCAACCTGCTCACTCTTC	3960
Qy	3961	TGCTTCTCACAGAGAGGTGACGTTCCCTCCACAGCGCTCTCAACCTGCTCACTCTTC	4020
Db	3961	TGCTTCTCACAGAGAGGTGACGTTCCCTCCACAGCGCTCTCAACCTGCTCACTCTTC	4020
Qy	4021	CTGGGGTCCGCAAGACCTTACAGACATACCGCTGACTGGAGAGTGTCTTAACCTGTTCA	4080
Db	4021	CTGGGGTCCGCAAGACCTTACAGACATACCGCTGACTGGAGAGTGTCTTAACCTGTTCA	4080
Qy	4081	CTGACGAGAGCAGCTATGTGTGGAGGTAGAGATGCTGGGGCGCGGTGGAGCG	4140
Db	4081	CTGACGAGAGCAGCTATGTGTGGAGGTAGAGATGCTGGGGCGCGGTGGAGCG	4140
Qy	4141	GGACCCGACCATCTGGGCCAGACGCTCCCGGAAGGAACTTCAGCACAAAAGGCTGAGC	4200
Db	4141	GGACCCGACCATCTGGGCCAGACGCTCCCGGAAGGAACTTCAGCACAAAAGGCTGAGC	4200
Qy	4201	TCATGGCCCTCACGCAAGCTTTGCGGTGGCGGAGGAAATTCATAAACATTTATACGG	4260
Db	4201	TCATGGCCCTCACGCAAGCTTTGCGGTGGCGGAGGAAATTCATAAACATTTATACGG	4260
Qy	4261	ACAGCAGGTATGCTTTGCGGACTGACACAGTACATGGGGCCATCTATATAACAAAGGGGT	4320
Db	4261	ACAGCAGGTATGCTTTGCGGACTGACACAGTACATGGGGCCATCTATATAACAAAGGGGT	4320

QY 4321 TGCCTTACCTCAGCAGGGAGGGAAAATAAGAAACAAAGAGGAAATTTCTAAGCCCTATTAGAAG 4380
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Db 4321 TGCCTTACCTCAGCAGGGAGGGAAAATAAGAAACAAAGAGGAAATTTCTAAGCCCTATTAGAAG 4380
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QY 4381 CGGTACATTTACCAAAAGGCTAGCTATTATACACTGCTCCTGGACATCAGAAGCTAAAG 4440
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Db 4381 CGGTACATTTACCAAAAGGCTAGCTATTATACACTGCTCCTGGACATCAGAAGCTAAAG 4440
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QY 4441 ATCTCATATCCAGAGAAACACAGATGGCTGACCGGGTTGCCAAGCAGGAGCCAGGGTG 4500
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Db 4441 ATCTCATATCCAGAGAAACACAGATGGCTGACCGGGTTGCCAAGCAGGAGCCAGGGTG 4500
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Db 4501 TTAACTCTTGCTTATPATAGAAATGCCCAAGCCCCAGAAACCCAGACGACGATACACCC 4560
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QY 4561 TAGAAGACTGGCAGAGATATAAAGATAGACAGGTTCTTGAGACTCCGGAGGGACCT 4620
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Db 4561 TAGAAGACTGGCAGAGATATAAAGATAGACAGGTTCTTGAGACTCCGGAGGGACCT 4620
|||||
QY 4621 GCTATACCTCAGATGGGAAGGAAATCCTGCCCAAGAAAGGGTTAGAAATATGTCGAAC 4680
|||||
Db 4621 GCTATACCTCAGATGGGAAGGAAATCCTGCCCAAGAAAGGGTTAGAAATATGTCGAAC 4680
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QY 4681 AGATACATCGTCTAACCCACCTAGGAACTAAACACCTGCAGCAGTTGGTCAGAAATCCC 4740
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Db 4681 AGATACATCGTCTAACCCACCTAGGAACTAAACACCTGCAGCAGTTGGTCAGAAATCCC 4740
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QY 4741 CTTATCATGTTCTGAGGCTACCAAGGAGTGCTGACTCGGTGGTCAAAACATTTGTGCCCCT 4800
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Db 4741 CTTATCATGTTCTGAGGCTACCAAGGAGTGCTGACTCGGTGGTCAAAACATTTGTGCCCCT 4800
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Db 4801 GCCAGCTGTTAATGCTAATCCTTCCAGAAATGCTCCAGGGAAGAGACTAAGGGGAAGCC 4860
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Db 4861 ACCCAGCGCTCACTGGGAAGTGGACTTCACTGAGGTAAGCCGGCTAAATACGGAAACA 4920
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Db 4921 AATACCTATGTTTTGTAGACACCTTTTCAGGATGGGTAGAGGCTTATCTCTACTAAGA 4980
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QY 4981 AAGAGACTTCAACCGTGGTGGCTTAAAAAAATCTCGAAGAAATTTTTCAGAAATTTGGAA 5040
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Db 4981 AAGAGACTTCAACCGTGGTGGCTTAAAAAAATCTCGAAGAAATTTTTCAGAAATTTGGAA 5040
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Db 5041 TACCTAAGGTAATAGGGTCAGACAAATGGTCCAGCTTTTGTGCCCAGGTAAGTCAGGGAC 5100
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Db 5101 TGGCCAAGATATTTGGGGATTTGTAAGAACTGATGATGCTGATACAGACCCCAAGCTCAG 5160
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QY 5161 GACAGGTAGAGGATGAATAGAACCAATTAAGAGACCCTTACTAAATTTGACCGCGGAGA 5220
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Db 5161 GACAGGTAGAGGATGAATAGAACCAATTAAGAGACCCTTACTAAATTTGACCGCGGAGA 5220
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Db 5221 CTGGCCCTTAATGATTTGGATAGCTCTCTGCCCCCTTTGTGCTTTTATAGGGTTAGGAAACACCC 5280
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Db 5281 CTGGACAGTTTGGGCTGACCCCCCTATGAATTAATCTACGGGGAGACCCCCCTTAGGTAG 5340
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QY 5341 AAAATGCTCTGTGATAGTGTGCTGCTTTCCAGACCTTTGTTCTCTAGGCTCA 5400
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Db 5341 AAAATGCTCTGTGATAGTGTGCTGCTTTCCAGACCTTTGTTCTCTAGGCTCA 5400
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Db 5401 AGGCACCTTGAAGTGGGTGAGACCAACGAGCGTGGAGGCAACTCCGGAGGGCTCTACTAGGAG 5460
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Db 5521 ACCGTGCAGAAACCTCGAGACTCGGTGGAGGGCCCTTATCTGTACTTTTTGACACAC 5580
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QY 5581 CAAACGCTGTGAAGTTCGAGAACTCCACCTGTGATCCATCGATCCCAAGTCTAAACCGG 5640
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Db 5581 CAAACGCTGTGAAGTTCGAGAACTCCACCTGTGATCCATCGATCCCAAGTCTAAACCGG 5640
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Db 5641 CCCCACCTCCCATTTCCGGGTGGAAGCGGAAAGACTGAAATCCCTTTAAGCTTCGCC 5700
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QY 5701 TCCATCGGTGGTTCTTACTCTGTCAATAACCTCTCAGACTAATGGTATGCGCATAGGA 5760
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Db 5761 GACAGCTGAATCCCATTAACCCCTTATCTCTCACTGGTTAATTAAGTCTCCGACCA 5820
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Db 5881 TAGCTTTGCTCAGATCAGTTATCTAGTCTGAACCTCAACCCAGATATCTCTCAATGCT 5940
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Db 5941 CACGGAATTTTATGTTGCCAGGACCAACCAATATAGGAAACATTCGCGAAATCCAGA 6000
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Db 6061 ACCTCTCAGCAGGATAGGGTAAGTTTCTTATGTCAACACCTATACAGCTCTGACAA 6120
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QY 6121 TTTAATTTACCTGACCTGGATTAGAACTGGAAGCCCCCAAGTCTCTCTTCAGACCTAGAT 6180
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Db 6121 TTTAATTTACCTGACCTGGATTAGAACTGGAAGCCCCCAAGTCTCTCTTCAGACCTAGAT 6180
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QY 6181 TACCTAAATAATAGTTTCACTGAGAAAGGAAACAAAGAAATATCTTAAATGGGTAAAT 6240
|||||
Db 6181 TACCTAAATAATAGTTTCACTGAGAAAGGAAACAAAGAAATATCTTAAATGGGTAAAT 6240
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QY 6241 GGTATGCTTTGGGGAATGGTATATTATGAGGCTCGGGTAAACAAACAGGCTCCAATCTA 6300
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Db 6301 ACTATTCGCTCAAAATAAACAGCTGGAGCCCTCCAATGGCTATAGGACCAATAACGGTC 6360
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QY 6361 TTAGCGGGTCAAGAACCCCAACCAAGGACCAAGGACCAATCTCTAACTTAACCTCTGGA 6420
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Db 6361 TTAGCGGGTCAAGAACCCCAACCAAGGACCAAGGACCAATCTCTAACTTAACCTCTGGA 6420
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QY 6421 TCAGACCCCACTGAGTCTAACAGCAGACTAAAAATGGGGGCAAAATTTTTAGGCTCATC 6480
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Db 6421 TCAGACCCCACTGAGTCTAACAGCAGACTAAAAATGGGGGCAAAATTTTTAGGCTCATC 6480
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QY 6481 CAGGGAGCTTTTCAAGCTCTTAACCTCAAGCTCCAGAGGCTACCTCTCTTGTGTGGCTA 6540
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Db	6481	CAGGAGCTTTTCAAGCTCTTAACCTCCACGACTCCAGAGGCTACCTCTTCTTGTGGCTA	6540
Qy	6541	TGCTTAGCTTGGGCCCCACCTTACTATGAGGAATGGCTAGAGGGAATCAATGTG	6600
Db	6541		6600
Qy	6541	TGCTTAGCTTGGGCCCCACCTTACTATGAGGAATGGCTAGAGGGAATCAATGTG	6600
Db	6541		6600
Qy	6601	ACAAAGAACATAGAGACCAATGCATGCGGATGCCAAATAAGCTTACCTTACTGAG	6660
Db	6601		6660
Qy	6601	ACAAAGAACATAGAGACCAATGCATGCGGATGCCAAATAAGCTTACCTTACTGAG	6660
Db	6601		6660
Qy	6661	GTTTCTGGAAAGGCACTGATAGGAAAGTTCCTCCCAACCAACACCTTTGTAAC	6720
Db	6661		6720
Qy	6661	GTTTCTGGAAAGGCACTGATAGGAAAGTTCCTCCCAACCAACACCTTTGTAAC	6720
Db	6661		6720
Qy	6721	CACACTGAAGCTTTAATCAAACTCTGAGAGTCAATATCTGGTACCTGGTTATGACAGG	6780
Db	6721		6780
Qy	6721	CACACTGAAGCTTTAATCAAACTCTGAGAGTCAATATCTGGTACCTGGTTATGACAGG	6780
Db	6721		6780
Qy	6781	TGTTGGGCGATGTAATCTGGAATTAACCCCTTGTGTTCCACCTTGGTTTAAACCAAACT	6840
Db	6781		6840
Qy	6781	TGTTGGGCGATGTAATCTGGAATTAACCCCTTGTGTTCCACCTTGGTTTAAACCAAACT	6840
Db	6781		6840
Qy	6841	AAAGATTTTGCATTAATGGTCCAAATGTTTCCCGAGTGTATTAATCTATCCGAAAGACA	6900
Db	6841		6900
Qy	6841	AAAGATTTTGCATTAATGGTCCAAATGTTTCCCGAGTGTATTAATCTATCCGAAAGACA	6900
Db	6841		6900
Qy	6901	ATCCTTGATGATGACTACAGAAATCATCGAACAAGAGAGAACCATATCTCTGACA	6960
Db	6901		6960
Qy	6901	ATCCTTGATGATGACTACAGAAATCATCGAACAAGAGAGAACCATATCTCTGACA	6960
Db	6901		6960
Qy	6961	CTTCTGTGATGCTCGGACTTGGAGTGGCAGAGGTAGGAAACAGAAACAGCTGCCCTG	7020
Db	6961		7020
Qy	6961	CTTCTGTGATGCTCGGACTTGGAGTGGCAGAGGTAGGAAACAGAAACAGCTGCCCTG	7020
Db	6961		7020
Qy	7021	GTACGGGACACAGCAGCTAGAAACAGGACTTAGTAACCTTACATCGAATTTGTAAACGAA	7080
Db	7021		7080
Qy	7021	GTACGGGACACAGCAGCTAGAAACAGGACTTAGTAACCTTACATCGAATTTGTAAACGAA	7080
Db	7021		7080
Qy	7081	GATCTCCAGGCTTAGAATAATCTGTCACTAAGTCTGGAGGATCCCTAACCTCTTATCT	7140
Db	7081		7140
Qy	7081	GATCTCCAGGCTTAGAATAATCTGTCACTAAGTCTGGAGGATCCCTAACCTCTTATCT	7140
Db	7081		7140
Qy	7141	GAAGTAGCTTACAGATAGAGAGGTTAGATTTATTTTCTAAAGAGAGGAGTTA	7200
Db	7141		7200
Qy	7141	GAAGTAGCTTACAGATAGAGAGGTTAGATTTATTTTCTAAAGAGAGGAGTTA	7200
Db	7141		7200
Qy	7201	TGTTAGCTTTGAAGGAGGATGCTGTTTTATGTGGATCATTCAGGGGCCATCAGAGAC	7260
Db	7201		7260
Qy	7201	TGTTAGCTTTGAAGGAGGATGCTGTTTTATGTGGATCATTCAGGGGCCATCAGAGAC	7260
Db	7201		7260
Qy	7261	TCCATGAACAAGCTTAGAGAAAGTTGGAGAGCGTCAAGGGAAGAACTACTCAA	7320
Db	7261		7320
Qy	7261	TCCATGAACAAGCTTAGAGAAAGTTGGAGAGCGTCAAGGGAAGAACTACTCAA	7320
Db	7261		7320
Qy	7321	GGTGGTTTGAAGGATGCTTCAACAGCTCTTTTGGTGGCTTACCTACTTTTCTGCTTTA	7380
Db	7321		7380
Qy	7321	GGTGGTTTGAAGGATGCTTCAACAGCTCTTTTGGTGGCTTACCTACTTTTCTGCTTTA	7380
Db	7321		7380
Qy	7381	ACAGGACCTTAAATAGTCTCTCTCTGTTACTCACAGTTGGGCCCATGTATTATTAACAG	7440
Db	7381		7440
Qy	7381	ACAGGACCTTAAATAGTCTCTCTCTGTTACTCACAGTTGGGCCCATGTATTATTAACAG	7440
Db	7381		7440
Qy	7441	TTAATTGCTTCAATTAGAGAACGAATAAGTGCAATCCAGATCATGGTACTTAGACAACAG	7500
Db	7441		7500
Qy	7441	TTAATTGCTTCAATTAGAGAACGAATAAGTGCAATCCAGATCATGGTACTTAGACAACAG	7500
Db	7441		7500
Qy	7501	TACCAAGCCCTTAGCAGGAGCTGCGCTAGCTCTACCACTTCTAGATTTAGAAC	7560
Db	7501		7560
Qy	7501	TACCAAGCCCTTAGCAGGAGCTGCGCTAGCTCTACCACTTCTAGATTTAGAAC	7560
Db	7501		7560
Qy	7561	TATTAAAGAGAGAGTGGGGAATGAAAGGATGAAATACAACTAAGCTTAATGAGAA	7620
Db	7561		7620
Qy	7561	TATTAAAGAGAGAGTGGGGAATGAAAGGATGAAATACAACTAAGCTTAATGAGAA	7620
Db	7561		7620

RESULT 2
US-10-113-664A-139
; Sequence 139, Application US/10113664A
; Publication No. US20030224350A1
; GENERAL INFORMATION:
; APPLICANT: Cui, Cunqi
; APPLICANT: Diamond, Lisa E.
; APPLICANT: Logan, John S.
; APPLICANT: Nextran, Inc.
; TITLE OF INVENTION: Elimination of Endogenous Porcine
; TITLE OF INVENTION: Retrovirus
; FILE REFERENCE: 630666.00009
; CURRENT APPLICATION NUMBER: US/10/113,664A
; CURRENT FILING DATE: 2002-03-28
; PRIOR APPLICATION NUMBER: US 60/279,337
; PRIOR FILING DATE: 2001-03-28
; NUMBER OF SEQ ID NOS: 139
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 139
; LENGTH: 8916
; TYPE: DNA
; ORGANISM: Sus scrofa
; FEATURE:
; OTHER INFORMATION: porcine endogenous retrovirus (PERV)
; OTHER INFORMATION: G28 locus; G28 PERV genome
US-10-113-664A-139

Query Match 85.2%; Score 6931.2; DB 6; Length 8916;
Best Local Similarity 91.4%; Pred. No. 0;
Matches 7574; Conservative 0; Mismatches 548; Indels 164; Gaps 15;
Qy 1 GCGTGGTGTAGACTGTGGGCCCGCCGCTTGAATATAAATCCTCTTCTGCTTTGCA 60
Db 559 GCGTGGTGTAGACTGTGGGCCCGCCGCTTGAATATAAATCCTCTTCTGCTTTGCA 618

QY 61 TCAGACCCGCTTCTCTGTGAGTGATTAAGGGAGTCGCCCTTTTCCGAGCCTGAGG----- 115
Db 619 TCAGACCCGCTTCTCTGTGAGTGATT-TGGGGTGTGCGCTCTTCCGAGTCAGGACGAGAGG 677
QY 116 ----TTCCTTTTTCCTGCTTCTTACATTTGGGGGCTCGTCGGGATCTGTGCGGCCACCCC 171
Db 678 GAATTTAACTCGACTGGCCCTTTCAGTTTGGTGGTGGCCGGGAAACCCCGCACTACCCC 737
QY 172 TAACACCCGAGAACCCGACTTGGAGGTAAAGAGATCCTCTTTTAACTGTATGCAATGA 231
Db 738 TCACACCTGAGAACCCGACTTGGAGGT-AAAGGATCCCTTTGGAACTGTGAGTGTGA 796
QY 232 --CCGGCCGGCGTCTCTGTTCTGAGTGTCTGTTTTCAGTGGTGCOCGCTTTCCGTTTGA 289
Db 797 TGTCCGCTGGCGTCTCTGTTCTGAGTGTCTGTTTTCGCTGATGTCGGCGCTTTCGGTTTGA 856
QY 290 GCTGTCTCTCAGGCCGTAAGGCTGGGGATCTGTGATCAGCAGAGCTGCTAGGAGATC 349
Db 857 GCTGTCTCTCAGACCGTAAGGACTGGGGACTGTGATCAGCAGACGTGCTAGGAGATC 916
QY 350 ACAGGCTGTGCGCTTGGGGACGCCCGGAGGTGAGGAGCCAGGGACGCTGGTGGT 409
Db 917 ACAGGCTGCAACCTTGGGGACGCCCGGAGGTGGGGAGCCAGGAGCGCTGGTGGT 976
QY 410 CTCCTACTGTGCGTCAAGGACCGAAATCTGTTGCTGAAAGCGAAAGCTTCCCGCTCCGG 469
Db 977 CTCCTTCTGTGCGTCAAGGACCGAGTCTGTTGTTGAAAGCGAAAGCTTCCCGCTCCGG 1036
QY 470 ACCGTCGAGCTCTTTTGGCTGTTGTTGGAAGAGCTGGACGGGTCACTGTGTCTGATCT 529
Db 1037 GCCGTCGAGCTCTTTTGGCTGCTGTGTGAAGACGCGGACGGGTGCGGTGTGTCTGGATCT 1096
QY 530 GTTGGTTTCTGTTTCTGTGTCTTTCTGTGTGTGCTTGTCTACAGTTTAAATATGG 589
Db 1097 GTTGGTTTCTGTTTCTGTGTCTTTGTCTGTGGCTTGTCTACAGTTTAAATATGG 1156
QY 590 ACAGCGGTGACACCCCTCTTAGTTTGTACTCTCGACCATTTGGACTGAAGTTAAATCCAG 649
Db 1157 ACAGCGGTGACACCCCTCTTAGTTTGTACTCTCGACCATTTGGACTGAAGTTAAATCCAG 1216
QY 650 GGCTCAATTTGTCTAGTTTCAAGTTAAGAGGACCTTGGCAGACTTCTGTGTCTCTGA 709
Db 1217 GGCTCAATTTGTCTAGTTTCAAGTTAAGAGGACCTTGGCAGACTTCTGTGTCTCTGA 1276
QY 710 ATGGCCGACATTCGATGTTGGATGGCCATCAGAGGGGACCTTTAATCTGAGATTATCT 769
Db 1277 ATGGCCGACATTCGATGTTGGATGGCCATCAGAGGGGACCTTTAATCTGAGATTATCT 1336
QY 770 GGCTGTTAAAGCAGTTATTTTTCAGACTGGACCCGGCTCTCATCCCGATCAGAGCCCTA 829
Db 1337 GGCTGTTAAAGCAATTTATTTTCAGACTGGACCCGGCTCTCATCCCGATCAGAGCCCTA 1396
QY 830 TATCTTTAGTGGCAAGATTTGGCAGAGATCTCCCGCATGGGTAAACCATTGGGTGA 889
Db 1397 TATCTTTAGTGGCAAGATTTGGCAGAGATCTCCCGCATGGGTAAACCATTGGGTGA 1456
QY 890 TAAGCCAGAAAGCCAGGTCCCGAATCTGCTTGGAGAGAAACAAACACATCGC 949
Db 1457 TAAGCCAGAAAGCCAGGTCCCGAATCTGCTTGGAGAGAAACAAACACATCGC 1516
QY 950 TGAAGAGTCAAGCCCTCTCTCATATCTACCCCGAGATTGAGGAGCCACCGCTTTGGCC 1009
Db 1517 TGAAGAGTCAAGCCCTCTCTCATATCTACCCCGAGATTGAGGAGCCCGCTTTGGCC 1576
QY 1010 GGAACCCCAATCTGTTTCCCGCAACCCCTTATCTGGCAAGGTTGCGGAGGGGACCTTT 1069
Db 1577 GGAACCCCAATCTGTTTCCCGCAACCCCTTATCTGGCAAGGTTGCGGAGGGGACCTTC 1636
QY 1070 TGCCTCTCTGAGCTCCGCGTGGAGGACCTGTCAGGGACCTCGGAGCCGAGGGG 1129
Db 1637 TGCCTCTCTGAGCTCCGCGTGGAGGACCTGTCAGGGACCTGTCAGGGACCTCGGAGCCGAGGGG 1696
QY 1130 CGCCACCCCGGAGGACAGACGAGATCGCGACATTAACCGCTGCGCACGTACGCGCCCTCC 1189

Db 1697 GCGCCACCCCGGAGCGGACAGAGATCGCGCATTTACCGCTGCGCACGTACGCGCCCTCC 1756
QY 1190 CACACGGGGGGCCAAATTTGCAGCCCTCCAGTATTTGGCCCTTTCTTCTGACAGATCTCTA 1249
Db 1757 CATACGGGGGGCCAAATTTGCAGCCCTCCAGTATTTGGCCCTTTCTTCTGACAGATCTCTA 1816
QY 1250 TAAATTTGGAATACTAAACCATCCCTTTCTCGAGGATCCCCAACCGCTCACCGGGTGGT 1309
Db 1817 TAAATTTGGAATACTAAACCATCCCTTTCTCGAGGATCCCCAACCGCTCACCGGGTGGT 1876
QY 1310 GGAGTCCCTTATGTTCTCTCACAGCTACTTTGGGATGATCTCAACAGCTGCTGCAGAC 1369
Db 1877 GGAGTCCCTTATGTTCTCTCACAGCTACTTTGGGATGATGTCAACAGCTGCTGCAGAC 1936
QY 1370 ACTCTTCAACCCGAGGAGCAGAGAGAAATTTCTATTAGAGGTAGAAAAAATTTTCTCTGG 1429
Db 1937 ACTCTTCAACCCGAGGAGCAGAGAGAAATTTCTGTTAGAGGTAGAAAAAATTTTCTCTGG 1996
QY 1430 GGCCTGAGCGGCGAACCCACCGGTTGCAAAATCAGATTTGACATGGGATTTCCCTTAACCTG 1489
Db 1997 GGCCTGAGCGGCGAACCCACCGGTTGCAAAATCAGATTTGACATGGGATTTCCCTTGACTCG 2056
QY 1490 CCCCGTTGGGACTACAAACACCGCTGAAGGTAGGAGAGCTTGAATACTATCGCCAGGC 1549
Db 2057 CCCCGTTGGGACTACAAACACCGCTGAAGGTAGGAGAGCTTGAATACTATCGCCAGGC 2116
QY 1550 TCTGTTGGCGGCTCTCCGGGCGCTCAAGAGCGGCCACTTAATTTGGCTTAAGTAAGAGA 1609
Db 2117 TCTGTTGGCGGCTCTCCGGGCGCTCAAGAGCGGCCACTTAATTTGGCTTAAGTAAGAGA 2176
QY 1610 AGTGTATCAGGGACCGAAATGAACCCCTCTGTTTTTTTGTAGAGGCTCTTGAAGCCCTT 1669
Db 2177 GGTGTATCAGGGACCGAAATGAACCTCCCTCAGTTTTTCTTGAGAGGCTCATGGAAGCCCTT 2236
QY 1670 CAGCGGCTACACCCCTTTTGTATCCACCTCAGAGGCCCAAAAGCCCTCAGTGGCTTTGGC 1729
Db 2237 CAGCGGCTTTCACCCCTTTTGTATCCCTCAGCTCGGAGGCTCAGAAAGCCCTCAGTGGCCCTGGC 2296
QY 1730 CTTTATAGGACAGTCAAGCTTGGATATTAGAAGAGGCTTCAAGAGCTCGAAGGGTTACA 1789
Db 2297 CTTTATAGGACAGTCAAGCTTGGATATTAGAAGAGGCTTCAAGAGCTCGAAGGGTTACA 2356
QY 1790 GGAGGCTGAGTTACGTGATCTAGTGAAGGAGCAGAGAAAGTATATTACAAAAGGGAGC 1849
Db 2357 GGAGGCTGAGTTACGTGATCTAGTGAAGGAGCAGAGAAAGTATATTACAAAAGGGAGC 2416
QY 1850 AGAAGAAAGAGGAAACAAAGAAAGAGAGAGAAAGAGAGAAAGGGAGAAAGACGTAA 1909
Db 2417 AGAAGAAAGAGGAAACAAAGAAAGAGAGAGAAAGAGAGAAAGGGAGAAAGACGTAA 2476
QY 1910 TAAACGGCAAGAGAGAAATTTTCAAGATCTTGGCTGAGTGGTTGAAGGGGAAAAAGCAA 1969
Db 2477 TAAACGGCAAGAGAGAAATTTTCAAGATCTTGGCTGAGTGGTTGAAGGGGAAAAAGCAA 2536
QY 1970 TACGGAAAAAGAGAGAGATTTTGTAGGAAAAATTAGTTCAGGCCCTTAGACGTACAGGGAACCT 2029
Db 2537 TAGGAAAAAGAGAGAGATTTTGTAGGAAAAATTAGTTCAGGCCCTTAGACGTACAGGGAACCT 2596
QY 2030 GGGCAATAGGACCCCTCAGCAAGGACCAATGTGATATTGTAAAGAAAGAGGACACTG 2089
Db 2597 GGGCAATAGGACCCCTCAGCAAGGACCAATGTGATATTGTAAAGAAAGAGGACACTG 2656
QY 2090 GGCAGGAATCTCCCAAGAGGAAACAAAGACCAAGATCCTAGCTCTAGAAGAGA 2149
Db 2657 GGCAGGAATCTCCCAAGAGGAAACAAAGATCTGAAGGCTTTAGCTCTGGAAGAGA 2716
QY 2150 TAAAGATTAGGGAGACGGGGTTTCGACCCCTCCCGAGCCAGGGTAACTTTGAAGGT 2209
Db 2717 TAAAGATTAGGGAGACGGGGTTTCGACCCCTCCCGAGCCAGGGTAACTTTGAAGGT 2776
QY 2210 GAGGGGCAACCAAGTTGAGTTCTGTGTTGATATCCGAGCGGAACATTCAGTGTACTACA 2269

Db 2777 GGAGGGCAACAGTTGAGTTTCGTGGTGTATACCGGAGCGAAACATTCAGTGTCTACTACA 2836
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2770 GCCATTTAGGAATACTAAAGATAAAATCTCTGGGTGATGGTGCCACAGGCGAAACAACA 2329
Db 2837 GCCATTTAGGAATACTAAAGATAAAATCTCTGGGTGATGGTGCCACAGGCGAAACAACA 2896
Qy 2330 GTATCCATGACTACCCGGAAGAACAGTTTGACTCTGGGAGTGGGACGGGTAAACCCACTCGTT 2389
Db 2897 ATATCCATGACTACCCGGAAGAACAGTTTGACTCTGGGAGTGGGACGGGTAAACCCACTCGTT 2956
Qy 2390 TCTGGTCATACCTGAGTGCCAGACACCCCTCTTTAGGTAGAGACTTATTTAGTACCAAGATGGG 2449
Db 2957 TCTGGTCATACCTGAGTGCCAGACACCCCTCTTTAGGTAGAGACTTATTTAGTACCAAGATGGG 3016
Qy 2450 AGCAAAATTTCTTTGAAACAGGGAACAGAGTGTCTGCAATTAACAAACCTATCAC 2509
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Qy 2510 TGTGTTGACCCCTCCAAATTTAGATGACGAATATCGACTATCTCTCCCTAGTAAAGCCTGA 2569
Db 3077 TGTGTTGACCCCTCCAAATTTAGATGACGAATATCGACTATCTCTCCCTAGTAAAGCCTGA 3136
Qy 2570 TCAAAATATACAAATTTCTGGTGGAAACAGTTTCCCAAGCCTGGGCGAAGAACCGCAGGGAT 2629
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Qy 2630 GGGTTTGGCAAGCAAGTTCCTCCCAAGTATTTCAACTGAAGGCCAGTGCCACACCACT 2689
Db 3197 GGGTTTGGCAAGCAAGTTCCTCCCAAGTATTTCAACTGAAGGCCAGTGCTGCACCACT 3256
Qy 2690 GTCACTCAGACAGTACCCCTTGAGTAAAGAGCTCAAGAGGAATTCGGCCGCAATGTCCA 2749
Db 3257 GTCACTCAGACAGTACCCCTTGAGTAAAGAGCTCGAGAGGAATTCGGCCGCAATGTCCA 3316
Qy 2750 AAGATTAAATCCAAACAGGCGATCTAGTTTCCTGTCCTCAATTCCTCCCTGGAAATCTCCCTGCT 2809
Db 3317 AAGATTAAATCCAAACAGGCGATCTAGTTTCCTGTCCTCAATTCCTCCCTGGAAATCTCCCTGCT 3376
Qy 2810 ACCGGTTAGAAAGCTGGGACTAATGACTATCGACAGTACAGACTTGAGAGAGTCAA 2869
Db 3377 ACCGGTTAGAAAGCTGGGACTAATGACTATCGACAGTACAGACTTGAGAGAGTCAA 3436
Qy 2870 TAAACGGGTGAGAGATACACCAACAGTCCCGAACCTTTATACCTTTGTGTCTCT 2929
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Qy 2930 CCCACCCCAACGGAGCTGGTATACAGTATTGGAATTTAAAGGATGCTTTCTCTGCTGAG 2989
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Qy 2990 ATTACACCCCACTAGCCAAACCACTTTTGGCTTTCGAATGGAGAGATCCAGGTACGGGAAG 3049
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Qy 3050 AACCGGCGAGCTCACTCGGACCGGCTCCCGCAAGGTTCAAGACTCCCGACCATCTT 3109
Db 3617 AACCGGCGAGCTCACTCGGACTCGGCTCCCGCAAGGTTCAAAACTCCCGACCATCTT 3676
Qy 3110 TGACGAAGCCCTACACAGAGACCTGGCCAACTTCAGGATCCAAACACCCCTCAGGTGACCCCT 3169
Db 3677 TGACGAAGCCCTACACAGAGACCTGGCCAACTTCAGGATCCAAACACCCCGAGGTGACCCCT 3736
Qy 3170 CCTCCAGTACGTGGATGACTGCTTCTGGCGGAGCCACCAACAGGACTGCTTTAGAAAGG 3229
Db 3737 CCTCCAGTACGTGGATGACTGCTTCTGGCGGAGCCACCAACAGGACTGCTTTAGAAAGG 3796
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Qy 3290 CCAGATTTGACGAGAGGTTAACTATCTGGGTACAGTTTGGCGGACGGGACCGGATG 3349
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Qy 3410 AATGAGAGAGTTTGTGGGACAGCTGGATTTTCAGACTGTGGATCCGGGGTTTGGGAC 3469
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Qy 3770 GGTCAAGAGCGCTGACAAAATTTGACTTTGGGACAGAAATAAATCTGTAAATAGCCCCCATATG 3829
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Qy 3830 ATTTGGGAACATCGTTCCGGCAGCCCCCAGACCGATGATGACCAACGCCGCCCATGACCCA 3889
Db 4397 GTTGGGAACATCGTTCCGGCAGCCCCCAGACCGATGATGACCAACGCCGCCCATGACCCA 4456
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Qy 3950 TGCCACTCTTCTGCTGCTGAAGAGACTGATGAACCAAGTCACTCATGATTCCTCAACTATT 4009
Db 4517 TGCCACTCTTCTGCTGCTGAAGAGACTGATGAACCAAGTCACTCATGATTCCTCAACTATT 4576
Qy 4010 GATTGAGAGACTGGGTCCGCAAGGACCTTTACAGACATACCGCTGCTGAGAGAGTGTCT 4069
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Qy 4070 AACCTGGTTCACTGACGGAAGCAGCTATGTGTGGAAGGTAAAGAGATGGCTGGGGCGGC 4129
Db 4637 AACCTGGTTCACTGACGGAAGCAGCTATGTGTGGAAGGTAAAGAGATGGCTGGGGCGGC 4696
Qy 4130 GGTGTGGAACGGGACCCGCAAGTCTGGGCCAGACGCTGCGGAGAGAACTTTCAGACACA 4189
Db 4697 GGTGTGGAACGGGACCCGCAAGTCTGGGCCAGACGCTGCGGAGAGAACTTTCAGACACA 4756
Qy 4190 AAAAGCTGAGCTCATGGCCCTCAAGAGCTTTGGGCTGGCCGGAAGGAAATCCATAAA 4249
Db 4757 AAAAGCTGAGCTCATGGCCCTCAAGAGCTTTGGGCTGGCCGGAAGGAAATCCATAAA 4816
Qy 4250 CATTTATACGACAGCAGGTATGCTTTGCGACTGACACAGTACATGGGGCCATCTATAA 4309
Db 4817 CATTTATACGACAGCAGGTATGCTTTGCGACTGACACAGTACATGGGGCCATCTATAA 4876
Qy 4310 ACAAGGGGGTGTCTTACTCTCAGCAGGAGGGAATAAAGAAACAAAGAGGAATTTCTAAG 4369
Db 4877 GCAAGGGGGTGTCTTACTCTCAGCAGGAGGGAATAAAGAAACAAAGAGGAATTTCTAAG 4936
Qy 4370 CCTATTAGAGCGGTACATTTTACAAAGGCTAGCTATTATACATCTGCTCTGGACATCA 4429
Db 4937 CCTATTAGAGCGGTACATTTTGGCCAAAAGGCTAGCTATTATACATCTGCTCTGGACATCA 4996

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Qy 6587 GGAATTCATGTGACAAAGACATAGACCAATCCACATGGGGATCCCAAAATAGC 6646
Db 7214 GGAATTCATGTGACAAAGACATAGACCAATGTATGGGATCCCAAAATAGC 7273
Qy 6647 TTACCCCTTACTGAGGTTTCTGGAAAGGCGACCTGTCATAGGAAAGGTTTCCCCCATCCACC 6706
Db 7274 TTACCCCTTACTGAGGTTTCTGGAAAGGCGACCTGTCATAGGAGGTTTCCCCCATCCACC 7333
Qy 6707 AACACCTTTGTAACCACTGAAGCCTTTAATCAAACTCTGAGAGTCAATATCTGTATC 6766
Db 7334 AACACCTTTGTAACCACTGAAGCCTTTAATCAAACTCTGAGAGTCAATATCTGTATC 7393
Qy 6767 CTGGTTATGACAGTGTGGGCGATGTAATCTGAGTAAACCCCTTGTTTCCACCTTGG 6826
Db 7394 CTGGTTATGACAGTGTGGGCGATGTAATCTGAGTAAACCCCTTGTTTCCACCTTGG 7453
Qy 6827 TTTTAAACCAACTAAAGATTTTGGCATTTATGGTCCAAATTTGTTCCCGGAGTGTATTACT 6886
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Qy 6887 ATCCGGAAGAAAGCAATCTTGATGAAATATGACTACAGAAATCATCGACAAAGAGAGAC 6946
Db 7514 ATCCGGAAGAAAGCAATCTTGATGAAATATGACTACAGAAATCATCGGCGCAAAAGAGAGC 7573
Qy 6947 CCATATCTGACACTTGTGATGCTCGGACTTGGAGTGGCGACGAGGTGTAGGAACAG 7006
Db 7574 CCATATCTGACACTTGTGATGCTCGGACTTGGAGTGGCGACGAGGTGTAGGAACAG 7633
Qy 7007 GAACAGCTGCCCTGTCAGCGGACCAACAGCAGCTAGAAACAGGACTTAGTAAACCTTACATC 7066
Db 7634 GAACAGCTGCCCTTAAATCAGAGACCGCAACAGCTGGAGAAAGGACTTAGTAAACCTTACATC 7693
Qy 7067 GAAATTGTAACAGAGATCTCAAGCCCTAGAAAATCTGTAGTAACTGTGAGGAATCCC 7126
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Qy 7127 TAACCTCTTATCTGAAGTAGTCTACAGATAGAGAGGCTTAGATTATTTCTAA 7186
Db 7754 TAACCTCTTATCTGAAGTAGTCTTACAGAAACAGAGAGGCTTAGATTATTTCTAA 7813
Qy 7187 AAGAGGAGGATTTATGCTAGCTTTGAAGGAGGATGCTGTTTATGTTGATCATTCAG 7246
Db 7814 AAGAGGAGGATTTATGCTAGCTTTGAAGGAGGATGCTGTTTATGTTGATCATTCAG 7873
Qy 7247 GGGCATCAGAGACTCCATGAACAGCTTAGAGAAAGGTTGGAGAGCGTCAAGGGAAA 7306
Db 7874 GAGCTATCAGGACTCCATGAGCAAGCTCAGAGAAAGGTTAGAAAACGTCAACAAAGAA 7933
Qy 7307 AGGAAACTACTCAAGGGTGGTTGAGGATGGTTCAACAGTCTCTTTGGTTGGTACCC 7366
Db 7934 AAGAGGCTGGCAAGAGTGGTTGAGGATGGTTCAACAGTCTCTTTGGTTGGTACCC 7993
Qy 7367 TACTTTCTGCTTTAAGAGGACCTTAAAGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 7426
Db 7994 TGCTTTCTGCTTTAAGAGGACCTTAAAGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 8053
Qy 7427 GTATTATTAAACAGTTAATGCTTCTTATAGAGAACGAATAGTCAAGTCCAGATCATGG 7486
Db 8054 GCTTAATTAAATCGGTTTGTGCTTTGTTAGAGAACAGTGAAGTCCGATCATGG 8113
Qy 7487 TACTTTAGAACAGTACCAAGCCGCTTACG --- AGGAGCTGGCGCTAGCTCTACC 7543
Db 8114 TACTTTAGAACAGTACCAAGCCGCTTCCAAAGTAAAGAGAACTGACCTTTAGCCCTTCT 8173
Qy 7544 AGTTCTAAGATTAGAACTATTAAACAGAGAGAGTGGGATGAAGAGTGAAGATACA 7603
Db 8174 AGTTCTAAGATTAGAACTATTAAACAGAGAGAGTGGGATGAAGAGTGAAGATACA 8233
Qy 7604 ACCT-----AAGCTAATCAGAGGCTTAAATTTGTTCTGAATTCAG 7644
Db 8234 ACCTGACTCTCCAGAACCCAGGAAGTTAATGAAGAGCTCTAATGCTCCCTCGAATCCAG 8293

Qy 7645 AGTTGTTCTCTATAGTAAAGATTAGGTTTTTTTGTCTGTTTTTAAATATGC----- 7696
Db 8294 ACCCTGTTCCCTATAGTAAAGATCATCTTTTGTCTGTTTGTAGGCTTGTCTTCTGCT 8353
Qy 7697 -----GGAAGTAAATAGGCTCTGAGTACATCTCTCTAGGCAATGA 7736
Db 8354 CTGTACAAAACCTTTGTGAAGGGGAAAAACAGGCCCTGAGTATGTGCTCTATGCTTGA 8413
Qy 7737 AACTTCTTTGAAA-----CTATTGTAGATAACA 7763
Db 8414 AACTTCTTTGAAACTGCTCCTAACTGCTTTGTTGCTTCTGTAACCTGCTTGCAATAGAT 8473
Qy 7764 AGAAAAGGAGTCTTCTAACTGCTTTGTTAGCTTCTGTAAACTGGTTGGCCCATAAAGAT 7823
Db 8474 AAAAAGAGGAGAGTCAATCGCCTAACCGACCCCAAGTATCGGGGTGCGCAAAAATG 8533
Qy 7824 GTTGAATGTGTATACATATCTTGTGTGACATATCTTGTGTGACATATCTCTCCCAACATCGC 7883
Db 8534 TTGAAAATCTGTATAAATATATCTTGTGTGACATATCTCTCCCAACATCGCAGACAGGCA 8593
Qy 7884 CAAATGTGTAACCTTAAACAAATTT-AAATTAATTTGGTCCACGAAGCGCGGCTCTCGAA 7942
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Qy 7943 GTTTTAAATTTGACTGTTGTTGATTAATTTGAAATGATTTGTTGT-AAAGCGCGGCTTT 8001
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Qy 8002 GTTGTGAACCCCATAAAGCTGTCCGACTCCACACTCGGGCCGCGAGTCTCTACCCCT 8061
Db 8714 GTTATGAACCCCATAAAGCTGTCCGACTCCACACTCGGGCCGCGAGTCTCTACCCCT 8773
Qy 8062 GCGTGTGTAGACTGTGGCCCGCCAGCGCTTGGATATAAAATCTCTGCTGTTTGA 8121
Db 8774 GCGTGTGTAGACTGTGGCCCGCCAGCGCTTGGATATAAAATCTCTGCTGTTTGA 8833
Qy 8122 TCAAAA 8127
Db 8834 TCAAGA 8839

RESULT 3
US-10-471-220-1
; Sequence 1, Application US/10471220
; Publication No. US2004014249A1
; GENERAL INFORMATION:
; APPLICANT: Tonjes, Ralf R.
; APPLICANT: Krach, Ulrich
; TITLE OF INVENTION: REPLICATION-COMPONENT MOLECULAR CLONES
; TITLE OF INVENTION: OF PORCINE ENDOGENOUS RETROVIRUS CLASS A AND CLASS B DERIVED
; TITLE OF INVENTION: FROM FIG AND HUMAN CELLS
; FILE REFERENCE: 11692-007US1
; CURRENT APPLICATION NUMBER: US/10/471,220
; CURRENT FILING DATE: 2003-09-08
; PRIOR APPLICATION NUMBER: PCT/EP02/02656
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: DE 101 11 433.8
; PRIOR FILING DATE: 2001-03-09
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 8918
; TYPE: DNA
; ORGANISM: Sus scrofa
; FEATURE:
; NAME/KEY: source
; LOCATION: (0)...(0)
; OTHER INFORMATION: Porcine cell line PK15; replication-competent
; OTHER INFORMATION: PERV-A clone PK15-PERV-A(58)
US-10-471-220-1
Query Match 85.2%; Score 6931.2; DB 7; Length 8918;

Best Local Similarity 91.4%; Pred. No. 0; Mismatches 548; Indels 164; Gaps 15;
Matches 7574; Conservative 0;

QY 1 GCGTGGTGTACGACTGTGGGCCCCACGGCGCTTGGAAATAAAATCCTCTTGTCTGTTTGA 60
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Db |||||
620 TCAAGACCGCTTCTCGTGTAGTGAAT--TGGGGTGTGCGCTCTTCCGAGTCAGGACGAGAGG 678
QY 116 ----TTCCTTTTGTCTGTGCTTAATTTGGGGGCTCGTCCGGGATCTGTGCGGCCACCCC 171
Db |||||
679 GAATTTTAACTCGACTGGCCCTTTCAGTTTGGTGGTGGCGGGGAAACCGCGCACTACCCC 738
QY 172 TAACACCCGAGAACCGACTTGGAGGTAAAGAGATCCTCTTTTAAACGTGT--ATGCATG 229
Db |||||
739 TACACCCGAGAACCGACTTGGAGGT-AAAGGATCCCCCTTTGGAACGTTGAGTGTGTG 797
QY 230 TACCGGCGCGGCTCTCTGTCTCAGTGTCTGTCTTTCAGTGTGTCGCGCTTTCGGTTTGA 289
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QY 290 GCTGTCTCTCAGCGCGTGAAGGCTGGGGACTGTGATCAGCAGAGCTGTAGGAGGATC 349
Db |||||
858 GCTGTCTCTCAGACCGTAAAGACTGGGGACTGTGATCAGCAGAGCTGTAGGAGGATC 917
QY 350 ACAGGCTGTGCGCTCGGCGGACGCCCGGGAGGTGAGGAGGCCACGGACGCTGTGTGT 409
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Db |||||
978 CTCCTTCTGCTCAGAGGACCGAGTCTGTGTGTGAAAGCGAAAGCTTCCCCCTCCGCG 1037
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Db |||||
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QY 650 GGCTCATATTTCTCAGTTTCAAGTGAAGAGGACCTTTGGCAGACTTTCTGTGTCTCTGA 709
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1218 GGCTCATATTTCTCAGTTTCAAGTGAAGAGGACCTTTGGCAGACTTTCTGTGTCTCTGA 1277
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Db |||||
1278 ATGGCCGACATTTGATGTTGGATGGCCATCAGAGGGGACCTTTAAATTTCTGAGATTATCCT 1337
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1398 TATCCTTACGTGCAAGATTTGGCAGAGGATCTCCGCCATGGGTTAAACCATTTGGCTGAA 1457
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1458 TAAGCCAGAAAGCCAGGTCCCGAATTTCTGGCTCTTGGAGAGAAACAAACACTTCGCG 1517
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Db 1578 GGAAACCCCAATCTGTTCCCCACACCCCTTATCCGGCAGAGGGTGTGCGAGGGGACCCCTC 1637
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Db |||||
2178 GGTGATGACGAGGACCGAATGAACCTCCCTCAGTCTTCTTGAGAGGCTCATGGAAGCCCT 2237
QY 1670 CAGGCGGTTACACCCCTTTTGATCCCACTCAGAGGCCCAAAAGCCCTCAGTGGCTTGGC 1729
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QY 1730 CTTTATAGACAGTCAAGCTTGGATATTAGAAAGAGCTTTCAGAGACTGGAAGGTTACA 1789
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QY 1850 AGAAGAAAGAAAGGAAACAAAGAAAGAGAGAGAAAGAGAGAAAGGAGAAAGAGCTAA 1909
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QY 2090 GGCAGGAATCTCCCAAGAGGGAACAAAGGACCAAGGATCTAGTCTTACGAAGAAGA 2149
Db |||||
2658 GGCAGGAATCTCCCAAGAGGGAACAAAGGACCTGAAGGCTTTAGTCTTGAAGAGAGA 2717

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QY	2210	GGAGGGCAACACAGTTGAGTTCTCTGGTTGATACCGAGCGGAAACATTCAGTGTCTACTACA	2269	QY	3290	CCAGATTTGACGAGAGAGGTAAACATCTTTGGGTTACAGTTTGGGACACGGGACCGGACCGATG	3349
Db	2778	GGAGGGCAACACAGTTGAGTTCTCTGGTTGATACCGAGCGGAAACATTCAGTGTCTACTACA	2837	Db	3858	CCAGATTTGACGAGAGAGGTAAACATCTTTGGGTTACAGTTTGGGACACGGGACCGGACCGATG	3917
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Db	2838	GCCATTTAGGAAACTAAAGATATAAATAAATCTCTGGGTGATGGGTGCCACAGGGCAACAACA	2897	Db	3918	GCTGACGAGGCAACGGAAGAAACTCTAGTCTCAGATACCGGCCCCCAACACACAGCAACAACA	3977
QY	2330	GTATCCATGAGTACCCGAGAAACAGTTGACTTCGGAGTGGGACGGGTAAACCCACTCGTT	2389	QY	3410	AATGAGAGAGTTTGTGGGACAGCTGATTTTGCAGACTGTGTGATCCCGGGTTTGGCAC	3469
Db	2898	ATATCCATGAGTACCCGAGAAACAGTTGACTTCGGAGTGGGACGGGTAAACCCACTCGTT	2957	Db	3978	AGTGAGAGAGTTTGTGGGACAGCTGATTTTGCAGACTGTGTGATCCCGGGTTTGGCAC	4037
QY	2390	TCTGGTCAATACCTGAGTGCCAGACCCCTCTCTAGGTAGAGACTTATTGACCAAGATGGG	2449	QY	3470	CTTAGCAGCCCACTCTACCCGCTTAACCAAGAAAGGGGAAATTTCTCTGGGCTCTCTGA	3529
Db	2958	TCTGGTCAATACCTGAGTGCCAGACCCCTCTCTAGGTAGAGACTTATTGACCAAGATGGG	3017	Db	4038	CTTAGCAGCCCACTCTACCCGCTTAACCAAGAAAGGGGAAATTTCTCTGGGCTCTCTGA	4097
QY	2450	AGCAAAATTTCTTTGAAACGAGGAAACGAAAGTGTCTGCAATTAACAAACCTATCAC	2509	QY	3530	GCACCAAGAGGCAATTTGATGCTATCAAAAAGGGCCCTGCTGAGCGCACCTGCTCTGGCCCT	3589
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QY	2510	TGTTGTGACCCCTCAATTTAGATGAGCAATATCGACTATATCTCTCCCTAGTAAAGCCCTGA	2569	QY	3590	CCCTGAGCTAAACCCCTTTACCCCTTTATGATGAGCGTAAAGGAGTAGCCCGGG	3649
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QY	2570	TCAAAATATACAAATCTGTTGGAAACAGTTTCCCAAGCCCTGGGACAGAAACCGCAGGGAT	2629	QY	3650	AGTTTAAACCCAAACCTTAGGACCATGAGAGAGCTGTGCGCTTACCTGTCAAAAGAGCT	3709
Db	3138	TCAAAATATACAAATCTGTTGGAAACAGTTTCCCAAGCCCTGGGACAGAAACCGCAGGGAT	3197	Db	4218	AGTTTAAACCCAAACCTTAGGACCATGAGAGAGCTGTGCGCTTACCTGTCAAAAGAGCT	4277
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Db	3198	GGGTTTGGCAAGCAAGTTCGCCCAAGTTATTCAACTGAAGGCCAGTGCACACCACT	3257	Db	4278	CGATCTGTAGCCAGTGTGGCCCATATGCTCAAGGCTATCGCAGCTGTGGGCCTACT	4337
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Db	3318	AAGATTATCAACAGGCGATCTAGTTCTCTGTCCTCAATCTCCCTGGAAATCTCCCTGCT	3377	Db	4398	GTTTGGAAACAATCTGTTGGGACGCCCCCAGACCGATGATGATGATGATGATGATGATGATG	4457
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Db	3438	TAAAGGGTGAGGATATACACCCAGTCCCGAACCTTTATACCTCTTGTGTCTCT	3497	Db	4518	TGCCACTCTTCTGCTGAAAGAGACTGATGAACCAAGTGAATCATGATGATGATGATGATGATG	4577
QY	2930	CCCAACCCCAAGGAGTATACAGTATGAGTAAAGGATGCTTCTTCTGCTGAG	2989	QY	4010	GATTGAGAGACTGGGTCCGCAAGGACCTTTACAGACATACCGCTGATGATGATGATGATGATG	4069
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QY	2990	ATTACACCCCAAGGAGTATACAGTATGAGTAAAGGATGCTTCTTCTGCTGAG	3049	QY	4070	AACCTGTTCTACACGAGAGCTATGCTGGAAGGATGATGATGATGATGATGATGATGATGATG	4129
Db	3558	ATTACACCCCAAGGAGTATACAGTATGAGTAAAGGATGCTTCTTCTGCTGAG	3617	Db	4638	AACCTGTTCTACACGAGAGCTATGCTGGAAGGATGATGATGATGATGATGATGATGATGATG	4697
QY	3050	AACCGGGGAGTCTACCTGGACCCGACTGCCCAAGGGTTCAAGAACTCCCGACCATCTT	3109	QY	4130	GGTGTGAGCGGACCCGACGATCTGGGCCAGACGCTGCGGGAAGGAACTTTCAGACACA	4189
Db	3618	AACCGGGGAGTCTACCTGGACCCGACTGCCCAAGGGTTCAAGAACTCCCGACCATCTT	3677	Db	4698	GGTGTGAGCGGACCCGACGATCTGGGCCAGACGCTGCGGGAAGGAACTTTCAGACACA	4757
QY	3110	TGACGAAGCCTTACACAGAGCCTGCCCACTTACAGGATCCAAACCCCTCAGGTGACCTT	3169	QY	4190	AAAGGCTGAGTCTATGGCCCTCAGCAAGCTTTGCGGTGCGGACGAGGAAATTCATATAA	4249
Db	3678	TGACGAAGCCTTACACAGAGCCTGCCCACTTACAGGATCCAAACCCCTCAGGTGACCTT	3737	Db	4758	AAAGGCTGAGTCTATGGCCCTCAGCAAGCTTTGCGGTGCGGACGAGGAAATTCATATAA	4817
QY	3170	CCTCCAGTACGTGATGCTCTTCTGGCGGGACCCAAACAGGACTGCTTTAGAAAGG	3229	QY	4250	CATTATACGGAACAGAGGATGCTTTGCGACTGTGCACACGATACGAGGCGGCTCTATAA	4309
Db	3738	CCTCCAGTACGTGATGCTCTTCTGGCGGGACCCAAACAGGACTGCTTTAGAAAGG	3797	Db	4818	CATTATACGGAACAGAGGATGCTTTGCGACTGTGCACACGATACGAGGCGGCTCTATAA	4877
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QY 6467 TTTTACCTCATCCAGGAGCTTTTCAAGCTCTTAACTCCAGACTCCAGAGGCTACCT 6526
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Db GGAATTCATGTGACAAAGAACATAGACCAATGTATATGGGGATCCCAAAATAGC 7274
QY 6647 TTACCTCTTACGAGGTTTCTGGAAGGCACTCTGATAGGAAGGTTTCCCCCATCCCAAC 6706
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8235 ACCTGACTCTCCAGAACCCAGGAAGTTAATAAGAGCTCTAAATGCCCTCGAATTCAG 8294
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7697 -----GGAAGTAAATAATAGCCCTGAGTACATGTCTCTAGGATGA 7736
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8475 AAAAGAGGAGAGTCAATTTGCTTAAACGACCCAGTAAGATCGGCGTGCACAAAATG 8534
7824 GTTGAATGTGTATACATATCTTGTGTGACAAATGTCTCTCCCAACCCGAAACATGCG 7883
8535 TTGAAATCTGTATAATAATATCTTGTGTGACAAATGTCTCTCCCAACCCGAGAGAGCA 8594
7884 CAATGTGTAACTCTAAACCAATTAATTAATTTGTTGTTGTTGTTGTTGTTGTTGTTG 7943
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7944 TTTTAAATTCAGTGTGTTTGTGATATTTT-GAAATGATTGTTTGT-AAAAGCGCGGCTTT 8001
8655 TTTTGAATTCAGTGTGTTTGTGATATTTTAAATGATTAGTTTGTAAAAGCGCGGCTTT 8714
8002 GTTGTGAACCCCAATAAAGCTGCTCCCACTCCCACTCGGGGCGGAGTCTCTACCCCT 8061
8715 GTTGTGAACCCCAATAAAGCTGCTCCCACTCCCACTCGGGGCGGAGTCTCTACCCCT 8774
8062 GCGTGTGTAGTGTGTTGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 8121
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8122 TCAAAA 8127
8835 TCAAGA 8840

RESULT 4
US-10-113-664A-138
; Sequence 138, Application US/10113664A
; Publication No. US20030224350A1
; GENERAL INFORMATION:
; APPLICANT: Cui, Cunqi
; APPLICANT: Diamond, Lisa E.
; APPLICANT: Logan, John S.
; APPLICANT: Nextran, Inc.
; TITLE OF INVENTION: Elimination of Endogenous Porcine
; TITLE OF INVENTION: Retrovirus
; FILE REFERENCE: 630666.00009
; CURRENT APPLICATION NUMBER: US/10/113,664A
; CURRENT FILING DATE: 2002-03-28
; PRIOR APPLICATION NUMBER: US 60/279,337
; PRIOR FILING DATE: 2001-03-28
; NUMBER OF SEQ ID NOS: 139
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 138
; LENGTH: 8919
; TYPE: DNA
; ORGANISM: Sus scrofa
; FEATURE:
; OTHER INFORMATION: porcine endogenous retrovirus (PERV)

; OTHER INFORMATION: G319 locus; G19 PERV genome			
US-10-113-664A-138			
Query Match 85.0%; Score 6915.6; DB 6; Length 8919;			
Best Local Similarity 91.4%; Pred. No. 0;			
Matches 7578; Conservative 0; Mismatches 544; Indels 166; Gaps 17;			
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Db	560	GGGTGGGTACGACTGTGGGCCCCAGCGCTCGGAATAAAATCCTTGTCTGTTTGA	619
QY	61	TCNAGACCGCTTCTCGTAGTGATTAAGGGGAGTCGCCCTTTCCGAGCCCTGGAGG----	115
Db	620	TCNAGACCGCTTCTCGTAGTGATTTGGGGTGTGCGCTCTTCCGAGTCAGGATGAGAG	678
QY	116	---TTCTTTTCTGCTGCTTACATTTGGGGGCTCGTCGGGATCTGTCCGGCCACCC	171
Db	679	GATTTTAACTCGACTGGCCCTTCAGTTTGGTGGTGGCGGGAAACCCGCGACTACCC	738
QY	172	TAAACCCGAGAACCGACTTGGAGGTAAAGAGATCCTCTTTTAAACGTGT--ATGCATG	229
Db	739	TCACACCCGAGAACCGACTTGGAGGT-AAAGGATCCCTTTGGAACGTGTGAGTGTGTG	797
QY	230	TACCGCGCGGCTCTCTGTCGAGTGTCTGTTTTCAGTGTGTGCGGCTTTCCGTTTGA	289
Db	798	TGTCCGCTGGCGTCTCTGTTCTGAGTGTCTGTTTTCGTTGATGCGGCTTTCCGTTTGA	857
QY	290	GCTGTCTCTCAGCGCTGAAGGCTCGGGGACTGTGATCAGCAGACGTCTAGGAGATC	349
Db	858	GCTGTCTCTCAGACCGTAAGGACTGGGGACTGTGATCAGCAGACGTCTAGGAGATC	917
QY	350	ACAGGCTGTCTGCGGAGACGCCCGGAGGTGAGGAGCAGCGACGCTGTGTGT	409
Db	918	ACAGGCTGCAACCTTGGGGAGCGCCCGGAGGTGGGAGGACGCGACGCTGTGTGT	977
QY	410	CTCTACTGTGCTGACAGGACCGAATTCCTGTGCTGCTGCTGAAGCGAAGCTTCCCGCT	469
Db	978	CTCTTCTGTGCTGACAGGACCGAGTCTGTGTTGTTGAAGCGAAGCTTCCCGCT	1037
QY	470	ACCGTCCGACTCTTTTGCCTGTGGAAGACGTGAGCGGGTCAAGTGTGCTGACT	529
Db	1038	GCGCTCCGACTCTTTTGCCTGTGGAAGACGTGAGCGGGTCCGCTGTGCTGACT	1097
QY	530	GTTGGTTTCTGTTTGTGTCTTTCTGTTGTGCTCTTGTCTACAGTTTTTAATGG	589
Db	1098	GTTGGTTTCTGTTTGTGTCTTTCTGTTGTGCTCTTGTCTACAGTTTTTAATGG	1157
QY	590	ACAGCGGTGACACCCCTTTAGTTTGAATCTCGACCAATGGACTGAAGTTAAATCCAG	649
Db	1158	ACAGCGGTGACACCCCTTTAGTTTGAATCTCGACCAATGGACTGAAGTTAAATCCAG	1217
QY	650	GGCTCATATTTCTCAGTTTCAGGTTAAGAGGACCTTGGCAGACTTCTGTCTCTGA	709
Db	1218	GGCTCATATTTCTCAGTTTCAGGTTAAGAGGACCTTGGCAGACTTCTGTCTCTGA	1277
QY	710	ATGGCCGACATTCGATTTGGATGGCCATCAGAGGGGACCTTTAAATCTGAGATTATCCT	769
Db	1278	ATGGCCGACATTTGATTTGGATGGCCATCAGAGGGGACCTTTAAATCTGAGATTATCCT	1337
QY	770	GGCTGTTAAAGCAGTTATTTTTTTCAGCTGACCCCGCTCTCATCCCGATCAGAGCCCTA	829
Db	1338	GGCTGTTAAAGCAATTTATTTTTCAGACTGGACCCGCTCTCATCCCGATCAGAGCCCTA	1397
QY	830	TATCTTACGTGCAAGATTTGCGAGGATCTCCGCGCATGGGTTAAACCATGGCTGA	889
Db	1398	TATCTTACGTGCAAGATTTGCGAGGATCTCCGCGCATGGGTTAAACCATGGCTGA	1457
QY	890	TAAAGCAAGAAACCGAGTCCCCGAATTCCTGGCTCTTGGAGAGAAAAACAAACCTCGGC	949
Db	1458	TAAAGCAAGAAACCGAGTCCCCGAATTCCTGGCTCTTGGAGAGAAAAACAAACCTCGGC	1517
QY	950	TGAAAAGTCAAGCCCTCTCTCATATCTACCCCGAGATTGAGGAGCCACCGCTTGGCC	1009
Db			

Db	1518	TCAAAAAGTCAAGCCCTCTCTCATATCTACCCCGAGATTGAGGAGCCCGCGCTTGGCC	1577
QY	1010	GGAAACCCCAATCTGTTCCCCACCCCTTATCTGCGACAGGTTGCGCGAGGGGACCCCT	1069
Db	1578	GGAAACCCCAATCTGTTCCCCACCCCTTATCTGCGACACAGGTTGCTGCGAGGGGACCCCT	1637
QY	1070	TGCCCTCTCTGAGCTCGCGGCTGGAGGACCTGCTGAGGAGACTCGAGGCGGAGGG	1129
Db	1638	TGCCCTCTCTGAGCTCGCGGCTGGAGGACCTGCTGAGGAGACTCGAGGCGGAGGG	1697
QY	1130	CGCCACCCCGAGCGACAGAGATCGCGCATTTACCGCTGCGCACCTAGCGGCCCTCC	1189
Db	1698	CGCCACCCCGAGCGAGACAGAGATCGCGCATTTACCGCTGCGCACCTAGCGGCCCTCC	1757
QY	1190	CACACCGGGGGCCAAATTGACAGCCCTCCAGTATTGGCCCTTTCTTCTGAGATCTCTA	1249
Db	1758	CATACCGGGGGCCAAATTGACAGCCCTCCAGTATTGGCCCTTTCTTCTGAGATCTCTA	1817
QY	1250	TAATTGGAAAACTAACCATCCCTTTCTCGAGAGATCCCCAACCGCTCACGGGTTGGT	1309
Db	1818	TAATTGGAAAACTAACCATCCCTTTCTCGAGGATCCCCAACCGCTCACGGGTTGGT	1877
QY	1310	GGAGTCCCTTATGTTCTCTCACAGCTACTTGGGATGATTGTCAACAGCTGCTGCAGAC	1369
Db	1878	GGAGTCCCTTATGTTCTCTCACAGCTACTTGGGATGATTGTCAACAGCTGCTGCAGAC	1937
QY	1370	ACTCTTCAACACCGAGGAGGAGAGAAATCTATTAGAGGCTAGAAAAATTTCTCTCG	1429
Db	1938	ACTCTTCAACACCGAGGAGGAGAGAAATCTATTAGAGGCTAGAAAAATTTCTCTCG	1997
QY	1430	GGCGACGGGCGACCCACCGGTTGCCAAATGAGATTGATGGGATTTCCCTTAACCTG	1489
Db	1998	GGCGACGGGCGACCCACCGAGTTGCCAAATGAGATTGATGGGATTTCCCTTAACCTG	2057
QY	1490	CCCCGTTGGGACTCAACACCGCTGAAGTGGGAGACTTGAATAATCTATCGCCAGGC	1549
Db	2058	CCCCGTTGGGACTCAACACCGCTGAAGTGGGAGACTTGAATAATCTATCGCCAGGC	2117
QY	1550	TCTGTGGCGGTCTCCGGGCGCTCAAGACGGCCCACTAATTTGGCTTAAGTAAGAGA	1609
Db	2118	TCTGTGGCGGTCTCCGGGCGCTCAAGACGGCCCACTAATTTGGCTTAAGTAAGAGA	2177
QY	1610	AGTGTAGCAGGACCAATGAACCCCTCTCTGTTTCTTGGAGGCTCTTGAAGCCCT	1669
Db	2178	AGTGTAGCAGGACCAATGAACCCCTCTCTGTTTCTTGGAGGCTCTTGAAGCCCT	2237
QY	1670	CAGCGGTACACCCCTTTGATCCACCTCAGAGGCCCAAAAGCCCTCAGTCGCTTGGC	1729
Db	2238	CAGCGGTACACCCCTTTGATCCACCTCAGAGGCCCAAAAGCCCTCAGTCGCTTGGC	2297
QY	1730	CTTTATAGGACAGTCAGCCCTTGGATATTAGAAAGAGCTTTCAGAGACTGGAAGGGTTACA	1789
Db	2298	CTTTATAGGACAGTCAGCCCTTGGATATTAGAAAGAGCTTTCAGAGACTGGAAGGGTTACA	2357
QY	1790	GGAGGCTGATTTAGTGTAGTGAAGGACAGAGAAAGTATTATTACAAAAGGAGAC	1849
Db	2358	GGAGGCTGATTTAGTGTAGTGAAGGACAGAGAAAGTATTATTACAAAAGGAGAC	2417
QY	1850	AGNAGAAAGAGGGAACAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	1909
Db	2418	AGNAGAAAGAGGGAACAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	2477
QY	1910	TAAACCGGCAAGAGAGAAATTTGACTTAAGATCTTTGGCTGAGTGGTTGAAGGGAAAAAGCAA	1969
Db	2478	TAAACCGGCAAGAGAGAAATTTGACTTAAGATCTTTGGCTGAGTGGTTGAAGGGAAAAAGCAA	2537
QY	1970	TACGGAAAGAGAGAGATTTTAGGAAATTTAGTTCAGGCCCTTAGCAGTCAGGGAACT	2029
Db	2538	TAGGGAAAGAGAGAGATTTTAGGAAATTTAGTTCAGGCCCTTAGCAGTCAGGGAACT	2597
QY	2030	GGGCAATAGGACCCCTCAGCAAGGACCAATGTGCATATTGTAAAGAAAGAGACACTG	2089
Db	2598	GGGCAATAGGACCCCTCAGCAAGGACCAATGTGCATATTGTAAAGAAAGAGACACTG	2657

Qy	2090	GGCAAGGAACTGCCCCAAGAGGGAACAAAGGACCAAGGATCCTAGCTCTTAGAAGA	2149	TCCTCAGTACGTGGATGACCTGCTTCTGGGGAGCCACCAACAGGACTGCTTAGAAG	3228
Db	2658	GGCAAGGAACTGCCCCCAAGAGGGAACAAAGGACTGAAGGTCTTAGCTCTGGAAGA	2717	TCCTCCAGTACGTGGATGACCTGCTTCTGGGGAGCCACCAACAGGACTGCTTAGAAG	3797
Qy	2150	TAAAGATTAGGGAGAGCGGGTTCGGACCCCTCCAGCCAGGCTTAAGGT	2209	GCACGAAGGCACTACTGCTGGAATTGCTGACCTAGGCTACAGAGCTCTCTCTAAGAAGG	3288
Db	2718	TAAAGACTAGGGAAGCGGGTTCGGACCCCTCCAGCCAGGCTTAAGGT	2777	GTACGAAGGCACTACTGCTGGAATTGCTGACCTAGGCTACAGAGCTCTCCGCTAAGAAGG	3857
Qy	2210	GGAGGGCAACCACTGAGTTCCTGGTTGATACCGGAGCGAAACATTCAGTGTACTACA	2269	CCACGATTTCCAGGAGAGAGGTAACTATCTTGGGGTACAGTTTGGGGACGGGACGCGAT	3348
Db	2778	GGAGGGCAACCACTGAGTTCCTGGTTGATACCGGAGCGAAACATTCAGTGTACTACA	2837	CCACGATTTCCAGGAGAGAGGTAACTATCTTGGGGTACAGTTTGGGGACGGGACGCGAT	3917
Qy	2270	GCACATTAAGGAAAACTAAAGATATAAAAAATCC- TGGGTGATGGGTGCCACAGGGCAACAAC	2328	GGCTGACGAGGCAACGGAAGAACTGTAGTCCAGATACCGGCCCCCAACCAACAGCCAAAC	3408
Db	2838	GCACATTAAGGAAAACTAAAGATATAAAAAATCC- TGGGTGATGGGTGCCACAGGGCAACAAC	2897	GGCTGACGAGGCAACGGAAGAACTGTAGTCCAGATACCGGCCCCCAACCAACAGCCAAAC	3977
Qy	2329	AGTATCCATGGACTACCCGAAGAAACAGTTGACTTTGGGAGTGGGACGGGTAAACCACTCGT	2388	AAATGACAGAGTTTTTTCGGGACAGCTGGATTTTTCAGACTGTGTGATCCCGGGGTTTGGCA	3468
Db	2898	AAATCCATGGACTACCCGAAGAAACAGTTGACTTTGGGAGTGGGACGGGTAAACCACTCGT	2957	AAGTGAGAGAGTTTTTTCGGGACAGCTGGATTTTTCAGACTGTGTGATCCCGGGGTTTGGCA	4037
Qy	2389	TTCTGGTCTATACCTGAGTGGCCAGCACCCCTCTTAGGTAGAGACTTATGACCAAGATGG	2448	CTTTAGCAGCCCCACTCTACCCACTAACCAAGAAAGGGAATTTCTCTGGGCTCCTG	4097
Db	2958	TTCTGGTCTATACCTGAGTGGCCAGCACCCCTCTTAGGTAGAGACTTATGACCAAGATGG	3017	AGCACCAAGAGGCACTTGTCTATCAAAAAGGCCCTGCTGAGCGCACCTCTCTGCGGCC	4157
Qy	2449	GAGCACAAATTTCTTTTGAACAAGGAAACAGAGGTGCTGCAAAATAACAAACCTATCA	2508	TCCCTGACGTAACTAAACCCCTTTTACCTTTATGTGGATGACGCTAAGGGAGTAGGCCCGG	3648
Db	3018	GAGCACAAATTTCTTTTGAACAAGGAAACAGAGGTGCTGCAAAATAACAAACCTATCA	3077	TCCCTGACGTAACTAAACCCCTTTTACCTTTATGTGGATGACGCTAAGGGAGTAGGCCCGG	4217
Qy	2509	CTGTGTTGACCTCCAAATTAGATGACGAATATCGACTATATCTCTCCCTAGTAAAGCTG	2568	GAGTTTTTAAACCAACCCCTTAGGACCATGGAAGAACCTGTGCGCTTCTCTCAAGAAGC	3708
Db	3078	CTGTGTTGACCTCCAAATTAGATGACGAATATCGACTATATCTCTCCCTAGTAAAGCTG	3137	GAGTTTTTAAACCAACCCCTTAGGACCATGGAAGAACCTGTGCGCTTCTCTCAAGAAGC	4277
Qy	2569	ATCAAAATATACAAATTCGTGTTGAAACAGTTTCCCAAGCTTGGGACAGAACCCGAGGA	2628	TCGATCCTGTAGCCAGTGGTGGCCGATATGCTGAGGCTATCGCAGCTGTGGCCATAC	4337
Db	3138	ATCAAAATATACAAATTCGTGTTGAAACAGTTTCCCAAGCTTGGGACAGAACCCGAGGA	3197	TGGTCAAGGAGCGTGACAAATTTGACTTTGGGACAGAAATATACCTGTAATAGCCCCCATG	3828
Qy	2629	TGGGTTGGCAAGCAAGTCCCCACAAAGTTATTCAACTGAAGCCAGTCCACACAG	2688	TGGTCAAGGAGCGTGACAAATTTGACTTTGGGACAGAAATATACCTGTAATAGCCCCCATG	4397
Db	3198	TGGGTTGGCAAGCAAGTCCCCACAAAGTTATTCAACTGAAGCCAGTCCACACAG	3257	CATTGGAGAACATCGTTCCGAGCCGCCAGATGGATGACCAACCCCGCATGATGCC	3888
Qy	2689	TGTCAGTACAGACGTACCCCTTGAGTAAAGAGCTCAAGAGGAATTCGGCCGATGCC	2748	CATTGGAGAACATCGTTCCGAGCCGCCAGATGGATGACCAACCCCGCATGATGCC	4457
Db	3258	TGTCAGTACAGACGTACCCCTTGAGTAAAGAGCTCAAGAGGAATTCGGCCGATGCC	3317	ACTATCAAGGCTCTCTTCTCAAGAGGGTCAAGTTCCGCTCCACAGCGGCTCTCAACC	3948
Qy	2749	AAAGATTAAATCCAAAGGGCATCCTAGTTCCTGTCCTCAATCTCCCTGGAATCTCCCTGC	2808	ACTATCAAGGCTCTCTTCTCAAGAGGGTCAAGTTCCGCTCCACAGCGGCTCTCAACC	4517
Db	3318	AAAGATTAAATCCAAAGGGCATCCTAGTTCCTGTCCTCAATCTCCCTGGAATCTCCCTGC	3377	CTGCCACTCTTCTGCTGGAAGACTGTATGAACCAAGTACTCATGATTTGCCATCAACTAT	4577
Qy	2809	TACCGGTTAGAAAGCCTGGGACTAATGACTATCGACAGTACGAGCTTGAGAGAGGTCA	2868	CTGCCACTCTTCTGCTGGAAGACTGTATGAACCAAGTACTCATGATTTGCCATCAACTAT	4637
Db	3378	TACCGGTTAGAAAGCCTGGGACTAATGACTATCGACAGTACGAGCTTGAGAGAGGTCA	3437	TAACTCTGTTCACTGACCGAGAGCTATGTGGTGAAGGTAAAGGATGGCTGGGGCGG	4697
Qy	2869	ATAAAGGGTGCAGGATATACACCAAGTCCCGAACCTTTATAACCTCTTTGTGCTC	2928	CGGTGGTGAACGGGACCCGCGACGATCTGGGGCCAGAGCTGCGGAGGAATTCATGAC	4188
Db	3438	ATAAAGGGTGCAGGATATACACCAAGTCCCGAACCTTTATAACCTCTTTGTGCTC	3497	CGGTGGTGAACGGGACCCGCGACGATCTGGGGCCAGAGCTGCGGAGGAATTCATGAC	4757
Qy	2929	TCCCAACCCCAAGGGAGCTGGTATACAGTATTGGACTTAAAGGATGCCCTTCTTCTGCTGA	2988	AAAAAGGCTGAGCTATGCGCCCTCAGCAAGCTTTTGGGCTGGCCGAGGGAATTCATGAA	4817
Db	3498	TCCCAACCCCAAGGGAGCTGGTATACAGTATTGGACTTAAAGGATGCCCTTCTTCTGCTGA	3557	AAAAAGGCTGAGCTATGCGCCCTCAGCAAGCTTTTGGGCTGGCCGAGGGAATTCATGAA	4817
Qy	2989	GATTACACCCCTAGCCAAACCACTTTTTCCTTCGAATGGAGATCCAGTACGGGAA	3048	ACATTTATACGACAGCAGGTATGCTTTTGGGCTGACACGATCATGCGGGCCATCTATA	4308
Db	3558	GACTACATCCCACTAGCCAAACCACTTTTTCCTTCGAATGGAGATCCAGTACGGGAA	3617		
Qy	3049	GAAACGGGAGCTACCTGAGCCGACTGCGCCCAAGGGTTCAAGAACTCCCGACCATCT	3108		
Db	3618	GAAACGGGAGCTACCTGAGCTGCGCCCAAGGGTTCAAGAACTCCCGACCATCT	3677		
Qy	3109	TTGACGAAGCCCTACACAGAGACCTGGCCAACTTCAGGATCCAAACCCCTCAGGTGACCC	3168		
Db	3678	TTGACGAAGCCCTACACAGAGACCTGGCCAACTTCAGGATCCAAACCCCTCAGGTGACCC	3737		

|||||
4818 ACATTATACAGACAGCGTATGCTTTGCGACTGCACACGTACACGGGCGCATCTATA 4877
QY
4309 AACAAAGGGGTTGCTTACTCTAGCAGGAGGAGAAATAAGAACAAAGAGGAAATCTTAA 4368
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Db
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QY
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5118 GACAGTACACCCCTAGAAGACTGGCAAGAAATAAAAAAGATAGACCAAGTTCTCTGAAACTC 5177
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Db
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Db
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6855 ATGCTTGGGGAATAGTGTACTATGAGGCTCTGGGAGAAAGAAAGATCTGTTCTGACT 6914
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6304 ATTCGCTCAAAAT---AAACAGCTGGAGCTTCAATGGCTATAGGACCAAAATACGGTC 6360
Db
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QY
6361 TTGACGGGTCAAGACCCCAACCAAGGACCCAGGACCACTCTCTAAC----- 6408
Db
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/ LENGTH: 8918
/ TYPE: DNA
/ ORGANISM: Sus scrofa
/ FEATURE:
/ NAME/KEY: source
/ LOCATION: (0)...(0)
/ OTHER INFORMATION: Porcine primary fibroblasts; replication-competent
/ OTHER INFORMATION: PERV-A clone PERV-A (Bac-130A12)
US-10-471-220-3

Query Match      84.0%; Score 6832.4; DB 7; Length 8918;
Best Local Similarity 91.0%; Pred. No. 0;
Matches 7542; Conservative 1; Mismatches 573; Indels 176; Gaps 19;

QY      1  GCGTGTGTACGACTGTGGGCCCCCAGCGGCTTGGGAATAAAATCCTCTTGCTGTTTGA 60
DB      560 GCGTGGCTACGACTGTGGGCCCCCAGCGGCTCGGAATAAAATCCTCTTGCTGTTTGA 619
QY      61  TCAAGACCGCTTCTCGTGTGATTAAGGGAGTGCCTTTTCCGAGCCTGGAGG----- 115
DB      620 TCAAGACCGCTTCTCGTGTGATTTGGGGTGTGCTCTTCCGAGTCAGGACGAGAGG 678
QY      116 ----TTCCTTTTGGCTGTCTTACATTTGGGGCTCGTCCGGATCTGTCCGGCCACCCC 171
DB      679 GATTTTAACTCGACTCGGCTTTCAGTTTGGTGGCGGGAAACCCCGCACTACCCC 738
QY      172  TTAACCCCGAGAACCGACTTGGAGGTAAAGAGATCCTCTTTTAAACGTGT--ATGCATG 229
DB      739 TCACACCCGAGAACCGACTTGGAGGT-AAAGGATCCCTTTGGAAACGTGTGAGTGTG 797
QY      230  TACCGCCGCGCTCTGTTCTGAGTGTCTGTTTTTCAGTGGTGGCGCTTTCGTTTGA 289
DB      798 TGTGCGCTGGCGTCTCTGTTCTGAGTGTCTGTTTTCGGTGATGCGCGCTTTCGTTTGA 857
QY      290  GCTGTCTCTCAGCCGCTTAAGGCTGGGGACTGTGATCAGCAGACGTCTAGGAGATC 349
DB      858 GCTGTCTCTTAAGCCGTAAGGACTGGGGA-----ATCAGCAGACGTCTAGGAGATC 912
QY      350  ACAGGCTGTGCCCTGGGGAGCCGCC-----GGGAGGTGAGGAGCAGGAGCCGCTG 404
DB      913 ACAGGCTGACCCCTGGGGAGCCGCCGCTGTGGGAGGTGGGGAGACCGAGGACGCTG 972
QY      405  GTGGTCTCTACTGTGCGGTGAGAGACCGAAATCTGTGTGTAAGCGAAAGCTTCCCTC 464
DB      973 GTGGTCTCTCTGTGCGGTGAGAGACCGAGTTCTGTGTGTAAGCGAAAGCTTCCCTC 1032
QY      465  CCGCGACCGTCCGACTCTTTTGTGCTGTTGTGGAAGACGTGAGCGGGTCAGTGTGTCG 524
DB      1033 CCGCGCCCGTCCGACTCTTTTGTGCTGTTGTGGAAGACGCGGTCGCGTGTGTCG 1092
QY      525  GATCTGTGTTTCTGTTTGTGTGCTTGTGCTGTGTGCTGCTGTCTACAGTTTAAAT 584
DB      1093 GATCTGTGTTTCTGTTTGTGTGCTTGTGCTGTGCTGCTGTCTACAGTTTAAAT 1152
QY      585  ATGGGACAGACGGTGAAGCCCTCTTAGTTTGACTCTCGACCATTTGAGCTGAAGTTAAA 644
DB      1153 ATGGGACAGACGGTGAAGCCCTCTTAGTTTGACTCTCGACCATTTGAGCTGAAGTTAAA 1212
QY      645  TCAGGGCTCATAAATTTGTGCTGAGTTTCAAGTTAAGAGGACCTTTGGCAGACTTCTGTGTC 704
DB      1213 TCAGGGCTCATAAATTTGTGCTGAGTTTCAAGTTAAGAGGACCTTTGGCAGACTTCTGTGTC 1272
QY      705  TCTGAATGCGGACATTCGATTTGGATGCGCATCAGAGGGACCTTTAATCTGAGATT 764
DB      1273 TCTGAATGCGGACATTCGATTTGGATGCGCATCAGAGGGACCTTTAATCTGAGATT 1332
QY      765  ATCCTGGCTGTTAAAGCAGTTATTTTTCAGACTGGACCCGGCTCTCATCCCGATCAGGAG 824
DB      1333 ATCCTGGCTGTTAAAGCAGTTATTTTTCAGACTGGACCCGGCTCTCATCCCGATCAGGAG 1392
QY      825  CCTTATATCTTACGTGGCAAGATTTTGGCAGAGGATCTTCCCGCATGGGTAAACATGG 884
DB      1393 CCTTATATCTTACGTGGCAAGATTTTGGCAGAGGATCTTCCCGCATGGGTAAACATGG 1452
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QY      885  CTGAATAAGCCAAAGAACCCAGGTCCCGAATTTCTGGCTCTTGGAGAGAAAAACAACAC 944
DB      1453 CTGAATAAGCCAAAGAACCCAGGTCCCGAATTTCTGGCTCTTGGAGAGAAAAACAACAC 1512
QY      945  TCGGCTGAAAAAGTCAAGCCCTCTCTCATATCTACCCGAGATTGAGGAGCCACCGGCT 1004
DB      1513 TCGGCTGAAAAAGTCAAGCCCTCTCTCATATCTACCCGAGATTGAGGAGCCACCGGCT 1572
QY      1005  TGGCCGGAAACCCCAATCTGTTCCCCACCCCTTATCTGGCACAGGGTCCCGAGAGGGA 1064
DB      1573 TGGCCGGAAACCCCAATCTGTTCCCCACCCCTTATCTGGCACAGGGTCTCGAGAGGGA 1632
QY      1065  CCTTTTGGCCCTCTCTGGAGTCCGCGGTGGAGGACCTGTCTGAGGAGACTCGGAGCCGG 1124
DB      1633 CCTCTGCCCCCTCTCTGGAGTCCGCGGTGGAGGACCTGTCTGAGGAGACTCGGAGCCGG 1692
QY      1125  AGGGGGCCACCCCGGAGCGGACAGACGAGATCGGACATTTACCGCTGCGCACGTACGGC 1184
DB      1693 AGGGGGCCACCCCGGAGCGGACAGACGAGATCGGACATTTACCGCTGCGCACGTACGGC 1752
QY      1185  CTTCCACACCCGGGGGCCAATTGACAGCCCTCCAGTATTGGCCCTTTTCTTCTGCAGAT 1244
DB      1753 CTTCCACATACCGGGGGCCAAATTGACGCCCTCCAGTATTGGCCCTTTTCTTCTGCAGAT 1812
QY      1245  CTCTATAATTGAAAACTAACCATCCCTTTCTCGAGGATCCCAACCGCCTCACGGGG 1304
DB      1813 CTCTATAATTGAAAACTAACCATCCCTTTCTCGAGGATCCCAACCGCCTCACGGGG 1872
QY      1305  TTGGTGGAGTCCCTTATGTTCTCTACAGCCCTACTTGGGATGATTTGTAACAGCTGCTG 1364
DB      1873 TTGGTGGAGTCCCTTATGTTCTCTACAGCCCTACTTGGGATGATTTGTAACAGCTGCTG 1932
QY      1365  CAGACACTCTTCAACAACCGAGGACGAGAGAAATCTATTAGAGGCTAGAAAAAATGTT 1424
DB      1933 CAGACACTCTTCAACAACCGAGGACGAGAGAAATCTCTGTAGAGGCTAGAAAAAATGTT 1992
QY      1425  CTTGGGGCCGACGGGCGACCCACGCGGTTGCAAAATGAGATTGACATGGGATTCCTTTA 1484
DB      1993 CTTGGGGCCGACGGGCGACCCACGCGAGTTGCAAAATGAGATTGACATGGGATTCCTTTG 2052
QY      1485  ACTCGCCCGGTTGGACTTACACACGCGCTGAAGGTAGGAGAGCTTTGAAATCTATCGC 1544
DB      2053 ACTCGCCCGGTTGGGACTTACAAACGCGCTGAAGGTAGGAGAGCTTTGAAATCTATCGC 2112
QY      1545  CAGGCTCTGCTGCGGCTCTCCGGGCGCTCAAGACGCCCACTAATTTGGCTAAGGTA 1604
DB      2113 CAGGCTCTGCTGCGGCTCTCCGGGCGCTCAAGACGCCCACTAATTTGGCTAAGGTA 2172
QY      1605  AGAGAAGTGTATGACGGGACCGAATGAACCCCTCTGTTTCTTGTGAGAGGCTCTTTGGA 1664
DB      2173 AGAGAAGTGTATGACGGGACCGAATGAACCTCTCCCTCAGTTTTTCTTGTGAGGCTCATGGA 2232
QY      1665  GCCTTCAGCGGTAACCCCTTTTGTATCCCACTCAGAGGCCCAAAAGCCTCAGTGGCT 1724
DB      2233 GCCTTCAGCGGTTTACCCCTTTTGTATCCCTCAGTCTTGTGAGGCTCAGAAAGCCTCAGTGGCT 2292
QY      1725  TTGGCTCTTATAGGACAGTCAGCCTTGGATATTAGAAAGAGCTTCAGAGACTGGAAGGG 1784
DB      2293 CTGGCTTTCATAGGACAGTCAGCCTTGGATATCAGAAAGAGCTTCAGAGACTGGAAGGG 2352
QY      1785  TTACAGAGGCTGAGTTAGTGTAGTGAAGGAGCGAGAAAGTATATTACAAAAGG 1844
DB      2353 TTACAGAGGCTGAGTTAGTGTAGTGAAGGAGCGAGAAAGTATATTACAAAAGG 2412
QY      1845  GAGACAGAGAAAGAAAGGAAACAAAGAAAGAGAGAGAAAGAGAGAAAGGGAGGAAAGA 1904
DB      2413 GAGACAGAGAAAGAAAGGAAACAAAGAAAGAGAGAGAAAGAGAGAAAGGGAGGAAAGA 2472
QY      1905  CGTAAATAACCGCAAGAGAGAAATTTGACTTAAGATCTTGGCTGAGTTGAGGAGGAAA 1964
DB      2473 CGTAAATAACCGCAAGAGAGAAATTTGACTTAAGATCTTGGCTGAGTTGAGGAGGAAA 2532
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QY	1965	AGCAATACGGAAGAGAGAGAGATTTTGTAGGAAATTTAGTTCAGGCCCTACAGTCAAGG	2024	Db	3613	GGAAAGACCGGCGAGCTCACTTGGACTCGACTGCCCCAGGGTTCAAAACTCCCGACC	3672
Db	2533	AGCAATAGGGAAGAGAGAGAGATTTTGTAGGAAATTTAGTTCAGGCCCTACAGTCAAGG	2592	QY	3105	ATCTTTTGAAGAACCCCTTACACAGAGACCTTGCCCAACTTTCAGGATCCAACACCTTCAGGTG	3164
QY	2025	AACCTGGGCAATAGGACCCCACTCGACAAGGACCAATGTGCATATTTGTAAAGAAAGGA	2084	Db	3673	ATCTTTTGAAGAACCCCTTACACAGAGACCTTGCCCAACTTTCAGGATCCAACACCCCGAGGTG	3732
Db	2593	AACCTGGGCAATAGGACCCCACTCGACAAGGACCAATGTGCATATTTGTAAAGAAAGGA	2652	QY	3165	ACCCTCTCCAGTACGTGAGTACCTGTCTCTGGCGGAGCCACCAACAGGAGTGTCTTA	3224
QY	2085	CACCTGGCAAGGAATCTCCCAAGAGAGGGAACAAAGGACCAAGGATCTCTAGTCTTAGAA	2144	Db	3733	ACCCTCTCCAGTACGTGAGTACCTGTCTCTGGCGGAGCCACCAACAGGAGTGTCTTA	3792
Db	2653	CACCTGGCAAGGAATCTCCCAAGAGAGGGAACAAAGGACCTGAAGTCTTAGTCTCGAA	2712	QY	3225	GAAGGACGGAAGCACTACTCTGCGAATTCGTCTGACCTAGGCTACAGAGCTCTGTCTAAG	3284
QY	2145	GAAGATAAAGATTTAGGGGAGACGGGTTTCGGACCCCTCCCGAGCCACAGGTAACCTTG	2204	Db	3793	GAAGGACGGAAGCACTACTCTGCGAATTCGTCTGACCTAGGCTACAGAGCTCTCGCTAAG	3852
Db	2713	GAAGATAAAGATTTAGGGGAGACGGGTTTCGGACCCCTCCCGAGCCACAGGTAACCTTA	2772	QY	3285	AAGGCCCAGATTTTCAGGAGAGAGAGTAAACATCTTGGGGGTACAGTTTTCGGGACCGGAG	3344
QY	2205	AAGGTGAGGGGCAACCAAGTTGAGTTCCTGGTTGATACCGGAGGGAACATTCAGTGTCTA	2264	Db	3853	AAGGCCCAGATTTTCAGGAGAGAGAGTAAACATCTTGGGGGTACAGTTTTCGGGCGGGCAG	3912
Db	2773	AAGGTGAGGGGCAACCAAGTTGAGTTCCTGGTTGATACCGGAGGGAACATTCAGTGTCTA	2832	QY	3345	CGATGGCTGACGAGGACCGAAGAAACCTGTGTAGTCCAGATACCGGCCCCCAACACAGCC	3404
QY	2265	CTACAGCCATTTAGGAAACTTAAAGATATAAAATCTCTGGGTGATGGGTGCCACAGGGCAA	2324	Db	3913	CGATGGCTGACGAGGACCGAAGAGAACTGTGTAGTCCAGATACCGGCCCCCAACACAGCC	3972
Db	2833	CTACAGCCATTTAGGAAACTTAAAGATATAAAATCTCTGGGTGATGGGTGCCACAGGGCAA	2892	QY	3405	AAACAAATGAGAGAGTTTTTCGGGACAGCTGGATTTTTCAGACTGTGGATCCCGGGGTTT	3464
QY	2325	CAACAGTATCCATGCACTACCCGAAGAACAGTTGACTTTGGGAGTGGGACGGGTAAACCCAC	2384	Db	3973	AAACAAATGAGAGAGTTTTTCGGGACAGCTGGATTTTTCAGACTGTGGATCCCGGGGTTT	4032
Db	2893	CAACAAATATCCATGCACTACCCGAAGAACAGTTGACTTTGGGAGTGGGACGGGTAAACCCAA	2952	QY	3465	GGGACCTTTAGCAGCCCACTCTACCCGCTAAACCAAGAAAGGGGGAATTTCTCTCGGGCT	3524
QY	2385	TCGTTTCTGGTCATACCTGAGTCCCGAGCACCCCTCTTAGGTAGAGACTTATTGACCAAG	2444	Db	4033	GGGACCTTTAGCAGCCCACTCTACCCGCTAAACCAAGAAAGGGGGAATTTCTCTCGGGCT	4092
Db	2953	TCGTTTCTGGTCATACCTGAGTCCCGAGCACCCCTCTTAGGTAGAGACTTATTGACCAACA	3012	QY	3525	CCTGAGCACACAGAGGCAATTTGATGTATCAAAAAGCCCTCTGTGAGGGGACCTGTCTCTG	3584
QY	2445	ATGGGAGCACAAATTTCTTTTGAACAGGGAACACAGAGTGTCTGCAATTAACAAACCT	2504	Db	4093	CCTGAGCACACAGAGGCAATTTGATGTATCAAAAAGCCCTCTGTGAGGGGACCTGTCTCTG	4152
Db	3013	ATGGGAGCCCAATTTTCTTTTGAACAGGGAACCCAGAGTGTCTGCAATTAACAAACCT	3072	QY	3585	GGCCTCCCTGACGTAACTAAACCCCTTTACCCCTTTATGTGATGAGCTGTAGGGAGTAGCC	3644
QY	2505	ATCACTGTGTGACCTCCCAATAGATGACGAATATGCACTATATCTCTCCCTAGTAAAG	2564	Db	4153	GGCCTCCCTGACGTAACTAAACCCCTTTACCCCTTTATGTGATGAGCTGTAGGGAGTAGCC	4212
Db	3073	ATCACTGTGTGACCTCCCAATAGATGACGAATATGCACTATATCTCTCCCTAGTAAAG	3132	QY	3645	CGGGGAGTTTAAACCCAAACCTTAGGACCATGAGGAGAGACTGTGTGCTTACTCTGTCAAG	3704
QY	2565	CCTGATCAAAATATACAAATCTGGTTGGAAACAGTTTCCCAAGCCTCGGCGAGAAACCGCA	2624	Db	4213	CGGGGAGTTTAAACCCAAACCTTAGGACCATGAGGAGAGACTGTGTGCTTACTCTGTCAAG	4272
Db	3133	CCTGATCAAAATATACAAATCTGGTTGGAAACAGTTTCCCAAGCCTCGGCGAGAAACCGCA	3192	QY	3705	AAGCTCGATCCTGTAGCAGTGTGGCCCAATATGCTGAAAGGCTATGCGAGCTGTGGCC	3764
QY	2625	GGGATGGTTTGGCAAGCAAGTTTCCCCCAACAGTTTATCACTGAAGGCCAGTGCCACA	2684	Db	4273	AAGCTCGATCCTGTAGCAGTGTGGCCCAATATGCTGAAAGGCTATGCGAGCTGTGGCC	4332
Db	3193	GGGATGGTTTGGCAAGCAAGTTTCCCCCAACAGTTTATCACTGAAGGCCAGTGCTGCA	3252	QY	3765	ATCTGTCAAGGACCGCTGACAAATTCATCTTTGGGACAGATATACTGTATATAGCCCC	3824
QY	2685	CCAGTGTCAAGTACAGACGATCCCTTGTAGTAAAGAGCTCAAGAGGAATTCGGCCGCAT	2744	Db	4333	ATCTGTCAAGGACCGCTGACAAATTCATCTTTGGGACAGATATACTGTATATAGCCCC	4392
Db	3253	CCAGTGTCAAGTACAGACGATCCCTTGTAGTAAAGAGCTCAAGAGGAATTCGGCCGCAT	3312	QY	3825	CATGCAATGGAGAACATCGTTTCGGCAGCCCGACGATGGATGACCAACGCGCCGCATG	3884
QY	2745	GTCCAAAGATTAATCCAAACAGGACATCTAGTTCCTGTCCAAATCTCCCTGGAATCTCCC	2804	Db	4393	CATGCAATGGAGAACATCGTTTCGGCAGCCCGACGATGGATGACCAACGCGCCGCATG	4452
Db	3313	GTTCAAGATTAATCCAAACAGGACATCTAGTTCCTGTCCAAATCTCCCTGGAATCTCCC	3372	QY	3885	ACCCACTATCAAAAGCCTGTCTTCTCACAGAGAGGCTCACGTTTCGCTCCACAGCGCTCTC	3944
QY	2805	CTGTACCGGTTAGAAAGCCTGGGACTAATGATATCGACACAGTACAGGACTTGAGAGAG	2864	Db	4453	ACCCACTATCAAAAGCCTGTCTTCTCACAGAGAGGCTCACGTTTCGCTCCACAGCGCTCTC	4512
Db	3373	CTGTACCGGTTAGAAAGCCTGGGACTAATGATATCGACATCGACAGTACAGGACTTGAGAGAG	3432	QY	3945	AACCTGCACTCTTCTGCTGGAAGAGACTGATGAACCAAGTGAATGATGATGATGATGATG	4004
QY	2865	GTCAATAACCGGTGCGAGATATACCCCAACAGTCCCGAACCCCTTATAACCTCTGTGT	2924	Db	4513	AACCTGCACTCTTCTGCTGGAAGAGACTGATGAACCAAGTGAATGATGATGATGATGATG	4572
Db	3433	GTCAATAACCGGTGCGAGATATACCCCAACAGTCCCGAACCCCTTATAACCTCTGTGT	3492	QY	4005	CTATTTGATTTAGGAGACTGGGGTCCGAAAGGACCTTACAGACATACCCCTGACTCGAGAA	4064
QY	2925	GCTCTCCCAACCCCAACGGAGTGTGTATACAGTATTGGACTTTAAAGGATGCTCTTCTTCG	2984	Db	4573	CTATTTGATTTAGGAGACTGGGGTCCGAAAGGACCTTACAGACATACCCCTGACTCGAGAA	4632
Db	3493	GCTCTCCCAACCCCAACGGAGTGTGTATACAGTATTGGACTTTAAAGGATGCTCTTCTTCG	3552	QY	4065	GTGCTAACCTGTTTCACTGACCGGAGCAGCTATGTGTGGAGGTAAGAGGATGCTCGG	4124
QY	2985	CTGAGATTAACCCCACTAGGCCAACCACTTTTGTGCTTCCGATGAGAGATCCAGGTACG	3044	Db	4633	GTGTTAACCTGTTTCACTGACCGGAGCAGCTATGTGTGGAGGTAAGAGGATGCTCGG	4692
Db	3553	CTGAGACTACATCCCACTAGGCCAACCACTTTTGTGCTTCCGATGAGAGATCCAGGTGCG	3612	QY	4125	CGGCGGTGTGTGGAGCGGACCCGACGATCTGTGGGCGACAGCTTCCCGGAAGGAACTTCA	4184
QY	3045	GGAAGAACCGGCGAGCTCACCTGGACCCGACTGCCCCCAAGGGTTTCAAGAACTCCCCGACC	3104				

Db 4693 CCGCCGGTGGTGA CCGGACCCGCA CGATCTGGGCCAGCAGCCTGCGGAAAGAACTTCA 4752
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Db 4753 GCACAAAAGCGTGAGCTCATGGCCCTCAGCGAAGCTTTGGGCTGGCCGAGGGAATCC 4812
QY ATAAACATTTATACGACAGCAGGATGCTTTGGCACTGCGACATGACATGATGCGGCAATC 4304
Db 4813 ATAAACATTTATACGACAGCAGGATGCTTTGGCACTGCGACATGACATGATGCGGCAATC 4872
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Db 4873 TATAAGCAAGGGGTTGCTTACCTCAGCAGGAGGGAATAAAGAACAAAGGGAATTT 4932
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Db 4933 CTAAGCCTATTAGAAGCGGTACATTTTGCCTAAGAGGCTAGCTATTATATACATGTCCTGGA 4992
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QY CAGGACGCCAGGGTGTAACTTCTGCCTATATAGAAATGCCCAAGCCCGCAGAACCC 4544
Db 5053 CAGGACGCCAGGGTGTAACTTCTGCCTATATAGAAACACCCAAAGCCCGCAGAACCC 5112
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Db 5113 GAGCGACAGTACACCCCTAGAAGACTGGCAAGAGATAAAAAGATAGACCAAGTTCTCTGAA 5172
QY ACTCCGGAAGGGAACCTGCTATACCTCAGATGGGAAGGAATCTTGCCCCACAAAGAGGG 4664
Db 5173 ACTCCGGAAGGGAACCTGCTATACCTCAGATGGGAAGGAATCTTGCCCCACAAAGAGGG 5232
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Db 5233 TTAGAAATATGTCMAACAGATACATGCTCTAACCCACTAGGAACCTAAACACCTGCGAGAG 5292
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QY AAATTCACCGGAGACTGGCGTTAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 5264
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; CURRENT FILING DATE: 2002-03-28
; PRIOR APPLICATION NUMBER: US 60/279,337
; PRIOR FILING DATE: 2001-03-28
; NUMBER OF SEQ ID NOS: 139
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 137
; LENGTH: 8764
; TYPE: DNA
; ORGANISM: Sus scrofa
; FEATURE:
; OTHER INFORMATION: porcine endogenous retrovirus (PERV)
; OTHER INFORMATION: G3 locus; G3 PERV genome
US-10-113-664A-137
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Query Match 78.0%; Score 6343.4; DB 6; Length 8764;
Best Local Similarity 87.2%; Pred. No. 0;
Matches 7175; Conservative 0; Mismatches 926; Indels 126; Gaps 15;

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QY 61 TCAAGACCGCTTCTCGTGAAGTAAAGGGAGTGCCTTTTCCGAGCCTGGAGG---- 115
DB 548 TCAAGACCGCTTCTCGTGAAGTAAAGGGAGTGCCTTTTCCGAGCCTGGAGGGGG 606
QY 116 ----TTCTTTTTCGTGCTTACATTTGGGGGCTCGTCCGGGATCTGTGCGGCCACCC 171
DB 607 GATTGTTCTTTTACTTGCCTTTCATTTGGTGTGCAATGGCCGGGAAACCCCTGCGACCC 666
QY 172 TTAACCCGAGAACCGACTTGGAGGTAAAGAGATCCTCTTTTAAAGTATGCAATGTA 231
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DB 784 TGTCTCTCTCAGACCGTAAAGGACTTGGAGGACTGTGATCAGCAGACGTGCTAGGAGGATCAC 843
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DB 844 AGGCTGCCACCTTGGGGGAGCGCCCCGGGAGGTGGGAGAGCCAGGACGCTGTGGTGTCT 903
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QY 472 CGTCCGACTCTTTTGCCTGTGTTGAAGACGTGGACGGGTCACTGTGTCTGGATCTGT 531
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QY 892 AGCCAAAGAAAGCAGGTCCCGAAATTCGGCTCTTGGAGAGAAACAAACACTCCGGCTG 951
DB 1384 AACCAAGAAAGCAGGTCCCGAAATTCGGCTCTTGGAGAGAAACAAACACTCCGGCCG 1443
QY 952 AAAAAAGTCAAGCCCTCTCTCATATCTACCCCGAGATTGAGGAGCCACCGGCTTGCCCG 1011
DB 1444 AAAAAAGTCAAGCCCTCTCTCTGATCTACCCCGAGATCGAGAGCGCCGACTTGGCCCG 1503
QY 1012 AACCCCAATCTGTTCCCGACCCCTTATCTGCGCAGAGGTGCGGAGGGAGCCCTTTCG 1071
DB 1504 AACCCCAATCTGTTCCCGACCCCTTATCCAGCAGAGGTGCTGTGAGGGGACCTCTCG 1563
QY 1072 CCCCTCTGAGCTCCGGGTGGAGGACCTGTGACGGGACTCGAGAGCCGAGGGGGCG 1131
DB 1564 CCCCTCTGAGCTCCGGGTGGAGGACCTGTGTCGGGACTCGAGAGCCGAGAGGGCG 1623
QY 1132 CCACCCCGAGGCGGACAGACGAGATCGCAGCATTTACCGCTGCGCACGTACGGCCCTCCCA 1191
DB 1624 CCACCCCGAGGCGGACAGACGAGATCGCGATATTACCGCTGCGCACCTATGSCCCTCCCA 1683
QY 1192 CACCGGGGGGCAATTTGACGCCCCCTCCAGTATTGGCCCTTTTCTCTGCGAGATCTCTATA 1251
DB 1684 TGCCGGGGGGCAATTTGACGCCCCCTCCAGTATTGGCCCTTTTCTCTGCGAGATCTCTATA 1743
QY 1252 ATTGGAAACTAACCATCCCCCTTCTCGGAGGATCCCAACGCTCAGGGGTTGCTGG 1311
DB 1744 ATTGGAAACTAACCATCCCCCTTCTCGGAGGATCCCAACGCTCAGGGGTTGCTGG 1803
QY 1312 AGTCCCTTATGTTCTCTACACGCTTACTTGGGATGATTGTCAACAGCTGCTGCAGACAC 1371
DB 1804 AGTCCCTTATGTTCTCTACACGCTTACTTGGGATGATTGTCAACAGCTGCTGCAGACAC 1863
QY 1372 TCTTCAACCCGAGGCGAGAGAGAAATTTCTATTAGAGCTAGAAAAATGTTTCTTGGGG 1431
DB 1864 TCTTCAACCCGAGGCGAGAGAGAAATTTCTGTTAGAGCTAGAAAAATGTTTCTTGGGG 1923
QY 1432 CGGAGGGGCGACCCACGCGGTTGCAAAATGAGATTGACATGGATTTCCCTTAACTCGCC 1491
DB 1924 CGGAGGGGCGACCCACGCGAGTTGCAAAATGAGATTGACATGGATTTCCCTTAACTCGCC 1983
QY 1492 CCGGTTGGGACTACAACACGCGTGAAGGTAGGAGAGCTTGAAAAATCTATCGCAGGCTC 1551
DB 1984 CCGGTTGGGACTACAACACGCGTGAAGGTAGGAGAGCTTGAAAAATCTATCGCAGGCTC 2043
QY 1552 TGGTGGCGGCTCTCGGGGCGCTCAAGACGGGCCCACTAAATTTGGCTAAGGTAAGAAG 1611
DB 2044 TGGTGGCGGCTCTCGGGGCGCTCAAGACGGGCCCACTAAATTTGGCTAAGGTAAGAAG 2103
QY 1612 TGATCGAGGAGCGAATGAACCCCTCTGTTTCTTCTGAGAGGCTTGGAGGCTTCA 1671
DB 2104 TGATCGAGGAGCGAATGAACCCCTCTGTTTCTTCTGAGAGGCTTGGAGGCTTCA 2163
QY 1672 GCGGTTACACCCCTTTTGTATCCACCTCAGAGGCCCAAAAAGCCTCAGTGGCTTTGGCCCT 1731
DB 2164 GCGGTTACACCCCTTTTGTATCCCTCAGAGGCCCAAAAAGCCTCAGTGGCCCTTGGCCCT 2223
QY 1732 TTATAGGACAGTCAGCTTTGGGATATTAGAAAGAGCTTCAGAGACTGGAAGGTTACAGG 1791
DB 2224 TCATTTGGGCGAGTCGGCTCTGGATATCAGAAAGAAACTTCAGAGACTGGAAGGTTACAGG 2283
QY 1792 AGGCTGAGTTACGTGATCTAGTGAAGGAGGAGGAGAACTATATTACAAAGAGGAGACAG 1851
DB 2284 AGGCTGAGTTACGTGATCTAGTGAAGGAGGAGGAGAACTATATTACAAAGAGGAGACAG 2343
QY 1852 AAGAAAGAAAGGAAACAAAGAAAGAGAGAGAAAGAGGAGGAGGAGGAGGAGGAGGAGG 1911
DB 2344 AAGAGGAGAGGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGGAGG 2403
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QY 1912 AACGGCAAGAGAGAAATTTGACTAAGATCTTGGCTGCAGTGGTTGAAGGGAAGCAATA 1971
DB 2404 GACGGCAAGAGAGAAATTTGACTAAGATCTTGGCCGAGTGGTTGAAGGGAAGCAGCA 2463
QY 1972 CGMAAGAGAGAGAGATTTAGGAAATTTAGTTCAGGCTCAGGAGGAGGAGGAGGAGG 2031
DB 2464 GGGAGAGAGAGAGAGATTTAGGAAATTTAGTTCAGGCTCAGGAGGAGGAGGAGGAGG 2523
QY 2032 GCAATAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2091
DB 2524 GCAATAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2583
QY 2092 CAAGGAACTGCCCAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2151
DB 2584 CAAGGAACTGCCCAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2643
QY 2152 AAGATTAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2211
DB 2644 AAGATTAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2703
QY 2212 AGGGGCAACAGATTGAGTTCCTGCTGATACCGGAGGAGGAGGAGGAGGAGGAGGAGG 2271
DB 2704 AGGGGCAACAGATTGAGTTCCTGCTGATACCGGAGGAGGAGGAGGAGGAGGAGGAGG 2763
QY 2272 CATTTAGGAAATCTAAAGATATAAAATCTCGGAGGAGGAGGAGGAGGAGGAGGAGG 2331
DB 2764 CATTTAGGAAATCTAAAGATATAAAATCTCGGAGGAGGAGGAGGAGGAGGAGGAGG 2823
QY 2332 ATCCATGGAGTACCCGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2391
DB 2824 ATCCATGGAGTACCCGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2883
QY 2392 TGGTCATCTGAGTGGCCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2451
DB 2884 TGGTCATCTGAGTGGCCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2943
QY 2452 GACAAATTTCTTTTGAACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2511
DB 2944 CTCAAATTTCTTTTGAACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 3003
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DB 3004 TGGTGACCTCCAAATTTAGATGATGATATCGACTATATCTCCCTCTAGTAAAGCTGATC 3063
QY 2572 AAAATATCAATCTCTGTTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2631
DB 3064 AAGATATACAGTCTGTTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 3123
QY 2632 GTTTGGCAAGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2691
DB 3124 GTTTGGCAAGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 3183
QY 2692 CAGTCAGACAGTACCCCTTGGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2751
DB 3184 CAGTCAGACAGTACCCCTTGGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 3243
QY 2752 GATTAAATCCAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2811
DB 3244 GATTAAATCCAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 3303
QY 2812 CGGTTAGAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2871
DB 3304 CGGTTAGAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 3363
QY 2872 AACGGGTCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2931
DB 3364 AAAGGGTCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 3423
QY 2932 CACCCCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2991
DB 3424 CGCCTGAACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 3483
QY 2992 TACACCCCACTAGCCAAACCACTTTTGGCTTCGAATGGAGAGATCCAGGTACGGGAAGAA 3051

DB 3484 TACACCCCACTAGCCAAACCGCTTTTGGCTTCGAATGGAGAGATCCAGGTACGGGAAGAA 3543
QY 3052 CCGGGCAGCTCAGCTTGGAGCCGAGTCCCAAGGGTTCAAGAACTCCCCGACCATCTTTG 3111
DB 3544 CCGGGCAGCTCAGCTTGGAGCCGAGTCCCAAGGGTTCAAGAACTCCCCGACCATCTTTG 3603
QY 3112 ACAGAGCCCTACACAGAGAGCTTGGCCCACTTTCAGGATCCAAACCCCTCAGGTGACCTCC 3171
DB 3604 ACAGAGCCCTACACAGAGAGCTTGGCCCACTTTCAGGATCCAAACCCCTCAGGTGACCTCC 3663
QY 3172 TCCAGTACGTTGGATGACCTGCTTCTGGCGGAGCCACCAACAGAGACTGCTTGAAGGCA 3231
DB 3664 TCCAGTACGTTGGATGACCTGCTTCTGGCGGAGCCACCAACAGAGACTGCTTGAAGGTA 3723
QY 3232 CGAAGGCACCTACTGCTGGAAATTTGCTGACCTAGGCTACAGAGCCCTGCTTAAGAGGCC 3291
DB 3724 CGAAGGCACCTACTGCTGGAAATTTGCTGACCTAGGCTACAGAGCCCTGCTTAAGAGGCC 3783
QY 3292 AGATTTGACAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 3351
DB 3784 AGATTTGACAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 3843
QY 3352 TGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 3411
DB 3844 TGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 3903
QY 3412 TGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 3471
DB 3904 TGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 3963
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DB 3964 TAGCAGCCCACTCTACCCGCTAACCAAGAAAGGGGAGGAGGAGGAGGAGGAGGAGGAGG 4023
QY 3532 ACAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 3591
DB 4024 ACCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 4083
QY 3592 CTGAGGTAACCTAAACCCCTTTTACCTTTATGTTGAGTGAAGGAGGAGGAGGAGGAGGAGGAG 3651
DB 4084 CTGAGGTAACCTAAACCCCTTTTACCTTTATGTTGAGTGAAGGAGGAGGAGGAGGAGGAGGAG 4143
QY 3652 TTTTAAACCCCAACCTAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 3711
DB 4144 TTTTAAACCCCAACCTAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 4203
QY 3712 ATCTGTAGCCAGTGGTTGGCCCATATGCTGTAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 3771
DB 4204 ATCTGTAGCCAGTGGTTGGCCCATATGCTGTAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 4263
QY 3772 TCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 3831
DB 4264 TCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 4323
QY 3832 TGGAGAACTCTGCTGGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 3891
DB 4324 TGGAGAACTCTGCTGGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 4383
QY 3892 ATCAAGCCCTCTCTCAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 3951
DB 4384 ATCAAGCCCTCTCTCAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 4443
QY 3952 CCACCTCTCTCTCTCAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 4011
DB 4444 CCACCTCTCTCTCTCAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 4503
QY 4012 TTGAG 4071
DB 4504 TTGAG 4563
QY 4072 CCTGTTCACTGACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 4131

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QY 4132 TGTGGACGGGACCCGACAGATCTGGCCGACGACCTCTGGGAAGAACTTCAGCACAAA 4191
Db 4624 TGTGGACGGGACCCACACGATCTGGCCGACGACCTGCGGAAGAACTTCAGCGCAA 4683
QY 4192 AGCTGAGCTCATGGCCCTCAGCAAGCTTTGGGGCTGGCGGAGGGAATCATAAACA 4251
Db 4684 AGGCTGAGCTCATGGCCCTCAGCAAGCTTTGGGGCTGGCGGAGGGAATCATAAACA 4743
QY 4252 TTTATACGACAGCAGGTATGCTTTGCGACTGCAACCTACATGGGGCCATCTATAAC 4311
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Db 4804 AAAGGGGGTGTCTTACCTCAGCAGGAGGGAATAAAGAAAGAAATTTCTAAGCC 4863
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Db 5284 GTGTGCCCTGCCAGCTGGTTAATGCTAATCCTTCCAGATGCCCTCCAGGAAGAGACTAA 5343
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Db 6541 TGAATGSCCGATCTCTCTCAGGACCGGGTAAATTTCTCTCTGTGCAA----- 6590
QY 6109 AGCTCTGGAACAATTTAATTTACCTGATCTGGAATAGAACTGGGAAGCCCAAGTGTCTCCT 6168
Db 6591 --TTCCGGCCCGGCAAGTACAAAGTATATAAAGATAAGAGTGTCTCCCA 6648
QY 6169 TCAGACTAGATTAACCTAAATAAGTTTCACTGAGAAAGGAAACCAAGAAATATCCTA 6228
Db 6649 TCAGACTAGATTAATCTAAGATAGTTTCACTGAAAAAGGAAAAAGGAAAAATATTCAA 6708
QY 6229 AAATGGGTAATGATGTTGGGAATGTTATATTTATGGAGGCTCGGTTAAACCAACCA 6288
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QY 6346 GGACCAATACGGTCTTGACGGGTCAAGACGCCCCCAACC----- 6385
Db 6826 GGACCCGATAAGTACTGGCTGAACAGGGGCCCGCGCCCTGGAGCCACCGCATAACTTG 6885
QY 6386 -----AAGGACCAGGACCATCTCTAAACATAACT 6414
Db 6886 CCGTGCCCAATTAACCTCGCTGGGCTGACATACAGCGCCCTAGCAACGGTACC 6945
QY 6415 TCTGATCAGACCCCACTGAGTCTAACAGACGAC-----TAAATGGGG 6459
Db 6946 ACTGGATTGATTCTTACCAACAGCGCTAGAACTCCCGAGGTGTTCTGTGTTAAGACAGGA 7005
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QY 6640 AATAAGCTTACCTTACTGAGGTTTCTGGAAGGACCTGCATAGGAAGGTTCCGCCA 6699
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QY 8002 GTTGTGAACCCCATPAAAGCTGTCCGACTCCACACTCGGGGCGGAGTCTCTTACCCCT 8061
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Db 8621 GCGTGTGTAGACTGTGGGCCCCAGCGGCTTGAATTAATAATCTTCTTCTGTTGCA 8680
QY 8122 TCABAAA 8128
Db 8681 TCAAGAA 8687

RESULT 7

US-10-471-220-2
; Sequence 2, Application US/10471220
; Publication No. US2004014249A1
; GENERAL INFORMATION:
; APPLICANT: Tonjes, Ralf R.
; APPLICANT: Krach, Ulrich
; TITLE OF INVENTION: REPLICATION-COMPONENT MOLECULAR CLONES
; TITLE OF INVENTION: OF PORCINE ENDOGENOUS RETROVIRUS CLASS A AND CLASS B DERIVED
; FILE REFERENCE: 11692-007US1
; CURRENT APPLICATION NUMBER: US/10/471,220
; CURRENT FILING DATE: 2003-09-08

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/ PRIOR APPLICATION NUMBER: PCT/EP02/02656
/ PRIOR FILING DATE: 2002-03-11
/ PRIOR APPLICATION NUMBER: DE 101 11 433.8
/ PRIOR FILING DATE: 2001-03-09
/ NUMBER OF SEQ ID NOS: 47
/ SOFTWARE: PASTSEQ for Windows Version 4.0
/ SEQ ID NO 2
/ LENGTH: 8763
/ TYPE: DNA
/ ORGANISM: Sus scrofa
/ FEATURE:
/ NAME/KEY: source
/ LOCATION: (0)...(0)
/ OTHER INFORMATION: Porcine cell line PK15; replication-competent
/ OTHER INFORMATION: PERV-B clone PK15-PERV-B(213)
/ FEATURE:
/ NAME/KEY: misc feature
/ LOCATION: (1)...(8763)
/ OTHER INFORMATION: n = A,T,C or G
US-10-471-220-2

Query Match 77.7%; Score 6319; DB 7; Length 8763;
Best Local Similarity 87.0%; Pred. No. 0;
Matches 7159; Conservative 0; Mismatches 941; Indels 126; Gaps 15;

QY 1 GCGTGTGTACGACTGTGGGCCCCAGCGGCTTGGAAATAAAATCCTTGTCTGTTGCA 60
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QY 61 TCAAGACCGCTTCTGTAGTGTAAAGGGAGTCGCTTTCGAGAGCTTGAGG----- 115
Db 548 TCAAGACCGCTTCTGTAGTGTATT-TGGGGTGTGCGCTTTCGAGCCCGACGAGGGG 606
QY 116 ----TTCCTTTTGTCTGCTTACATTTGGGGCTCTGCGGGATCTGTCGGCCACCCC 171
Db 607 GATTGTCTTTTACTGGCCCTTCATTGTGTGCTTGGCCGGGAAATCCTGCGACACCCC 666
QY 172 TAACACCCGAGAACCGACTTGGAGGTAAAGAGATCCTCTTTTAACTGTATGCAATGTA 231
Db 667 TTACACCCGAGAACCGACTTGGAGGT-AAAGGATCCCTTTTGGACGTGTGTG--TG 723
QY 232 CGGCGCGGCTCTGTCTGTAGTGTCTGTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 291
Db 724 TCGGCGCGGCTCTGTCTGTAGTGTCTGTCTGTGTGTGTGTGTGTGTGTGTGTGTGT 783
QY 292 TGTCTCTCAGGCGGTAAAGGCTGGGGAGTGTGATCAGCAGACGTGTAGGAGGATCAC 351
Db 784 TGTCTCTCAGACCGTAAAGACTTGGAGGACTGTGATCAGCAGACGTGTAGGAGGATCAC 843
QY 352 AGGCTGTGCTGCGCTGGGGAGCGCCCGGAGGTGAGGAGAGCCAGGACGCTGTGTGTCT 411
Db 844 AGGCTGCGACCTTGGGAGCGCCCGGAGGTGGGAGAGCCAGGAAAGCGCTGTGTGTCT 903
QY 412 CTTACTGTGCGTCAGAGGACCGAAATCTGTGTGTGTAAGCGAAAGCTTCCCGCTCCG 471
Db 904 CTTACTGTGCGTCAGAGGTCGAGTCTGTGTGTGTAAGCGAAAGCTTCCCGCTCCG 963
QY 472 CGTCCGACTCTTTTGTGCTGTGTAAGCGGTGAGGAGTGTGCTGTGTGTGTGTGTGT 531
Db 964 CGTCCGACTCTTTTGTGCTGTGTAAGCGGAGCGGTCGCGTGTGTGTGTGTGTGTGT 1023
QY 532 TGTGTTTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 591
Db 1024 TGTGTTTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1083
QY 592 AGACGTGACGACCCCTCTTAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 651
Db 1084 AGACGTGACACCCCTCTTAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1143
QY 652 CTCATAATTTGTCTAGTGTAAAGAGGACCTTGGCAGACTTCTGTGTGTCTCTGAAT 711
Db 1144 CTCATAATTTGTCTAGTGTAAAGAGGACCTTGGCAGACTTCTGTGTGTCTCTGAAT 1203

712 GCGCGACATTTCGATGTGTGATGCGCATCAGAGGGGACCTTTAAATTTCTGAGATTATCCTGG 771
1204 GCGCAACATTTCGATGTGTGATGCGCATCAGAGGGGACCTTTAAATTTCTGAAATTTATCCTGG 1263
772 CTGTTAAAGCAGTATTTTTCAGACTGGACCGGGCTCTCATCCCGATCAGGAGCCCTATA 831
1264 CTGTTAAAGCAATCATTTTTCAGACTGGACCGGGCTCTCATCTGTATCAGGAGCCCTATA 1323
832 TCTTTACGTGGCAAGATTGGCAGAGGATCTCTCCGCAATGGGTAAACCATGGCTGAATA 891
1324 TCTTTACGTGGCAAGATTGGCAGAGGATCTCTCCGCAATGGGTAAACCATGGCTGAATA 1383
892 AGCCAGAAAGCCAGGTCCTCCGAAATTCGTCTCTTGGAGAGAAAAACAAACACTCGGCTG 951
1384 AAACAAGAAAGCCAGGTCCTCCGAAATCTCTGGCTCTTGGAGAGAAAAACAAACACTCGGCG 1443
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1012 AAACCCCAATCTGTTCCCCACCCCTTATCTGGCAGAGGTGCGCGAGGGGACCTTTG 1071
1504 AAACCCCACTGTTCCCCACCCCTTATCTCAGACAGAGGTGCTGTGAGGGACCTCTG 1563
1072 CCCCTCTCGAGCTTCGGCGGTGGAGGACCTGTGTCAGGAGACTCGGAGCCGAGGGGG 1131
1564 CCCCTCTCGAGCTTCGGGTGGTGGAGGACCTGTGTCGGGACCTCGGAGCCGAGAGGG 1623
1132 CCACCCCGAGCGGACAGACGAGATCGCGACATTAACCGCTGCGCAGCTACGGGCCCTCCCA 1191
1624 CCACCCCGAGCGGACAGACGAGATCGCGATATTACCGCTGCGCAGCTATGGCCCTCCCA 1683
1192 CAACCGGGGGCCAAATTCAGACCCCTCCAGTATTGGCCCTTTTCTTCGAGATCTCTATA 1251
1684 TCGCAGGGGGCCAAATTCAGACCCCTCCAGTATTGGCCCTTTTCTTCGAGATCTCTATA 1743
1252 ATTGAAAACTAAACATCCCTTCTCGAGAGATCCCAACCGCTCAGGGGTTGGTGG 1311
1744 ATTGAAAACTAAACATCCCTTCTCGAGAGATCCCAACCGCTCAGGGGTTGGTGG 1803
1312 AGTCCCTTATGTCTCTCAGACGCTTCTGGAGTATGTCACAGCTGTCTGACACAC 1371
1804 AGTCCCTTATGTCTCTCAGACGCTTCTGGAGTATGTCACAGCTGTCTGACACAC 1863
1372 TCTTCAACACCGAGGAGCAGAGAGAAATCTATTAGAGCTAGAAAAAATGTTCTCTGGGG 1431
1864 TCTTCAACACCGAGGAGCAGAGAGAAATCTCTGTAGAGCTAGAAAAAATGTTCTCTGGGG 1923
1432 CGCAGGGGCGACCCAGCGGTTGCAAAATGAGATTGACATGGGATTTCCCTTAACCTGCC 1491
1924 CGCAGGGGCGACCCAGCGAGTTGCAAAATGAGATTGACATGGGATTTCCCTTTGACTCGCC 1983
1492 CGGTTTGGAGCTACAAACCGCTGAGGTAGGAGAGCTTGAAAAATCTATCGCCAGGCTC 1551
1984 CGGTTTGGAGCTACAAACCGCTGAGGTAGGAGAGCTTGAAAAATCTATCGCCAGGCTC 2043
1552 TGTGTGCGGCTCTCGGGGCGCTCAAAGACGGCCCACTAAATTTGGCTAAGGTAAGAGAAG 1611
2044 TGTGTGCGGCTCTCGGGGCGCTCAAAGACGGCCCACTAAATTTGGCTAAGGTAAGAGAAG 2103
1612 TGAATGAGGAGCGAAATGAACCCCTCTGTGTTTCTTGTAGAGGCTCTTGGAAAGCCTTCA 1671
2104 TGAATGAGGAGCGAAATGAACCCCTCTGTGTTTCTTGTAGAGGCTCTTGGAAAGCCTTCA 2163
1672 GCGGTTACACCCCTTTTGTATCCCACTCAGAGSCCAAAAAAGCTCAGTGGCTTTTGGCCT 1731
2164 GCGGTTTACCCCTTTTGTATCTTACCTCAGAGSCCCAGAAAGCTCAGTGGCTTGGCCT 2223
1732 TTATAGGACAGTCAGCCTTTGGATATTAGAAAGAGCTTTCAGAGACTTGGAGGGTTACAGG 1791
2224 TCATTGGGCGAGTCGGCTCTGGATATCAGAAAGAACTTTCAGAGACTTGGAGGGTTACAGG 2283
1792 AGGCTGAGTTACGTGATCTAGTGAAGGAGCGAGAAAGTATATTACAAAGAGGAGACAG 1951
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QY	4012	TTGAGGAGACTGGGGTCCGCAAGGACCTTACAGACATACCGCTGACTGGAGAGTGTCTAA	4071
Db	4504	TTGAGGAGACTGGGGTCCGCAAGGACCTTACAGACATACCGCTGACTGGAGAGTGTCTAA	4563
QY	4072	CCTGGTTCACTGACGGAAGCAGCTATGTGGTGAAGGTGAAGGATGGCTGGGGCGGCGG	4131
Db	4564	CCTGGTTCACTGACGGAAGCAGCTATGTGGTGAAGGTGAAGGATGGCTGGAGCGGCGG	4623
QY	4132	TGGTGAACGGGACCCGACGATCTGGCCGAGCAGCCTGGGGAAGAACTTCAGCACARA	4191
Db	4624	TGGTGAACGGGACCCGACGATCTGGCCGAGCAGCCTGGGGAAGAACTTCAGCGCAAA	4683
QY	4192	AGGCTCAGCTCATGGGCCCTCACGCAAGCTTTGGCGTGGCCGGAAGGAAATCCATAACA	4251
Db	4684	AGGCTCAGCTCATGGGCCCTCACGCAAGCTTTGGCGTGGCCGGAAGGAAATCCATAACA	4743
QY	4252	TTTATACGGAACGACAGGTATGCTTTGCGACTGCACACGTAACATGCGGCGCATCTATAAC	4311
Db	4744	TTTATACGGAACGACAGGTATGCTTTGCGACTGCACACGTAACATGCGGCGCATCTATAAC	4803
QY	4312	AAAGGGGTTGCTTACTCAGCAGGAGGGAATTAAGAACAAAGAGGAAATCTTAAGCC	4371
Db	4804	AAAGGGGTTGCTTACTCAGCAGGAGGGAATTAAGAACAAAGAGGAAATCTTAAGCC	4863
QY	4372	TATTAGAAGCCGTACATTTACCAAAAAGGTAGCTATTATACATCTCTCTGGACATCAGA	4431
Db	4864	TATTAGAAGCCGTACATTTGCCCCAAAAGGTAGCTATTATACATCTCTCTGGACATCAGA	4923
QY	4432	AAAGCTAAAGATCTCATATCCAGAGGAACACAGATGCTGACCGGGTTGCAAGCAGGCAG	4491
Db	4924	AAAGCTAAAGATCTCATATCCAGAGGAACACAGATGCTGACCGGGTTGCAAGCAGGCAG	4983
QY	4492	CCGAGGTTGTAACCTTCTGCTTATTAATAGAAATGCCAAAGCCGACAGACCCAGACGAC	4551
Db	4984	CCGAGGTTGTAACCTTCTGCTTATTAATAGAAATGCCAAAGCCGACAGACCCAGACGAC	5043
QY	4552	AGTACACCTTAGAAGACTGGCAAGAGATAAAAAGATAGACAGTTCTCTGAGACTCCGG	4611
Db	5044	AGTACACCTTAGAAGACTGGCAAGAGATAAAAAGATAGACAGTTCTCTGAGACTCCGG	5103
QY	4612	AAAGGACCTGCTATACCTCAGATGGGAAGGAATCTGCCCCCAAAAAGAGGGTTAGAAT	4671
Db	5104	AAAGGACCTGCTATACCTCAGATGGGAAGGAATCTGCCCCCAAAAAGAGGGTTAGAAT	5163
QY	4672	ATGTCCAAACAGATACATCGTCTAACCCACCTAGGAACCTAAACACCTGACGAGTTGGTCA	4731
Db	5164	ATGTCCAAACAGATACATCGTCTAACCCACCTAGGAACCTAAACACCTGACGAGTTGGTCA	5223
QY	4732	GAAATCCCTTATCATGTTCTGAGGCTACGAGAGTGGCTGACTCGGTGGTCAAAACATT	4791
Db	5224	GAAATCCCTTATCATGTTCTGAGGCTACGAGAGTGGCTGACTCGGTGGTCAAAACATT	5283
QY	4792	GTGTGCCCTGCCAGCTGGTTAATGCTTAATCCCTCCAGAAATACCTCCAGGGAAGAGACTAA	4851
Db	5284	GTGTGCCCTGCCAGCTGGTTAATGCTTAATCCCTCCAGAAATACCTCCAGGGAAGAGACTAA	5343
QY	4852	GGGGAAGCCACCCAGCGCTCACTGGGAAGTGAACCTCACTGAGGTAAAGCCGGCTAAAT	4911
Db	5344	GGGGAAGCCACCCAGCGCTCACTGGGGAAGTGAACCTCACTGAGGTAAAGCCGGCTAAAT	5403
QY	4912	ACGGAAACAAATACCTATTGTTTGTAGACACCTTTTCAGGATGGGTAGAGGCTTATC	4971
Db	5404	ACGGAAACAAATATCTATTGTTTGTAGACACCTTTTCAGGATGGGTAGAGGCTTATC	5463
QY	4972	CTACTAAGAAAGAGACTTCAACCGTGGTGGCTTAAAAAATACTCGGAAGAAATTTTCCAA	5031
Db	5464	CTACTAAGAAAGAGACTTCAACCGTGGTGGCTTAAAAAATACTCGGAAGAAATTTTCCGA	5523
QY	5032	GATTGGAAATACCTAAGGTAAATAGGTGACAGAAATGCTCCAGCTTTTGTGCCCCAGTAA	5091
Db	5524	GATTGGAAATACCTAAGGTAAATAGGTGACAGAAATGCTCCAGCTTTTGTGCCCCAGTAA	5583

QY	5092	GTCAAGGACTGCGCCAAAGATATTGGGGATTGATTGAAAATCTGCATTGTGTGATACAGACCCC	5151
Db	5584	GTCAAGGACTGCGCCAAAGATATTGGGGATTGATTGAAAATCTGCATTGTGTGATACAGACCCC	5643
QY	5152	AAAGCTCAGGACAGGTAGAGAGATCAATAGAACCAATTAAGAGACCCCTTACTTAATTTGA	5211
Db	5644	AAAGCTCAGGACAGGTAGAGAGATCAATAGAACCAATTAAGAGACCCCTTACTTAATTTGA	5703
QY	5212	CCGCGGAGACTGGCGTTAATGATTGGATAGCTCTCTCGCCCTTTGTGCTTTTGTAGGGTTA	5271
Db	5704	CCACAGAGACTGGCATTAATGATTGGATAGCTCTCTCGCCCTTTGTGCTTTTGTAGGGTTA	5763
QY	5272	GGAAACACCCCTCGACAGTTTGGGCTGAACCCCTATGAATTACTCTACGGGGACACCCCCC	5331
Db	5764	GGAAACACCCCTCGACAGTTTGGGCTGAACCCCTATGAATTACTCTACGGGGACACCCCCC	5823
QY	5332	CATTGGTAGAAATTTGCTTCTGTACATAGTGTGACGCTGTGCTTTTCCAGCCCTTTGTTCT	5391
Db	5824	CATTGGTAGAAATTTGCTTCTGTACATAGTGTGACGCTGTGCTTTTCCAGCCCTTTGTTCT	5883
QY	5392	CTAGGCTCAAGGCACCTTGAGTGGGTGAGACAAACGAGCGTGGAGGCAACTCCGCGGAGGCCT	5451
Db	5884	CTAGGCTCAAGGCCTGAGTGGGTGAGGCAACGAGCGTGGAGGCAACTCCGCGGAGGCCT	5943
QY	5452	ACTCAGGAGGAGAGACTTTGCAGATCCCAATCGTTTCCAAAGTGGGAGATTCAGTCTACG	5511
Db	5944	ACTCAGGAGGAGAGACTTTGCAGATCCCAATCGTTTCCAAAGTGGGAGATTCAGTCTACG	6003
QY	5512	TTAGAGCCACCGTGCAGGAAACCTCGAGACTCGGTGGAGAGCCCTTATCTCGTACTTT	5571
Db	6004	TTAGAGCCACCGTGCAGGAAACCTCGAGACTCGGTGGAGAGCCCTTATCTCGTACTTT	6063
QY	5572	TCAGCACACCAACCGCTGTGAAGTGAAGGATCTCCACCTGGATCCATGATCCACG	5631
Db	6064	TCAGCACACCAACCGCTGTGAAGTGAAGGATCTCCACCTGGATCCATGATCCACG	6123
QY	5632	TTAAACACCGCGCACCTCCGATTCGGGTGGAAAGCCGAAAGACTGAAATTCCTTTA	5691
Db	6124	TTAAAGCTGGCGCCACCTCCGACTCGGGTGGAGAGCCGAAAGACTGAAATTCCTTTA	6183
QY	5692	AGCTTCGCTCATCGCTGGTTCCTTACTCTGCTCAATTAACCTCTCAGACTAATGATG	5751
Db	6184	AGCTTCGCTCATCGCTGGTTCCTTACTCTGCTCAATTAACCTCTCAGACTAATGATG	6243
QY	5752	CGCATAGGAGAGACGCTGAACTCCCAATAAACCTTCTCTCACCTGGTGTAAATTA	5811
Db	6244	CGCTTTATAGACAGCTCGAAACCCCAATAGACCTTTATCCCTTACCTGGCTGATTA	6303
QY	5812	TCGCGCACAGGTATTAATATCAACAACTCAAGGGAGGCTCTCTTTAGGAACTCGGTG	5871
Db	6304	CTGTATACGGGTGCTCACTGTAAATAGCACTCGAGGTGTGCTCTCTAGAGGACCTG	6363
QY	5872	CCTGATCTATAGCTTTGGCTCAGATCAGTTATTC---CTAGTCTGACCTCACCCCGAT	5928
Db	6364	CCTGAACTGCAATTTCTGCTCCGCTCGGATTAACCCCGCTGTTAAAGAGCACCTCCCAAC	6423
QY	5929	ATCCTCCATGCTCACGGATTTTATGTTCCCGAGGACCCCAATAATTAATGAAACATTCG	5988
Db	6424	CTAGTCCGTAGTTATGGGTCTATTGCTGCCAGG---CACAGAGAAAGAAATTA	6480
QY	5989	GGAAATCCAGAGATTTCTTTTGTAAACAACTGGAACCTGTAACTTAATGATGATAT	6048
Db	6481	GGGGTTCCTGGGGAATCTTCTCTAGGAGATGGAGCTGCTGCTCACTCCAAAGTGGAGAC	6540
QY	6049	TGAAATGGCCAACTCTCAGAGGATAGGTAAGTTTCTTCTGTCGAACCTATACC	6108
Db	6541	TGAAATGGCCGATCTCTCTCAGGACCGGGTAAATTTCTCTTTCTCAA-----	6590
QY	6109	AGCTCTGGAACAAATTTAATTAACCTGACCTGATTTAGAACTGGAGCCCGGCTCTCT	6168
Db	6591	---TTCCGGCCCGGCAAGGTACAAAGTGAAGAACTATATAAGATAGAGGCTGCTCCCA	6648
QY	6169	TCAGACCTAGATTAACCTAAAAATAAGTTTCACTGAGAAAGGAAACAAAGAAATATCTCTA	6228

APPLICANT: Krach, Ulrich
; TITLE OF INVENTION: REPLICATION-COMPONENT MOLECULAR CLONES
; TITLE OF INVENTION: OF PORCINE ENDOGENOUS RETROVIRUS CLASS A AND CLASS B DERIVED
; FILE OF INVENTION: FROM PIG AND HUMAN CELLS
; FILE REFERENCE: 11692-007U51
; CURRENT APPLICATION NUMBER: US/10/471,220
; CURRENT FILING DATE: 2003-09-08
; PRIOR APPLICATION NUMBER: PCT/EP02/02656
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: DE 101 11 433.8
; PRIOR FILING DATE: 2001-03-09
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 8840
; TYPE: DNA
; ORGANISM: Sus scrofa
; FEATURE:
; NAME/KEY: source
; LOCATION: (0)...(0)
; OTHER INFORMATION: Porcine primary fibroblasts; replication-competent
; OTHER INFORMATION: PERV-B clone PERV-B(Bac-192B9)
US-10-471-220-4

Query Match 77.3%; Score 6288.8; DB 7; Length 8840;
Best Local Similarity 86.8%; Pred. No. 0;
Matches 7173; Conservative 0; Mismatches 932; Indels 155; Gaps 17;

QY 1 GCGTGTGTACGACTGTGGGCCCCAGCGCGCTTGGAAATAAAATCCTCTTGTGTTTGA 60
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QY 61 TCAAGACCGCTTCTCGTAGTGATTAAAGGGAGTCGCTTTCCGAGCGCTGGAGG- 115
DB 586 TCAAGACCGCTTCTCGTAGTGATT-TGGGGTGTGCGCTTCTCCGAGCCCGACGAGGGG 644
QY 116 ---TTCTTTTCTGCTGCTTCAATTTGGGGGCTCGTCGGGACTGTGCGCGGCCACCC 171
DB 645 GATTGTTCTTTTACTGCGCTTTCATTTGGTGGCTGGCGGGAAATCCTGGACACCC 704
QY 172 TAAACCCGAGAACCGACTTGGAGGTAAAGAGATCCTCTTTTAAAGTATATGATGTA 231
DB 705 TTAACCCGAGAACCGACTTGGAGGT-AAAGGATCCCTTTGGAAACGTGTGTG--TGTG 761
QY 232 CGGGCGGGCTCTGTTCTGAGTGTCTGTTTTCAGTGTGGCGCTTTTCGTTTTCAGC 291
DB 762 TCGGCGGGGCTCTGTTCTGAGTGTCTGTTTTCGGTGTATGCGCGCTTTCGGTTTCAGC 821
QY 292 TGTCTCTCAGGCGGTAAAGGCTGGGGACTGTGATCAGCAGACGTGCTAGGAGGATCAC 351
DB 822 TGTCTCTCAGACCGTAAAGACTGGAGGACTGTGATCAGCAGACGTGCTAGGAGGATCAC 881
QY 352 AGCTGCTGCTCGGGGAGCGCCCGGGAGGTGAGAGAGCAGGAGCGCTGGTGGTCT 411
DB 882 AGGCTGCCACCTCGGGGAGCGCCCTGGAGGTGGGAGAGCCAGGAGCGCTGGTGGTCT 941
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DB 942 CTTACTGTGGTCTGAGAGGACCGAATCTGTTGTTGAAGCGAAGCTTCCCTCCCGGAC 1001
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DB 1002 CGTCCGACTCTTTTGGCTGCTTGGAAAGACCGCGGAGCGGTGCGTGTGCTGGATCTGT 1061
QY 532 TGGTTTCTGTTTGTGTGTTTGTCTTGTGTGTCTGCTGATATATATATATATATATATAT 591
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DB 1122 AGACGCTGAGCGACCCCTCTAGTTTCTGACTCTGACCATTTGGACTGAAGTTAATCCAGGG 1181
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DB 1182 CTCATAAATTTGTCAGTTTCAGGTTTAAAGAGGACCTTGGCAGACTTTTCTGTGCTCTGAAT 1241
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DB 1242 GCGCAACATTCGATGTTGATGGCCATCAGAGGGACCTTTAATCTCTGAAATATCTCTGG 1301
QY 772 CTGTTAAAGCAGTTAATTTTTCAGACTGGACCCGGCTCTCATCCCGATCAGGAGCCCTATA 831
DB 1302 CTGTTAAAGCAGTTAATTTTTCAGACTGGACCCAGCTCTCATCTGATCAGGAGCCCTATA 1361
QY 832 TCTTTACGTGGCAAGATTGGCAGAGGATCTCCGCCATGGGTGTTAAACCATGCTGTAATA 891
DB 1362 TCTTTACGTGGCAAGATTGGCAGAGGATCTCCACCATGGGTGTTAAACCATGCTGTAATA 1421
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QY 952 AAAAAGTCAAGCCCTCTCTCATATCTACCCGAGATTGAGGAGCCACCGGCTTGGCCCG 1011
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QY 1192 CACCGGGGGGCAATTTGACGCGCTTCAAGTATTTGGCCCTTTTCTTCTGAGATCTCTATA 1251
DB 1722 TGCAGGGGGGCAATTTGACGCGCTTCAAGTATTTGGCCCTTTTCTTCTGAGATCTCTATA 1781
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QY 1312 AGTCCCTTATGTTCTCTCAGCGCTTACTTGGATGATTGTCAACAGCTGCTGCAGACAC 1371
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QY 1432 CCGAGGGGAGCCCGCGGTTGCAAAATGAGATTGCAATGGATTTCCCTTAACCTCGCC 1491
DB 1962 CCGAGGGGAGCCCGCGGTTGCAAAATGAGATTGCAATGGATTTCCCTTAACCTCGCC 2021
QY 1492 CCGGTTGGGACTACAACCGGCTGAAGGTAGGAGAGCTTGAATACTATTCGCGAGGCTC 1551
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QY 1552 TGTGTGCGGGTCTCCGGGGCGCTCAAGACGGGCCCTAATTTGGCTAAGGTAAGAGAAG 1611
DB 2082 TGTGTGCGGGTCTCCGGGGCGCTCAAGACGGGCCCTAATTTGGCTAAGGTAAGAGAAG 2141
QY 1612 TGAATCAGGAGCGGAAATGAACCCCTCTGTTTCTTCTGAGAGGCTTCTGGAGGCTTCA 1671
DB 2142 TGAATCAGGAGCGGAAATGAACCCCTCTGTTTCTTCTGAGAGGCTTCTGGAGGCTTCA 2201
QY 1672 GCGGTTACACCCCTTTGATCCACCTCAGAGGCCCAAAAAAGCCTCAGTGGCTTTGGCCCT 1731
DB 2202 GCGGTTTACCCCTTTTGTATCTTCTGAGGCCCAAAAAAGCCTCAGTGGCCCTGGCCT 2261
QY 1732 TTAATAGGACAGTCTGAGCTTTGGATATTAGAAAGAGCTTCAGAGACTGGAAAGGTTACAGG 1791

Db	2262	TCATTGGGAGTCGGCTCTGGATATACAGAAAGAACTTCAGAGACTGGAAAGGGTTACAGG	2321
Qy	1792	AGGCTGAGTTACGTTAGTCTAGTGAAGGAGGAGAGAAAGTATATTACAAAGGGAGACAG	1851
Db	2322	AGGCTGAGTTACGTTAGTCTAGTGGGAGGAGGAGAAAGGTTATTACGAAAGGGAGACAG	2381
Qy	1852	AAGAAGAAAGGGAAACAAAGAAAGAGAGAGAAAGAGAGAAAGGGAGAAAGACGTAAATA	1911
Db	2382	AAGAGGAGAGGAACACAGAGAAAGAAAGAGAGAGAAAGGAGAAAGGAGAAAGACGTGATA	2441
Qy	1912	AACGGCAAGAGAGAAATTTGATTAAGATCTTGGCTGCAAGTGGTTGAAGGGAAAGCAATA	1971
Db	2442	GACGCAAGAGAGAAATTTGATTAAGATCTTGGCCGCAAGTGGTTGAAGGGAAAGACAGCA	2501
Qy	1972	CGGAAACAGAGAGAGATTTTAGGAAATTTAGGTCAGGCCCTTAGACAGTCAGGGAACCTGG	2031
Db	2502	GGGAGAGAGAGAGATTTTAGGAAATTTAGTCAAGCCCTTAGACAGTCAGGGAACCTGG	2561
Qy	2032	GCAATAGGACCCCACTCGACAAAGACCAATGTGCATATTGTAAAGAAAGAGACACTGGG	2091
Db	2562	GCAATAGGACCCCACTCGACAAAGACCAAGTGTGGTATTGTAAAGAAAGAGACACTGGG	2621
Qy	2092	CAAGGAATGCCCCAAGAGGAAACAAAGGACCAAGGATCTTAGTCTCTAGAGAAAGATA	2151
Db	2622	CAAGGAATGCCCCAAGAGGAAACAAAGGACCAAGGATCTTAGTCTCTAGAGAAAGATA	2681
Qy	2152	AAGATTAGGGAGACGGGGTTCGAGCCCCCTCCCGAGCCAGGGTAACTTTGAAGGTGG	2211
Db	2682	AAGATTAGGGAGACGGGGTTCGAGCCCCCTCCCGAGCCAGGGTAACTTTGAAGGTGG	2741
Qy	2212	AGGGCAACACAGTTGAGTTCCTGTTGATACCGAGCGCAACATTCAGTGTCTACTACAGC	2271
Db	2742	AGGGCAACACAGTTGAGTTCCTGTTGATACCGAGCGGAGCATTCAGTGTCTACTACAC	2801
Qy	2272	CATTAGGAAACCTAAAGATAAAATCTCGGGTATGGGTGTCACAGGGGCAACAAACAGT	2331
Db	2802	CATTAGGAAACCTAAAGATAAAATCTCGGGTATGGGTGTCACAGGGGCAACCGGAGT	2861
Qy	2332	ATCCATGGACTACCGAAGAACAGTTGACTTGGGAGTGGGACGGGTAAACCCACTCGTTTC	2391
Db	2862	ATCCATGGACTACCGAAGAACCGTTGACTTGGGAGTGGGACGGGTAAACCCACTCGTTTC	2921
Qy	2392	TGGTCATACCTGAGTGGCCAGCACCCCTCTTAGGTAGAGACTTATGCACAAAGATGGAG	2451
Db	2922	TGGTCATACCTGAGTGGCCAGTACCCCTTCTAGGTAGAGACTTATGCACAAAGATGGAG	2981
Qy	2452	CACAAATTTCTTTTGAACAAAGGAAACAGAAAGTGTCTGCAATTAACAAACCTATCACTG	2511
Db	2982	CTCAAAATTTCTTTTGAACAAAGGAAACAGAAAGTGTCTGCAATTAACAAACCTATCACTG	3041
Qy	2512	TGTTGACCTTCAATTTAGATGAGCAATATCGACTATATCTCTCCCTAGTAAAGCTGATC	2571
Db	3042	TGTTGACCTTCAATTTAGATGAGCAATATCGACTATATCTCTCCCTAGTAAAGCTGATC	3101
Qy	2572	AAATATACAAATCTGGTGAACAGTTTCCCAAGCTGGGAGAGAAACCGCAGGGATGG	2631
Db	3102	AAGATATACAGTCTCGTGGAGAGTTTCCCAAGCTGGGAGAGAAACCGCAGGGATGG	3161
Qy	2632	GTTTGGCAAGCAAGTTTCCCAAGCTGGGAGAGAAATTCAACTGAAGGCCAGTGCACACAGTGT	2691
Db	3162	GTTTGGCAAGCAAGTTTCCCAAGCTGGGAGAGAAATTCAGCTGAAGGCCAGTGCACACAGTAT	3221
Qy	2692	CAGTCAGACAGTACCCCTTGAAGAGAGTCAAGAGGAAATTCGGCCGCGCATGTCCAAA	2751
Db	3222	CAGTCAGACAGTACCCCTTGAAGAGAGTCAAGAGGAAATTCGGCCGCGCATGTCCAAA	3281
Qy	2752	GATTAAATCCACAGGGCATCTAGTTCCTGTGCCAATCTCCCTGGAATCTCCCTGCTAC	2811
Db	3282	GATTAAATCCACAGGGCATCTAGTTCCTGTGCCAATCTCCCTGGAATCTCCCTGCTAC	3341
Qy	2812	CGGTTAGAAAGCTGGGACTAATGACTATCGACAGTACAGGACTTGAGAGAGGTCAATA	2871
Db	3342	CGGTTAGAAAGCTGGGACTAATGACTATCGACAGTACAGGACTTGAGAGAGGTCAATA	3401
Qy	2872	AACGGGTGACAGGATATACACCCCAACAGTCCCGAAACCTTTATAACCTTTGTGTGCTCTCC	2931
Db	3402	AAAGGGTGCAGGACATACACCCCAACAGTCCCGAAACCTTTATAACCTTTGTGTGCTCTCC	3461
Qy	2932	CACCCCAACGGAGCTGGTATACAGTATTGACACTTAAAGAGTGCCTTTCTGTGCTGAGAT	2991
Db	3462	CGCTGAACCGAACTGGTATACAGTATTGACACTTAAAGAGTGCCTTTCTGTGCTGAGAT	3521
Qy	2992	TACACCCCACTAGCCCAACACTTTTGGCTTCGAATGGAGAGATCCAGGTACCGGGAAGAA	3051
Db	3522	TACACCCCACTAGCCCAACACTTTTGGCTTCGAATGGAGAGATCCAGGTACCGGGAAGAA	3581
Qy	3052	CCGGGAGCTCACCTCGACCCCGACTGCCCAAGGGTTCAAGAACTCCCCGACCATCTTTTG	3111
Db	3582	CCGGGAGCTCACCTCGACCCCGACTGCCCAAGGGTTCAAGAACTCCCCGACCATCTTTTG	3641
Qy	3112	ACGAAGCCCTACACAGAGACTGCGCAACTTCAGGATCCAAACCCCTCAGGTGACCTCTCC	3171
Db	3642	ACGAAGCCCTACACAGAGACTGCGCAACTTCAGGATCCAAACCCCTCAGGTGACCTCTCC	3701
Qy	3172	TCCAGTACGTGGATGACCTCTCTGCGGGAGCCACCAACAGGACTGCTTAGAAGGCA	3231
Db	3702	TCCAGTACGTGGATGACCTCTCTGCGGGAGCCACCAACAGGACTGCTTAGAAGGTA	3761
Qy	3232	CGAAGGCATCTACTGCTGGAAATTTGTGACCTTAGGCTACAGAGCCTCTGCTAAGAGGCC	3291
Db	3762	CGAAGGCATCTACTGCTGGAAATTTGTGACCTTAGGCTACAGAGCCTCTGCTAAGAGGCC	3821
Qy	3292	AGATTTGACGAGAGAGGTAAACATATCTGGGGTACAGTTTGGGGACGGGACGGCATGGC	3351
Db	3822	AGATTTGACGAGAGAGGTAAACATATCTGGGGTACAGTTTGGGGACGGGACGGCATGGC	3881
Qy	3352	TGACGGGACACGGAGAAACTGTAGTCCAGATACCGGCCCAACACACAGCCCAACAA	3411
Db	3882	TGACGGGACACGGAGAAACTGTAGTCCAGATACCGGCCCAACACACAGCCCAACAA	3941
Qy	3412	TGAGAGAGTTTGGGGACAGCTGGATTTTGCAGACTGTGGATCCCGGGGTTTCGACCT	3471
Db	3942	TGAGAGAGTTTGGGGACAGCTGGATTTTGCAGACTGTGGATCCCGGGGTTTCGACCT	4001
Qy	3472	TAGCAGCCCACTCTACCCGCTAACCAAGAAAGGGGAATTCCTCTGGGCTCTGAGC	3531
Db	4002	TAGCAGCCCACTCTACCCGCTAACCAAGAAAGGGGAATTCCTCTGGGCTCTGAGC	4061
Qy	3532	ACCAGAAGGCAATTGATGCTATCAAAAGGCCCTGCTGAGCGCACTGCTGCGCCCTCC	3591
Db	4062	ACCAGAAGGCAATTGATGCTATCAAAAGGCCCTGCTGAGCGCACTGCTGCGCCCTCC	4121
Qy	3592	CTGACGTAACCTAAACCCCTTTTACCTTTTATGTGGATGAGCGTAAAGGGAGTAGCCCGGGGAG	3651
Db	4122	CTGACGTAACCTAAACCCCTTTTACCTTTTATGTGGATGAGCGTAAAGGGAGTAGCCCGGGGAG	4181
Qy	3652	TTTTAAACCCCAACCTTAGGACCATGGAGAGACCTGTGCGCTACTCTGTCAAAAGAGTCG	3711
Db	4182	TTTTAAACCCCAACCTTAGGACCATGGAGAGACCTGTGCGCTACTCTGTCAAAAGAGTCG	4241
Qy	3712	ATCCTGTAGCCAGTGGTGGCCCATATGCTGAAGGCTATCGAGCTGTGCGCATCTG	3771
Db	4242	ATCCTGTAGCCAGTGGTGGCCCATATGCTGAAGGCTATCGAGCTGTGCGCATCTG	4301
Qy	3772	TCAGGAGCGGTGACAAATTCGACTTTGGGACAGAAATATACTGTAATAGCCCCCATGAT	3831
Db	4302	TCAGGAGCGGTGACAAATTCGACTTTGGGACAGAAATATACTGTAATAGCCCCCATGAT	4361
Qy	3832	TGAGAAACATCGTTTGGGACGCCCCCAGACCGATGGATGACCAACGCCCGCATGACCCACT	3891
Db	4362	TGAGAAACATCGTTTGGGACGCCCCCAGACCGATGGATGACCAACGCCCGCATGACCCACT	4421
Qy	3892	ATCAAGCCCTGCTTCTCACAGAGAGGTGACGTTTGGCTTCCACACAGCGCTCTCAACCCCTG	3951
Db	4422	ATCAAGCCCTGCTTCTCACAGAGAGGTGACGTTTGGCTTCCACACAGCGCTCTCAACCCCTG	4481

3952 QY CCACTCTTCTGCTGAAGAGACTGATGAACCAAGTCACTCATGATTGCCATCAACTATTGA 4011
4482 Db CCACTCTTCTGCTGAAGAGACTGATGAACCAAGTCACTCATGATTGCCATCAACTATTGA 4541
4012 QY TTGAGGAGACTGGGTCGCCAAGGACTTACAGACATACCGCTGACTGAGAGAGTGTCTAA 4071
4542 Db TTGAGGAGACTGGGTCGCCAAGGACTTACAGACATACCGCTGACTGAGAGAGTGTCTAA 4601
4072 QY CTTGGTTCACTGACGGAAGCAGCTATGTGTTGGAAGTAAAGAGGATGGCTGGGGGGCGG 4131
4602 Db CTTGGTTCACTGACGGAAGCAGCTATGTGTTGGAAGTAAAGAGGATGGCTGGGGGGCGG 4661
4132 QY TGTGTGACGGGACCCGACAGATCTGGGCCAGCAGCCTGCCGGAAGAACTTCAGCACAAA 4191
4662 Db TGTGTGACGGGACCCGACAGATCTAGCCAGCAGCCTGCCGGAAGAACTTCAGCGCAAA 4721
4192 QY AGGCTAGCTCATGGGCCCTCAGCAAGCTTTGGGGCTGGCCGAGGAAATCGATAAACA 4251
4722 Db AGGCTAGCTCATGGGCCCTCAGCAAGCTTTGGGGCTGGCCGAGGAAATCGATAAACA 4781
4252 QY TTTATACGACACGACGATGCTTTGCGACTGCACACGTFACATGGGGCCATCTATAAC 4311
4782 Db TTTATACGACACGACGATGCTTTGCGACTGCACACGTFACATGGGGCCATCTATAAC 4841
4312 QY AAAGGGGGTTGCTTACTCAGCAGGAGGGAATAAAGAAACAAAGAGGAAATTTCTAAGCC 4371
4842 Db AAAGGGGGTTGCTTACTCAGCAGGAGGGAATAAAGAAACAAAGAGTAAATTTCTAAGCC 4901
4372 QY TATTAGAAGCGGPACATTTTACCAAAAAGGCTAGCTATTATACATGCTCTCGACATCAGA 4431
4902 Db TATTAGAAGCGCTTACATTTGCCAAAAGGCTAGCTATTATACATGCTCTCGACATCAGA 4961
4432 QY AAGCTAAGATCTCATATCCAGAGGAACACGATGCTGACCGGGTTGCCAAGCGGCAG 4491
4962 Db AAGCCAAAGATCTCATATCTAGAGGGAACACGATGCTGACCGGATTTGCCAAGCGGCAG 5021
4492 QY CCAGGGGTGTAACTTCTGCTTATATAGAAATGCCAAAGTCCCAAGCCCCAGAACCCAGACGAC 4551
5022 Db CCAGGGGTGTAACTTCTGCTTATATAGAAACGCCAAAGCCCCAGAACCCAGACGAC 5081
4552 QY AGTACACCTTAGAAGACTGGCAAGAGATAAAGATAGACACGATTTCTCTGAGACTCCGG 4611
5082 Db AGTACACCTTAGAAGACTGGCAAGAGATAAAGATAGACACGATTTCTCTGAGACTCCGG 5141
4612 QY AAGGACCTGCTATACCTCAGATGGGAGGAAATCTGCCCCCAAGAGGGTTAGAAAT 4671
5142 Db AAGGACCTGCTATACCTCATATGGGAAGGAAATCTGCCCCCAAGAGGGTTAGAAAT 5201
4672 QY ATGTCCAAACAGATACATCGTTAAACCCACCTAGGAACATAACACCTGCAGCAGTTGGTCA 4731
5202 Db ATGTCCAAACAGATACATCGTTCAACCCACCTAGGAACTAAACACCTGTAGCAGTTGGTCA 5261
4732 QY GAAACATCCCCTTATCATGTTCTGAGGCTACAGAGTGGCTGACTCGGTGGTCAAAACATT 4791
5262 Db GAAACATCCCCTTATCATGTTCTGAGGCTACAGAGTGGCTGACTCGGTGGTCAAAACATT 5321
4792 QY GTGTGCCCTGCCAGCTGGTTAATGCTTAATCCTTCCAGAAATGCCCTCCAGGGAAGAGACTAA 4851
5322 Db GTGTGCCCTGCCAGCTGGTTAATGCTTAATCCTTCCAAAGTACCTCCAGGGAAGAGACTAA 5381
4852 QY GGGGAAGCCACCCAGGCGCTCACTGGGAAGTGACTTCACTGAGGTAAAGCCCGGTAAAT 4911
5382 Db GGGGAAGCCACCCAGGCGCTCACTGGGAAGTGACTTCACTAAGTAAAGCCCGGTAAAT 5441
4912 QY ACGGAAACAAATACCTATTGGTTTTGTAGACACCTTTTCAGGATGGGTAGAGGCTTATC 4971
5442 Db ACGGAAACAAATACCTATTGGTTTTGTAGACACCTTTTCAGGATGGGTAGAGGCTTATC 5501
4972 QY CTACTAAGAAAGAGACTTCAACCGTGGCTTAAAGAAATACCTGGAAGAAATTTTCCAA 5031
5502 Db CTACTAAGAAAGAGACTTCAACCGTGGCTTAAAGAAATACCTGGAAGAAATTTTCCCA 5561
5032 QY GATTTGGAAATACCTAAGGTAATAGGGTACAGAAATGGTCCAGCTTTTGTGGCCCAAGTAA 5091

5562 Db GATTTGGAAATACCTAAGGTAATCGGGTCAGAAATGGTCCAGCTTTTGTGGCCCAAGTAA 5621
5092 QY GTACGGGACTGGCCAAAGATATTGGGGATTGATTGAAAACCTGATTTGTGCATACAGACCCC 5151
5622 Db GTACGGGACTGGCCAAAGATATTGGGGATTGATTGAAAACCTGATTTGTGCATACAGACCCC 5681
5152 QY AAAGCTCAGGACAGGTAGAGAGGATGAATAGAACCAATTAAAGAGACCCCTTACTAAATTGA 5211
5682 Db AAAGCTCAGGACAGGTAGAGAGGATGAATAGAACCAATTAAAGAGACCCCTCACCAAATTGA 5741
5212 QY CCGCGGAGACTGGCGGCTTAATGATTGGATAGCTCTCTGCCCTTTGTGCTTTTATAGGGTTA 5271
5742 Db CCACAGAGACTGGGCATTAATGATTGGATAGCTCTCTGCCCTTTGTGCTTTTATAGGGTTA 5801
5272 QY GGAAACACCCCTGACAGTTTGGGCTGACCCCTCATGAATTAATCTACGGGGGACCCCCCC 5331
5802 Db GGAAACACCCCTGACAGTTTGGGCTGACCCCTCATGAATTAATCTACGGGGGACCCCCCC 5861
5332 QY CATTCGTAGAAATTGCTTCTGTACATAGTGTGCTGCTGCTTTTCCAGCCCTTTGTCT 5391
5862 Db CGTTGCTAGAAATTGCTTCTGTACATAGTGTGCTGCTGCTTTTCCAGCCCTTTGTCT 5921
5392 QY CTAGGCTCAAGCACTTGAGTGGGTGAGACAAAGAGCGTGGAGGCAATCTCCGGGAGGCT 5451
5922 Db CTAGGCTCAAGCGCTCGAGTGGGTGAGGACGAGCGTGGAGGAGCTCCGGGAGGCT 5981
5452 QY ACTCAGGAGGAGGAGACTTGCAGATCCCAATCTGTTTCCAACTGGGAGATTCAGTCTACG 5511
5982 Db ACTCAGGAGAGGAGACTTGCAGATCCCAATCTGTTTCCAACTGGGAGATTCAGTCTATG 6041
5512 QY TTAGACGGCCACCGTCGAGGAAACCTCGAGACTCGGTGGAGGGCCCTTATCTCGTACTTT 5571
6042 Db TTAGACGGCCACCGTCGAGGAAACCTCGAGACTCGGTGGAGGGCCCTTATCTCGTACTTT 6101
5572 QY TGACACACCAACCGGTGAAAAGTGAAGGATCTCCACCTGGATCCATGATCCACG 5631
6102 Db TGACACACCAACCGGTGAAAAGTGAAGGATCTCCACCTGGATCCATGATCCACG 6161
5632 QY TTAAACCGGCGCACCTCCGATTCGGGTGAAAAGCGAAAGACTGAAAATCCCTTTA 5691
6162 Db TTAAAGTGGCGCACCTCCGACTCGGGTGAAGGCCGAAAGACTGAGAATCCCTTTA 6221
5692 QY AGCTTCGCTCCATCGCTGGTTCCTTACTCTGTCAATAACCTCTCAGACTAATGGTATG 5751
6222 Db AGCTTCGCTCCATCGCTGGTTCCTTACTCTTAAACAATTAACCTCCAGGCGAGTAGTAA 6281
5752 QY CGCATAGGAGACAGCGCTGAACTCCCAATAAACCTTATCTCTCACCTGGTTAATTAAGTAC 5811
6282 Db CGCCTTATAGACAGCTCGAAACCCCATAGACCTTTATCCCTTACCTGGCTGATTAATGAC 6341
5812 QY TCGGACACAGGTATTAATATCAACACACTCAAGGGGAGGCTCTTTTAGGAACCTGGTGG 5871
6342 Db CTGTATACGGGTGTCATCTGTAAATAGCACTCGAGGTGTGCTCTTAGAGACCTGGTGG 6401
5872 QY CTTGATCTTATAGCTTTGCTTCCCTCAGATCAGTTATTC---CTAGTCTGACCTCACCCCGAGT 5928
6402 Db CTTGATCTTATAGCTTTGCTTCCCTCCGATTTGATTAACCCCGCTGTTAAAGACACCTCCCAAC 6461
5929 QY ATCTCCCATGCTCAGGATTTTATGTTTCCCGAGGACCAACAAATTAATGAAAACATTCG 5988
6462 Db CTAGTCCGTAGTATGGGTTCCTATTGCTGCCAGG---CACAGAGAAAGAGAAATCTGT 6518
5989 QY GGAAATCCAGAGATTTCTTTTGTAAACAATCGAACTGTGAACCTCTAATGATGATAT 6048
6519 Db GGGGGTCTGGGGAATCTCTCTGTAGGAGATGGAGCTGGCTCACCTTCCAAATGAGAC 6578
6049 QY TGGAAATGCCCAACCTCTCAGCAGGATAGGGTAAGTTTTTCTTATGTCAACACCTATACC 6108
6579 Db TGGAAATGCCCGATCTCTCTCCAGGACCGGGTAAATTTCTCTTTGTAAA----- 6628
6109 QY AGCTCTGGAACAATTTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 6168

6629	--TTCCGGCCGGGCAAGTACAAAGTGTAGAACTATATAAGATTAAGAGCTGCTCCCCA	6680	6629	TCAGACCTAGATTACCTAAAAATAAGTTTCACTGAGAAAGGAAAAACAAGAAAATATCTTA	6228
6169	TCAGACCTAGATTACCTAAAAATAAGTTTCACTGAGAAAGGAAAAACAAGAAAATATCTTA	6228	6169	TCAGACCTAGATTATCTAAGATTAAGTTTCACTGAAAAAGGAAAAACAGGAAAATATTTCAA	6746
6687	TCAGACCTAGATTATCTAAGATTAAGTTTCACTGAAAAAGGAAAAACAGGAAAATATTTCAA	6746	6687	AAATGGGTAAATGGTATGTCTTCGGGGAATGGTATATATTGGAGGCTCGGGTAAACAACCA	6288
6229	AAATGGGTAAATGGTATGTCTTCGGGGAATGGTATATATTGGAGGCTCGGGTAAACAACCA	6288	6229	AAGTGGATAAATGGTATGAGCTGGGGAATAGTTTTTTTATAAA---TATCGCGGGGAGCA	6803
6747	AAGTGGATAAATGGTATGAGCTGGGGAATAGTTTTTTTATAAA---TATCGCGGGGAGCA	6803	6747	GGCTCCATTCTAACTATTGCGCTCAAAATAAAACACAGCTG---CAGCGCTCCAAATGGGTATA	6345
6289	GGCTCCATTCTAACTATTGCGCTCAAAATAAAACACAGCTG---CAGCGCTCCAAATGGGTATA	6345	6289	GGGTCCACTTTTAACCAATTCGCTTAGGATAGACGGGNACAGAACCCCTCTGGCGAGTG	6863
6804	GGGTCCACTTTTAACCAATTCGCTTAGGATAGACGGGNACAGAACCCCTCTGGCGAGTG	6863	6804	GGACCAATAACGGTCTTTGACGGGTCAAAGACCCCAACCCCAACGGAACAGGAACCATCTCT	6405
6346	GGACCAATAACGGTCTTTGACGGGTCAAAGACCCCAACCCCAACGGAACAGGAACCATCTCT	6405	6346	GGACCCGATAAAGTACTGTGCTGAACAGGGGCCCGCGCCCTGGAGCCACCGCATAACTTG	6923
6864	GGACCCGATAAAGTACTGTGCTGAACAGGGGCCCGCGCCCTGGAGCCACCGCATAACTTG	6923	6864	-----ACATAA	6414
6406	-----ACATAA	6414	6406	CCGGTCCCCCAATTAACCTCGCTCGGCTTGACATAACACAGCGCGCTAGCAACGGTACC	6983
6924	CCGGTCCCCCAATTAACCTCGCTCGGCTTGACATAACACAGCGCGCTAGCAACGGTACC	6983	6924	TCGTGGATCAGACCCCACTGAGTCTAAACAGCA-----CGACTAAAAATGGGG	6459
6415	TCGTGGATCAGACCCCACTGAGTCTAAACAGCA-----CGACTAAAAATGGGG	6459	6415	ACTGGATTGATTCCTTACCAACACCGCTAGAAACTCCCGAGTGTTCTGTGTTAGACAGGA	7043
6984	ACTGGATTGATTCCTTACCAACACCGCTAGAAACTCCCGAGTGTTCTGTGTTAGACAGGA	7043	6984	GCAAACTTTTATAGCCTCATCCAGGAGCTTTTCAAGCTCTTAACCTCCAGACTCCAGAG	6519
6460	GCAAACTTTTATAGCCTCATCCAGGAGCTTTTCAAGCTCTTAACCTCCAGACTCCAGAG	6519	6460	CAGAGACTCTTCAGTCTCATCCAGGAGCTTTCCAGGCCATCAACTCCACCGACCTGAT	7103
7044	CAGAGACTCTTCAGTCTCATCCAGGAGCTTTCCAGGCCATCAACTCCACCGACCTGAT	7103	7044	GCTAACCTCTTCTGTTGGCTATGCTTAGCTTTGGGCCCACTTACTATGTAAGAAATGGCT	6579
6520	GCTAACCTCTTCTGTTGGCTATGCTTAGCTTTGGGCCCACTTACTATGTAAGAAATGGCT	6579	6520	GCCACTCTTCTTGTGTTGGCTTGTCTATCCTCAAGGCTCTCTTATTATGAGGGGATGGCT	7163
7104	GCCACTCTTCTTGTGTTGGCTTGTCTATCCTCAAGGCTCTCTTATTATGAGGGGATGGCT	7163	7104	AGAAGAGGAAATTCATATGTGCACAAAGACATAGAGACCAATGCACATGGGATCCCCA	6639
6580	AGAAGAGGAAATTCATATGTGCACAAAGACATAGAGACCAATGCACATGGGATCCCCA	6639	6580	ANAAGAGGAAAAATTCATATGTGCACAAAGACGCTAGAAATCAATGTATGGGGTCCCCA	7223
7164	ANAAGAGGAAAAATTCATATGTGCACAAAGACGCTAGAAATCAATGTATGGGGTCCCCA	7223	7164	AATAAGCTTACCCTTACTGAGTGTTCGTAAGGAGGACCTGCATAGAAAGTTTCCCCCA	6699
6640	AATAAGCTTACCCTTACTGAGTGTTCGTAAGGAGGACCTGCATAGAAAGTTTCCCCCA	6699	6640	AATAAGCTTACCCTTACTGAGTGTTCGTAAGGAGGACATGATAGGAAAGCTCCCCCA	7283
7224	AATAAGCTTACCCTTACTGAGTGTTCGTAAGGAGGACATGATAGGAAAGCTCCCCCA	7283	7224	TCCCACCAACACCTTTGCTAGTACTGTGTTTATGAGCAGGCTCAGAAAAATCAGTAT	6759
6700	TCCCACCAACACCTTTGCTAGTACTGTGTTTATGAGCAGGCTTAAATCAAACTCTGAGAGTCAATAT	6759	6700	CTGGTACTCGTTATGACAGGTGGTGGGCATGTATTAATCTGGATTAACCCCTTGTTTTC	6819
7284	TCCCACCAACACCTTTGCTAGTACTGTGTTTATGAGCAGGCTCAGAAAAATCAGTAT	7343	7284	TTAGTACTCGTTTATAACAGGTGGTGGGCATGCAATACTGGGTTAACCCCTGTGTTTTC	7403
6760	CTGGTACTCGTTATGACAGGTGGTGGGCATGTATTAATCTGGATTAACCCCTTGTTTTC	6819	6760	ACCTTGTTTATTAACCAAACTTAAAGATTTTTTGCAATATGGTCCAAATTTGTTCCCGAGTG	6879
7344	TTAGTACTCGTTTATAACAGGTGGTGGGCATGCAATACTGGGTTAACCCCTGTGTTTTC	7403	7344	ACCTCAGTCTTCAACCAATCCAAAGATTTCTGTCTATGTTCCAAATCGTCCCCCGAGTG	7463
6820	ACCTTGTTTATTAACCAAACTTAAAGATTTTTTGCAATATGGTCCAAATTTGTTCCCGAGTG	6879	6820	TATTACTATCCGAAAAAGCAATCCTTTGATGAATATGACTACAGAAATCATTCGCAAAAG	6939
7404	ACCTCAGTCTTCAACCAATCCAAAGATTTCTGTCTATGTTCCAAATCGTCCCCCGAGTG	7463	7404	TACTACCACCTCGAGGAAGTGGTCTTGTGATGAATATGACTATCGGTATAACCGACCGAAA	7523
6880	TATTACTATCCGAAAAAGCAATCCTTTGATGAATATGACTACAGAAATCATTCGCAAAAG	6939	6880	AGAAACCCCATATCTCTGACACTTGTCTGTGATGCTCGGACTTGGAGTGGCAGCAGGTGTA	6999
7464	TACTACCACCTCGAGGAAGTGGTCTTGTGATGAATATGACTATCGGTATAACCGACCGAAA	7523	7464	AGAAACCCGCTATCCCTTACCTAGCTGTAAATGCTCGGATTTAGGGACGGCGTTTGGCATA	

Qy	7180	TTTCTAAAGAAAGGAGATTTATCTGTAGCCTTCAAGAGAGAAATGCTGTTTTTATGTGGAT	7233
Db	7764	TTTCTAAGAAAGGTGGGTATGTGACGCTTTAAAGAAAGATTTGCTCTCTATGTAGAT	7823
Qy	7240	CAATCAGGGCCCATCAGAGACTCCATGAAACAAGCTTAGAGAAAAGTTGGAGAAAGCGTCGA	7299
Db	7824	CACTCAGAGCCCATCAGAGACTCCATGAGCAAGCTTAGAGAAAAGTTAGAGAGCGCTCGA	7883
Qy	7300	AGGAAAGAAACTACTCAAGGGTGGTTGAGGGATGGTTCAACAGGTCTCTTTGGTTG	7359
Db	7884	AGGAAAGAGAGGCTGACCAAGGGTGGTTGAAAGGATGGTTCAACAGGTCTCTTTGGATG	7943
Qy	7360	GCATACCCCTACTTTCTGCTTTAAACAGGACCTTAATAGTCCCTCTCTCTGTTTACTCACAGTT	7419
Db	7944	ACACCCCTGCTTTCTGCTCTGACGGGACCCCTAGTAGTCTGCTCTGTTTACTTACAGTT	8003
Qy	7420	GGGCCATGTATTATTAACAAGTTAAATGTCCTTCAATTAGAGAAACAATAAGTCAGTCCAG	7479
Db	8004	GGGCTTTGCTTAATTAATAGTTTGTGCTCTTGTAGAGAACGAGTGAAGTCCAG	8063
Qy	7480	ATCATGTGTTACTAGACAAAGTACCAAGCCGCTCTAGC---AGGGAAGCTGCGCCCTAG	7536
Db	8064	ATCATGTGTTACTAGGCAACAGTACCAAGGCTTCTGAGCCAAAGGAAACTGACCTCTAG	8123
Qy	7537	CTCTACCAAGTTCTAAGATTAGAACTATTAAACAGAGAAAGTGGGAAATGAAAGGATGA	7596
Db	8124	CTTCCAGATTCTAAGATTAGAACTATTAAACAGAAAGTGGGAAATGAAAGGATGA	8183
Qy	7597	AAATACAAACCT-----AAGCTAATGAGAGCTTTAAATTTGTTCTGA	7637
Db	8184	AAATGCAACCTTAACCCCTCCAGAACCCAGGAAGTTAATAAAAGCTCTAAATGCCCCGA	8243
Qy	7638	ATTCAGAGTTTGTTCCTT-----ATAGTTAAAGATTAGGTTTTTTTCTGTTTTTAA	7689
Db	8244	ATTCAGACCCCTGCTGCTGCCAGTAATAGGTAGAAGGTCACACTTCTATTGTTCCAG	8303
Qy	7690	AATATGCGGAAGT---AAAATAGCCCTCAGTACATGTCTTAGGCATGAAACTTCTTG	7745
Db	8304	GGCTGTATCTCTGCTGCTAGTAGATAACAGGAAATGAGTTGACTAATGCTTATCTGG	8363
Qy	7746	AAACTATTGTGAGATAACAGAAAGGAGTTTCTAACCTGCTGTTGTTTACTGTGTAAAC	7805
Db	8364	ATTCTGTAAAACCTGACTGGCACCATAGAAGAAATGATTACACATTGACAGCCCTAGTGAC	8423
Qy	7806	TGGTTGGCCATAAAGATGTTGAATGTTGATACACATATCTTGGTCGACACATGTCTCC	7865
Db	8424	CTATCTCAACTGCAATCTGTCACTCTGCCAGGAGCCACGAGATGGGACCTCCGGAG	8483
Qy	7866	CCACCCCGAAACATGGCGAAA---TGTTGAATCTTAAACTTAAATTTAAATTTGTTGTC	7922
Db	8484	CTATTTTAAATGATTTGTTCCACGGAGCGGGCTCTCGATATTTTAAATGATTTGTTGTC	8543
Qy	7923	ACGAAGCGCGGCTCTCGAAGTTTAAATTTAAATTTAAATTTAAATTTGTTGATGA	7967
Db	8544	ACGGAGCGCGGCTCTCGATATTTTAAATTTAAATTTAAATTTAAATTTGTTGATGA	8603
Qy	7968	TTTTTGAATGATGTTTGTAAAGCGGGGCTTTGTTGTAACCCCATATAAGCTGTCCC	8027
Db	8604	TTTTTAAATGATTTGTTGTGACGACAGGCTTTTGTGTAACCCCATATAAGCTGTCCC	8663
Qy	8028	GACTCCACACTCGGGGCGCAGTCTCTACCCCTCGCTGGTGTGACGACTGTGGGCCCGAG	8087
Db	8664	GATTCGCACTCAGGGCGCAGTCTCTACCCCTCGCTGGTGTGACGACTGTGGGCCCGAG	8723
Qy	8088	CGCGTTTGAATAAAATTCCTCTGCTGTTTGTGATCAAAA	8127
Db	8724	CGCGTTTGAATAAAATTCCTCTGCTGTTTGTGATCAAGA	8763

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; GENERAL INFORMATION:
; APPLICANT: Jay A. Fishman
; TITLE OF INVENTION: MOLECULAR SEQUENCE OF SWINE RETROVIRUS
; AND METHODS OF USE
; NUMBER OF SEQUENCES: 74
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 60 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/723,552
; FILING DATE: 26-Nov-2003
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/661,858
; FILING DATE: 14-Sep-2000
; APPLICATION NUMBER: 08/766,528
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Louis Myers
; REGISTRATION NUMBER: 35,965
; REFERENCE/DOCKET NUMBER: MGP-038CP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)227-5941
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8060 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
; PS-10-723-552-1

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Query Match	67.1%	Score 5460;	DB 8;	Length 8060;
Best Local Similarity	99.7%;	Pred. No. 0;		
Matches 5521;	Conservative 0;	Mismatches 10;	Indels 5;	Gaps 5;
Qy 1	GCCTGGTGTACGACTGTGGCCCCCAGCGCGCTTGGGATAAAATCCTTCCTGCTGGTTGCA	60		
Db 2528	GCCTGGTGTACGACTGTGGCCCCCAGCGCGCTTGGGATAAAATCCTTCCTGCTGGTTGCA	2587		
Qy 61	TCAAGACCGCTTCTCGTGAGTGATTAAGGGAGTCGCGCTTTTCGAGCCTGGAGGTTCTT	120		
Db 2588	TCAAGACCGCTTCTCGTGAGTGATTAAGGGAGTCGCGCTTTTCGAGCCTGGAGGTTCTT	2647		
Qy 121	TTTGTCTGCTTACATTTGGGGGCTCGTCCGGATCTGTCCGGCCACCCCTAACACCG	180		
Db 2648	TTTGTCTGCTTACATTTGGGGGCTCGTCCGGGATCTGTCCGGCCACCCCTAACACCG	2707		
Qy 181	AGAACCGACTTGGAGGTAAGAAGATCCTCTTTTAAACGTGTATGATGTACCGCGCGC	240		
Db 2708	AGAACCGACTTGGAGGTAAGAAGATCCTCTTTTAAACGTGTATGATGTACCGCGCGC	2767		
Qy 241	GTCTCTCTCTGAGTGTCGTGTTTTCAGTGTGCGCGCTTTTCGGTTTCAGCTGTCCTTC	300		
Db 2768	GTCTCTCTGTCAGTGTCGTGTTTTCAGTGTGCGCGCTTTTCGGTTTCAGCTGTCCTTC	2827		
Qy 301	AGGCCGTAAAGGCTCGGGGACTGTGATCAGCAGACGTCTAGGAGGATCACAGCTGCTG	360		
Db 2828	AGGCCGTAAAGGCTCGGGGACTGTGATCAGCAGACGTCTAGGAGGATCACAGCTGCTG	2887		
Qy 361	CCCTGGGGGAGCCGCCGGGAGGTGAGGAGGCCAGGACCGCTGGTGTCTCCTACTGTCT	420		

6186	Db		AAACCCCTAGGACCATGAGAGACCTGTGCGCTACCTGTCAAAGAAGCTCGATCCTGTAG	6245
3721	QY		CCAGTGGTGTGGCCCATATGCTGAAGGCTATCGCAGCTGTGGCCATACTGTCCAAGGACG	3780
6246	Db		CCAGTGGTGTGGCCCATATGCTGAAGGCTATCGCAGCTGTGGCCATACTGTCCAAGGACG	6305
3781	QY		CTGACAAATTGACTTTTGGGAC - AGAATAATAACTGTAAATAGCCCCCATGCAATTTGGAGAAC	3839
6306	Db		CTGACAAATTGACTTTTGGGACAAGAATATAACTGTAAATAGCCCCCATGCAATTTGGAGAAC	6365
3840	QY		ATCGTTTGGCAGCCGCCAGACCGATGATGACCAACGCCCGCATGACCCCACTATCAAAGC	3899
6366	Db		ATCGTTTGGCAGCCGCCAGACCGATGATGACCAACGCCCGCATGACCCCACTATCAAAGC	6425
3900	QY		CTGCTTCTCACAGAGAGGGTCACGTTTCGCTCCACACGCGCTCTCAACCCCTGCCACTCTT	3959
6426	Db		CTGCTTCTCACAGAGAGGGTCACGTTTCGCTCCACCAACCGCTCTCAACCCCTGCCACTCTT	6485
3960	QY		CTGCTTGAAGAGACTGATGAACCACTGACTCATGATTGCCATCAACTATTGATTGAGGAG	4019
6486	Db		CTGCTTGAAGAGACTGATGAACCACTGACTCATGATTGCCATCAACTATTGATTGAGGAG	6545
4020	QY		ACTGGGTTCGCAAGGACCTTTACAGACATACCGCTGACTGCGAGAGTGCTAACTGGTTC	4079
6546	Db		ACTGGGTTCGCAAGGACCTTTACAGACATACCGCTGACTGCGAGAGTGCTAACTGGTTC	6605
4080	QY		ACTGACCGAGACGCTATGTGGTGGAGGTAAAGAGTATGCTGGGCGCGGTGGTGAC	4139
6606	Db		ACTGACCGAGACGCTATGTGGTGGAGGTAAAGAGTATGCTGGGCGCGGTGGTGAC	6665
4140	QY		GGGACCCGACGATCTGGGCCAGCAGCGCTGCGGAGAGAACTTCAGCACAAAAGGCTGAG	4199
6666	Db		GGGACCCGACGATCTGGGCCAGCAGCGCTGCGGAGAGAACTTCAGCACAAAAGGCTGAG	6725
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6726	Db		CTCATGCGCCTCACGCAAGCTTTTCGGCTGGCCGAGAGGAAATCCATAACATTTATACG	6785
4260	QY		GACAGCAGGTATGCTTTGCGACTGCAAGTACATGGCGGCATCTATAACAAAGGGGG	4319
6786	Db		GACAGCAGGTATGCTTTGCGACTGCAAGTACATGGCGGCATCTATAACAAAGGGGG	6845
4320	QY		TTGCTTACCTCAGCAGGAGGGAATAAAGAAACAAAGAGGAAATTCCTAAGCTATTAGAA	4379
6846	Db		TTGCTTACCTCAGCAGGAGGGAATAAAGAAACAAAGAGGAAATTCCTAAGCTATTAGAA	6905
4380	QY		GCCGTACATTTACCAAAAGGCTAGCTATTATACACTGTCTTGACATCAAGAAAGCTAAA	4439
6906	Db		GCCGTACATTTACCAAAAGGCTAGCTATTATACACTGTCTTGACATCAAGAAAGCTAAA	6965
4440	QY		GATCTCATATCCAGAGNAAACGATGGCTGACCGGTTGCCAGCAGGCGAGCCAGGCT	4499
6966	Db		GATCTCATATCCAGAGNAAACGATGGCTGACCGGTTGCCAGCAGGCGAGCCAGGCT	7025
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7026	Db		GTTAACCTTCTGCTTATAATAAGAAATGCCAAAGCCCGAGAACCCAGACGACGATACCC	7085
4560	QY		CTAGAAGACTGGCAAGAGATAAAAAGATAGACCAAGTTCTCTGAGACTCCGGAAGGAGCC	4619
7086	Db		CTAGAAGACTGGCAAGAGATAAAAAGATAGACCA - TTCTCTGAGACTCCGGAAGGAGCC	7144
4620	QY		TGCTATACCTCAGATGGGAAGGAAATCTCTGCCCCACAAAGAGGGTTAGAAATATGTCAA	4679
7145	Db		TGCTATACCTCAGATGGGAAGGAAATCTCTGCCCCACAAAGAGGGTTAGAAATATGTCAA	7204
4680	QY		C - AGATACATCGTCTAACCCACCTAGGAACTAAACACCTGCAGCAGTTGGTCAGAACATC	4738
7205	Db		CAAGATACATCGTCTAACCCACCTAGGAACTAAACACCTGCAGCAGTTGGTCAGAACATC	7264
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Db	7325	CTGCCAGCTGGTTAAATGCTTAATCTCTCCAAATGCGCTCCAGGGAAGAGACTAAGGGGAAG	7384
QY	4859	CCACCCAGGCGCTCACTGGGAAGTGGACTTCTAGTGGGTAAAGCCGGCTAAATACGGAAA	4918
Db	7385	CCACCCAGGCGCTCACTGGGAAGTGGACTTCTAGTGGGTAAAGCCGGCTAAATACGGAAA	7444
QY	4919	CAAAATACCTATTTGGTTTTTGTGTAGACACCTTTTCAGAGTGGGTAGAGGCTTATCCTACTAA	4978
Db	7445	CAAAATACCTATTTGGTTTTTGTGTAGACACCTTTTCAGAGTGGGTAGAGGCTTATCCTACTAA	7504
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Db	7505	GAAGAGACATTCACCGTGGTGGCTAAAAAATACTGGGAAGAAATTTTTCCAAAGATTGG	7564
QY	5039	AATACCTAAGGTAAATAGGGTCAGACAATGGTCAGAGCTTTTGTGGCCAGAGTAAGTCAGGG	5098
Db	7565	AATACCTAAGGTAAATAGGGTCAGACAATGGTCAGAGCTTTTGTGGCCAGAGTAAGTCAGGG	7624
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Db	7685	AGGACAGGTAGAGAGGATGAATAGAACCAATTAAGAGAGACCTTTACTAAATGTGACCGGGA	7744
QY	5219	GACTGGCGTTAAATGATTGGATAGCTCTCGCCCTTTGTGCTTTTGTAGGGTTAGGAACAC	5278
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QY	5279	CCCTGGACAGTTTGGGCTGACCCCTATGAATTTACTCTACGGGGGACCCCGCCCATTTGTT	5338
Db	7805	CCCTGGACAGTTTGGGCTGACCCCTATGAATTTACTCTACGGGGGACCCCGCCCATTTGTT	7864
QY	5339	AGAAATGCTTCTGTACATAGTGTGACGTGCTTTTCCAGCCTTTGTCTCTAGGCT	5398
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Db	8045	CCACCGTGCAGGAAAC	8060

RESULT 10
US-10-723-552-2
; Sequence 2, Application US/10723552
; Publication No. US20040185435A1
; GENERAL INFORMATION:
; APPLICANT: Jay A. Fishman
; TITLE OF INVENTION: MOLECULAR SEQUENCE OF SWINE RETROVIRUS
; AND METHODS OF USE
; NUMBER OF SEQUENCES: 74
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 60 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING APPLICATION NUMBER: US/10/723,552
FILING DATE: 26-Nov-2003
PRIOR APPLICATION NUMBER: US/09/661,858
FILING DATE: 14-Sep-2000
APPLICATION NUMBER: 08/766,528
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Louis Myers
REGISTRATION NUMBER: 35,965
REFERENCE/DOCKET NUMBER: MGP-038CP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)227-5941
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 7333 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
SEQUENCE DESCRIPTION: SEQ ID NO: 2:

us-10-723-552-2
Query Match 61.1%; Score 4970.8; DB 8; Length 7333;
Best Local Similarity 79.4%; Pred. No. 0;
Matches 6531; Conservative 0; Mismatches 702; Indels 989; Gaps 15;
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Db 69 TCAAGACCGCTTCTGTGTAGTGATT-TGGGGTGTGCGCTCTTCGAGCCCGGACGAGGG 127
Qy 116 ----TTCTTTTGTGTCTTACATTTGGGGGCTGTCTCGGGATCTGTTCGGCGCACCCC 171
Db 128 GATTGTTCTTTTACTGGCCCTTCATTTGGTGGCGGGGAAATCTCGGACCACCCC 187
Qy 172 TAAACCCGAGAACCGACTTGGAGGTAAAGAGTCTCTTTTAAAGTGTATCATGTA 231
Db 188 TTACACCCGAGAACCGACTTGGAGGT-AAAGGGATCCCTTTGGAAC--ATATGTGTG 244
Qy 232 CCGGCGCGGCTCTGTCTCAGTGTCTGTTTTCAGTGTGCGCGCTTTCGGTTTGCAGC 291
Db 245 TCGGCGCGGCTCTGTCTCAGTGTCTGTTTTCAGTGTGCGCGCTTTCGGTTTGCAGC 304
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Db 785 CTGTTAAGCAGTTATTTTTCAGACTGGACCCGCTCTCATCCGATCAGAGGACCTTATA 844
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Qy 1132 CCACCCCGAGCGGACAGAGATCGGACATTTACCGCTGCGCAGCTACGGCCCTCCCA 1191
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Qy 1192 CACCGGGGCGCAATTCAGCCCTCCAGTATTTGGCCCTTTCTTCTGACATCTCTATA 1251
Db 1205 TGCAGGGGCGCAATTCAGCCCTCCAGTATTTGGCCCTTTCTTCTGACATCTCTATA 1264
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Db 1325 AGTCCCTTATGTTCTCTCAACGCTTATTTGGGATGATTTCAACAGCTGTCTGACAGAC 1384
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Db 1565 TGGTGGGCGTCTCGGGGCGCTCAAGACGGCCCACTAAATTTGGCTAAGGTAGAGAG 1624
Qy 1612 TGATGAGGAGCGGAAATGAAACCCCTCTGTTTCTTTGAGAGGCTCTTTGGAAGCTTCA 1671
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Dbb 1685 GCGGTTACCCCTTTTGATCTCCTCAGAGCCGAGAAAGCCTCAGTGGCCCTGGCCT 1744

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QY 1852 AAGAAGAAAGGGAACAAAGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1911

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QY 1972 CGGAAAGAGAGAGAGATTTTGAAGAAATTAAGTTCAGGCCCTAGACAGTCAGGGAACCTGG 2031

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QY 3352 TGAACGAGGACCGGAAGAAAACCTGATCCAGATACCGGCCCAACCAACAGGCAAAACAA 3411

Dbb 3365 TGAACGAGGACCGGAAGAAAACCTGATCCAGATACCGGCCCAACCAACAGGCAAAACAA 3424

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Dbb 3425 TGAGAGAGTTTGGGACAGCTGGATTTTGCAGACTGTGGATCCCGGGTTTGGACCT 3484

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QY 3832 TGGAGAACATCGTTCCGACAGCCCGACAGCCGATGGATGACCAACGCCCGCATGACCCACT 3891

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QY 3892 ATCAAAGCCTGCTTCTCACAGAGAGGCTCACGTTTCGCTCCACGAGCGCTCTCAACCCCTG 3951
 Db 3517 ----- 3516
 QY 3952 CCACTCTTCTGCTGAAGAGACTGATGAACCAAGTACTCATGATGGCCATCAACTATTGA 4011
 Db 3517 ----- 3516
 QY 4012 TTGAGGAGACTGGGCTCGCAAGGACCTTACAGACATACCGCTGACTGAGAGAAGTGCTAA 4071
 Db 3517 ----- 3516
 QY 4072 CTTGGTTCACTGACGGAAGCAGCTATGTGTGGAAGGTAAGAGATGGCTGGGGCGCGG 4131
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 QY 4132 TGGTGGACGGGACCCGCAAGCAGATCTGGGCCAGCAGCCTGCCGGAAGAACTTCAGCACAAA 4191
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 QY 4192 AGGCTGAGCTCATGGCCCTCAGCAAGCTTTTGGGCTGGCGGAAGGAAATCCATAAACA 4251
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 QY 4312 AAAGGGGTTGCTTACTCAGCAGGAGGGAATAAAGAAACAAAGAGGAATAATCTTAAGCC 4371
 Db 3517 AAAGGGGTTGCTTACTCAGCAGGAGGGAATAAAGAAACAAAGAGGAATAATCTTAAGCC 3576
 QY 4372 TATTAGAACGGTCACTTACCAAAAGGCTAGCTATTATACACTGCTCTGGACATCAGA 4431
 Db 3577 TATTAGAACGGCTTACATTTGCAAAAGGCTAGCTATTATACACTGCTCTGGACATCAGA 3636
 QY 4432 AAGCTAAAGATCTCATATCCAGAGAAACAGATAGGCTGACCGGGTTGCCAAGCAGGCAG 4491
 Db 3637 AAGCAAAAGATCTCATATCTAGAGGGAACAGATAGGCTGACCGGGTTGCCAAGCAGGCAG 3696
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 Db 3757 AGTACACCTTAGAAGACTGGCAAGAGATAAAAGATAGACCTTCTCTGAGACTCGG 3816
 QY 4612 AAGGACCTGTATACCTCAGATGGGAAGAAATCCTGCCCAACAAAGAGGGTTAGAAT 4671
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 QY 4672 ATGTCCAAACAGATACATCGTCTAAACCCACTAGGAATTAACAACCTGCAGCAGTTGGTCA 4731
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 Db 3937 GAAATCCCTTATCATGTTCTGAGCTTACAGAGTGGCTGACTCGTGGTCAAAACATT 3996
 QY 4792 GTGTGCTGCTGAGCTGTATGCTAATCTTCCAGAAATGCTTCCAGGGAAGAGACTAA 4851
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 QY 4852 GGGGAAGCACCACCGGCTCTCACTGGGAAGTGGACTTCACTCAGGTAAAGCCGGCTAAAT 4911
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 QY 4912 ACGGAAAACAAATACCTATGTTGTTTGTAGACACCTTTTTCAGGATGGGTAGAGGCTTATC 4971
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 Db 4237 GATTTGGAATACCTTAAGGTAAATAGGCTCAGACAAATGCTCAGCTTTTGTGCCCAGGTAA 4296
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 QY 5212 CCCGGGAGACTGGCGTTAATGATTGGATAGCTCTCTCGCCCTTTGTGCTTTTTHAGGTTA 5271
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 QY 5272 GGAACACCCCTGACAGTTTGGGCTGACCCCTTATGAAATTAATCTACGCGGGGACCCCCC 5331
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 QY 5692 AGCTTCGCTCCTCATCGGCTGCTTACTTCTGTCAATAACCTCTCAGACTAATGGTATG 5751
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 QY 5752 GGCATAGGAGACAGCTGAACCTCCATAAACCTTATCTCCTCAGCTGTAAATTAATGAC 5811
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 QY 5812 TCCGGCAGAGTATTAAATATCAACAACCTCAAGGGAGGCTCTTTTAGAACCTGGTGG 5871
 Db 4935 TCCGGTACAGGTATTAAATATTAACAGCACTCAAGGGAGGCTCCCTTGGGAGCTGGTGG 4994
 QY 5872 CCTGATCTATAGTTTGCCTCAGATCAGTTATTCTAGTCT- - - - -GACCTCACCC 5922
 Db 4995 CCTGAAATATATGTCTGCTTTCGATCAGTAATCCCTGCTCAATGACAGGCCACACCC 5054
 QY 5923 CCAGATATCTCCTCAGTCTCAGGATTTTATGTTTGGCCAGGACCAACCAATAATGGAAAA 5982
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 QY 5983 CATTTGCGAAATCCAGAGATTTCTTTTGTAAACAAATGGAACTGTGTAACTCTTAATGAT 6042
 Db 5115 TATTGTGGAATCTCAGGATTTCTTTTGAAGCAATGGAGCTGCATAACTTCTTAATGAT 5174
 QY 6043 GGATATTGGAATGGCCAACTCTCAGCAGGATAGGGTAAAGTTTCTTATGCTCAACACC 6102

Db 5175 GGGAAATGGAAATGGCCAGTCTCTCAGCAAGACAGAGTAAGTTACTCTTTTGTAAACAAT 5234
Qy 6103 TATACAGCTCTGGCAAAATTTAAATTAACCTGACCTGGATTAGAACTGGAAAGCCCAAG--- 6159
Db 5235 CCTACCAAGTTAATCAATTTAATATAGCCATGGGAGATGGAAGATTGGCAACAGCGG 5294
Qy 6160 -----TGCTCTCCTTTAGACCTAGATTACCTA 6186
Db 5295 GTACAAAAAGATGTACGAAATAGCAAAATAAGCTGTCAITTCGTTAGACCTAGATTACTTA 5354
Qy 6187 AAAATAGCTTCACTGAGAAAGGAAAACAAGAAATATCCTAAAATGGGTAAATGCTATG 5246
Db 5355 AAAATAGCTTCACTGAAAAAGGAAAAAAGAAAAATATTCAAAAGTGGGTAAATGGTATA 5414
Qy 6247 TCTTGGGAATGGTATATTATGAGGCTCGGGTAAACAACACAGGCTCCATTTCTAACTATT 6306
Db 5415 TCTTGGGAATAGTGTACTATGAGGCTCTGGGAGAAAGAGATCTGTTCTGACTATT 5474
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Qy 6364 ACGGTCAAAGACCCCAACCCCAAGGACAGGACCAATCTCTTAAC----- 6408
Db 5535 GCGGAACAAGGACCTCCAAATCCAAGAACAGAGCCCATCTCTTAACCCCTCTGATTACAAT 5594
Qy 6409 ATAACTTCTGGATCAGACCCCACTGAGTCTTAACAGCACGACTAAAATGGGGCAAACTT 6468
Db 5595 ACNACCTCTGGATCAGTCCCCACTGAGCTTAACATCACTATTAAACACAGGGCGAACTT 5654
Qy 6469 TTTAGCCTCATCAGGGAGCTTTTCAAGCTCTTAACTCCACGACTCCAGAGGCTACCTCT 6528
Db 5655 TTTAGCCTCATCAGGGAGCTTTTCAAGCTCTTAACTCCACGACTCCAGAGGCTACCTCT 5714
Qy 6529 TCTTGTGGTATGCTTAGCTTCGGGCCACCTTACTATGAAGGAATGSGTAGAAGGG 6588
Db 5715 TCTTGTGGCTTTGCTTAGCTTCGGGCCACCTTACTATGAGGGAATGSGTAGAGAGGG 5774
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Qy 6709 CACCTTTGTAAACCACTGAAAGCTTTAATCGAAACCTCTGAGAGTCAATATCTGCTACCT 6768
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Db 5955 GGTATGACAGGTGGGTCATGTAATCTGGATTAAACCCCTTGCTTTCCACTTGGTT 6014
Qy 6829 TTTAACCAAACTAAAGATTTTTCGATTATGGTCCAAATTTGTTCCCGAGTGTATTACTAT 6888
Db 6015 TTAACCAAACTAAAGATTTTTCGATTATGGTCCAAATTTGTTCCCGAGTGTACTACTAT 6074
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Db 6075 CCGGAAAAAGCAATCTTGATGAAATGACTACAGAAATCATCGAAAAAGAGAGAGCCC 6134
Qy 6949 ATATCTCTGACACTTCTGATGCTCGGACTTGGAGTGGCAGCAGGTGAGGAAACAGGA 7008
Db 6135 ATATCCCTGACACTAGCTGTAATGCTCGGATTGGGAGTGGCTCGACGGTGGGAAACAGGA 6194
Qy 7009 ACAGCTGCCCTGCTCAGGACCAACAGAGCTAGAAAAAGGACTTAGTAACCTTACATCGA 7068
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Qy 7069 ATTGTAACAGAGATCTCCAGCCCTAGAAAAAATCTGTCAGTAACTCGAGGGAATCCCTA 7128
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Db 6315 ACCTCCTTATCTGAAGTGGTTCTACAGAAACAGAGGGGGTTAGATCTGTTATTTCTAAAA 6374
Qy 7189 GAAGGAGGATTAATGTAGTACCTTTGAAGGAGGAATGCTGTTTTTATGTGATCATTCAGGG 7248
Db 6375 GAAGGAGGTTAATGTAGTACCTTTAAAGAGGAATGCTGTTCTTATGTAGATCACTCAGGA 6434
Qy 7249 GCATCAGAGACTCCATGAACAAAGCTTTAGAGAAAGGTTGGAGAGCGTCAAGGGGAAAAAG 7308
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Qy 7309 GAAACTTACTCAAGGGTGGTTTGAAGGATGTTCAACAGAGTCTCTTTTGGTGGCTACCCCTA 7368
Db 6495 GAGGCTGACCAAGGGTGGTTTGAAGGATGTTCAACAGAGTCTCTTTGGATGACCACTCCTG 6554
Qy 7369 CTTTCTGCTTTAACAGGACCTTTAATAGTCTCTCTCTCTGTTACTACAGTTGGGCCATGT 7428
Db 6555 CTTTCTGCTCTGACGGGGCCCTTAGTAGTCTCTCTCTGTTACTTACAGTTGGGCCCTTG 6614
Qy 7429 ATTATTAAACAAGTTAATTCGCTTTTATTAGAGAACGAATAAGTSCAGTCCAGATCATGGTA 7488
Db 6615 TTAATTAATAGTTTGTGCTTTTGTAGAGAACGAGTGAAGTCACTCAGATCATGGTA 6674
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Db 6675 CTTAGGCAACAGTACCAAGCCCTCTGAGCCAGGAGAACTGACCTCTAGCCTTCCAG 6734
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Qy 7666 AGATTAGGTTTTTGTGTTTTTAAATATCGGGAAGTAAATAGGCCCTGAGTACATGTC 7725
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Db 6915 TCTGCGCCT-AAAGTAAGATAACAGGAAATGAGTTGAC----TAATCGCTTATCTGGATT 6969
Qy 7786 TTGTTTAGCTTCTGTAATACTGTTGCGCCATAAAGATGTTGAAATGTTGATACACATAT 7845
Db 6970 TGTAAACCTGACTGGCACCAATAGAGAAATGATTACATTTGACAGCCCTAGTGACCTAT 7029
Qy 7846 CTTGTTGACAAACATGTTCTCCCCACCCGAAACATGCGCAAAATGTTAACTCTTAAACAA 7905
Db 7030 CTCACCTGCAATCTGTCACTCTGCCCAGGAGCCACGAGATGCGGACCTCCCGAGCTAT 7089
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Qy 7960 -----TTGTGATATTTTGAATGATTGTTTGTAAAGCGCGGCTTTGTTGTGAAC 8010
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Qy 8011 CCATAAAAGCTGTCTCCGACTCCACACTCGGGGCCGAGTCTCTTACCCCTCGGTGGTGT 8070
Db 7210 CCATAAAAGCTGTCTCCGACTCGGGGCCGAGTCTCTTACCCCTCGGTGGTGT 7269
Qy 8071 ACAGCTGTGGGCCCAAGCGGCTTGAATAAAATCCTCTTGTGTTTGCATCAAAAAA 8130
Db 7270 ACAGCTGTGGGCCCAAGCGGCTTGAATAAAATCCTCTTGTGTTTGCATCAAAAAA 7329
Qy 8131 AA 8132
Db 7330 AA 7331

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; APPLICANT: Brockman, Jeffrey
; APPLICANT: Evans, David
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; APPLICANT: Rajan, Prithi
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Best Local Similarity 60.58; Pred. No. 0;
Matches 4377; Conservative 0; Mismatches 2575; Indels 285; Gaps 31;

Qy	461	CCCTCCGCGACCGTCCGACTCTTTGGCTGCTGTGGAAGACGFTGGACGGGTCACTGCTG	520
Db	601	CCGACCCCATCTCATCTGAATCTTTAAGTTGCTGTGTCGACGGCGAAGTCGCGCGGTT	660
Qy	521	TCGTGATC-TGTTGGTTCTGTTTGTGTGCTTTGTGCTGTTGTGCTGCTGCTGCTGCTG	579
Db	661	TTGGTTTCTTTTGTCTCAGTCTCGTGTCCGCTCTTTGTTGTGCTGCTATTTT	716
Qy	580	TTAATATGGGACACGACGTCGACACCTCTTAGTTTGTGCTCTCGACCATTTGACTCAAG	639
Db	717	TAGAAATGGGACATCTGTCTCACTCCCTTCTTAACTTCTTAACTTCTTAACTTCTTAA	776
Qy	640	TTAATATCCAGGCTCATAATTTGTCAAGTTTCAAGTTTAAAGAGGACCTTGGCAGACTTCT	699
Db	777	TAAATATCAGACACACATCAGTCACTGAGGTTAGGAAAGGCCCATGCAACTTTT	836
Qy	700	GTGCTCTGAATGCCGACATTCGATGTTGATGCCATCAGAGGGACCTTTAAATCTG	759
Db	837	GCGCTCCGAGTGGCCAACTTTGGAGTGGGCTGCGACCGGAGGCTTTTGTGCTGCTG	896
Qy	760	AGATTATCTGCTGTTTAAAGCACTTTTTCAGCTGACCTGACCTGACCTGCTCTCATCCGATC	819
Db	897	CACGTATCGCGCCGCTCAGGCGAATTTGTTTTTCAG---GAAGAAGGGGGTCACTGATC	953
Qy	820	AGGAGCCCTATATCTTACGTGGCAAGATTTGGCAGAGGATCTCCCGCATGGGTAAAC	879
Db	954	AGATCCCTTACATTTGTGACCTTGGCAGAGTCTCGTCCAGTTCCTCCAGCTTCGTGGTCAAGC	1013
Qy	880	CATGG---CTGAATTAAGCAAGAACGACGCTCCCGCAATTTCTGGCTCTTTGGAGAGAAA	936
Db	1014	CCTGGACCCCAATCTCTTGGAACTGACGCGTTGCGAGTTGCGCAGTCCGACGATCGAGTGA	1073

Qy	937	ACAAACACTCGGCTGAAAGAGTCAAGCCCTCTCTCATATATCTACCCCGAGATTGAGAGC	996
Db	1074	AATCTGTCCTGTCAGCACCCCCCAAGATTATTCAGAGATTGACGACTCTCTCTGGATGG	1133
Qy	997	CACCGGCTTGGCGGAACCCCAATCTGTTCCCCACCCCTTATCTCGGCACAGGTCGCG	1056
Db	1134	ACTCCCAACCTCC---CCCTTACCCCTGCCCAGAGCCACCTTGCAGCAGCCCCACCTG	1190
Qy	1057	CGAGGGGACCCCTTTGCCCCCTCTCGAGCTCCGCGGTGGAGGACCTGCTGCAAGGACTC	1116
Db	1191	TGGCAGCCCTCAGCGGAACCAACAGCAAGCGGGCTCAGGGACCGCGGGAGGACTC	1250
Qy	1117	GGAGCGGAGGGCGGCCACCCCGAGGGGACACAGAGATCGGACATTAACCGTTCGCGCA	1176
Db	1251	GGAGCGCGCGGGTCGGAGCCC---TGCAGAGGAGGGGGGCCAGATTTCCACAGTTGCTT	1308
Qy	1177	CGTACGGCCCTCCACACACCGGGGGCCAAATTGACGCCCCCTC-----CA	1219
Db	1309	GCCCCCTTAGAGCTCATGTGGAGGGCCACGCCAGAGCCTTAATGATCTCATTCCTTTACA	1368
Qy	1220	GTATTGGCCCTTTCTTCTGCAGATCTCTATAATTGAAAACTAAACCATCCCTTTCTC	1279
Db	1369	GTACTGGCTTTTCTTCTGATTTATATAATTGAAAACTAAACCATCCCTCTCCTCTC	1428
Qy	1280	GGAGGATCCCAACGCTCAACGGGTTGGTGGAGTCCCTTATGTTCTCTCACAGCCTAC	1339
Db	1429	AGAAAAACCCCTCTGGGCTTAAGTGGCTCTTGAATCACTTATGTTCTCTCATCAGCCAC	1488
Qy	1340	TTGGGATGATGTCAACAGCTGCTGCAGACACTCTTACACACCGAGGAGCGAGAGAGAT	1399
Db	1489	TTGGGATGATGTGACAGCTTTTGCAGGTTCTTACACAGAGAGAAAGGAGAGAGAT	1548
Qy	1400	TCTATTAGAGGCTAGAAAAAATGTTCTGGGGCGCACGGCGACCCACGCGGTTGCAAAA	1459
Db	1549	CCTGATGGAGGCAAGAAAAACGTTCTAGAGAGGACGGCACACCTGCTCTCCCTAA	1608
Qy	1460	TGAGATTGACATGGGATTTCCCTTAATCTCCCGCGTTGGGACTTACAAACGCGCTGAAG	1519
Db	1609	CCTCGTGGACGAGGCTTTCCCTTTGAACCCGCCCACTGGGACTTACAACTGCGGAAG	1668
Qy	1520	TAGGAGAGCTTGAANAATCTATCGCCAGGCTCTGGTGGCGGCTCTCGGGCGCTCAAG	1579
Db	1669	TAGGGAGCGCTCTTGTCTACCGTCTGAGTCTGTTGGAGGCTCTCAGAGAGCGCGCAG	1728
Qy	1580	ACGCGCCACTAATTTGGCTAAGGTAAAGAGTATGATCAGGAGCCGGAATGAACCCCTC	1639
Db	1729	ACGCGCCACCAATTTGGCTAAGGTAAAGAGTCTTGCAGGGGCGAGCTGAACACCCCTC	1788
Qy	1640	TGTTTTTCTTGAGAGCTTTGGAAGCTTCAAGCGGTACACCCCTTTTGTATCCACCTC	1699
Db	1789	AGTCTTTCTGGAGCGCTTATGGAGCGTATAGGAGGTACACCCCTTTGATCCCTCGTC	1848
Qy	1700	AGAGGCCAAAAAGCCTCAGTGGCTTTGGCTTTTATAGGACAGTCAGCCTTGGATATTAG	1759
Db	1849	AGAGGGACAGAAAGCCGCTGAGCCATGGCTTTCAITGGCCAGTCTCTCCCGATATTA	1908
Qy	1760	AAAGAGCTTTCAGAGCTGGAAGGTTTACAGGAGGCTGAGTTACGTGATCTAGTGAAGGA	1819
Db	1909	GAAGAGCTACAGAGGCTGGAGGGCTCCAAAGATTATACGCTCCAAAGTTTGTGAAGGA	1968
Qy	1820	GGCAGAGAAAGTATATTACAAAAAGGGGAGACAGAGAGAAAGGAAACAAAGAAAGAG	1879
Db	1969	AGCAGAGAAAGTTTATCAGAGAGAGAAACAGAGAGAGAGAGGCGAGAGAGAGAGAA	2028
Qy	1880	AGAAAGAGAGAAAGGAGAGAAAGACCTAATAACCGGCAAGAGAGAAATTTGACTAAGAT	1939
Db	2029	AGAAATAGAGAGAGAGAGAAATAGCCGAGATCGCCGTGAGGAGAGAAATTTGACTAAGAT	2088
Qy	1940	CTTGGCTGCAATGTTGAAGGAGAAACCAATACGGAAGAGAGAGAGATTTTAGGAAAT	1999
Db	2089	TCTGGCCGCACT-----TATAAATGATAGGACGTGAGAAAGGAGAGAGAGATTT	2139
Qy	2000	TAGGTACGGCCCTAGACAGTCAGGGAACCTGGGCAATAGGACCCCACTCGACAAGGACCA	2059

Db	2140	CCTGGGCAACAGGGCAGTGAACCGCCAGGTGGCAGAAAGACGCCGCTGGAAAAAGACCA	2199	Db	3208	ACAGGGGTTCAAAAACCTCCCTACCTGTTTGAAGAGCCCTCCATCGGGATTTAGCACC	3267
Qy	2060	ATGTGCATATGTAAAGAAAGAGGACACTGGGCAAGAACTGCCCCAAGAAGGAAACAA	2119	Qy	3140	CTTCAGGATCCAACACCCCTCAGTGAACCTCTCCAGTAGTGGATGAGCTGCTTCTGGC	3199
Db	2200	ATGCGCTTTTGAAGAAAAAGGACACTGGGCTAAAGACTGCCCCTAAGAAAAAGAGGCA	2259	Db	3268	CTTTCGGCTCAAAACCCGCCCTTACCTACTGCGAGTAGTAGATGATCTTTTAATCGC	3327
Qy	2120	AGGACCAAGGATCCTAGCTCTAGAAGAAGATAAGATTAGGGGAGACGGGGTTTCGGACCC	2179	Qy	3200	GGGAGCCACAAACAGGACTGCTTGAAGGCAAGAAAGGCACTACTGCTGGAAATGTCTGA	3259
Db	2260	A-----TTCAGGTCCTGACCCCTAGAGACGATTAGGGAAGTCGGGGCTCAGACCC	2310	Db	3328	AGCCGCTCAAAAGAGCTATGTCAACAGGGGACTGAGAGACTCTCACAAGACTGGGAA	3387
Qy	2180	CCTCCCGAGCCAGGGTAACTTTGAAGGTGAGGGGCAACGATTTGAAGTTCCTGTTGA	2239	Qy	3260	CCTAGGCTACAGAGCTCTGCTAAGAAAGCCAGATTTTCAGGAGAGAGTAACATCTT	3319
Db	2311	CCTCCCTGAGCCTAGGGTAACTTTGTCTGTGGAGGGGACTCCCGTTAAATTTCTGATAGA	2370	Db	3388	TTTGGGATATCGAGTTTCGGCTAAAAAGGCAAAATTTGTCAAACGTAGGTAATCTACTT	3447
Qy	2240	TACCGAGCGAAACATTCAGTGTCTACTACAGCCATTAGGAACATAAAGATAAAAAATC	2299	Qy	3320	GGGGTACAGTTTTCGGGAGCGGACGATGGCTGACGAGGCAACGGAAGAAAACTGTAGT	3379
Db	2371	TACTGGAGCAGAGCATTCGGTACTCACAGCCCTTGGGCAAACTAGGCTCTAAAGAGAC	2430	Db	3448	GGGTATATACTTTTCGAGGAGGTAAAGATGGCTCACTGAAGCCCGGAAAAAGACTGTCT	3507
Qy	2300	CTGGGTGATGGGTGCCACAGGGCAACACAGTATCCATGCACTTACCCGAAGAACAGTTGA	2359	Qy	3380	CCAGATAACGGGCCCAACACACAGCCAAACAAATGAGAGAGTTTTTCGGGACAGCTGGATT	3439
Db	2431	CATAGTGGTTGGAGCCACTGGGAGTAACTTTTACCCCTGGACAAACAAAGAGCCTTACA	2490	Db	3508	GATGATTCACCGCCCAACACACACGCGAGGTACGTGAGTTTCTGGGACTGCTGGCTT	3567
Qy	2360	CTTGGAGTGGGACGGTAAACCACTGTTTCTGTGTCATACCTGAGTGCCCGACACCCCT	2419	Qy	3440	TTGCGAGCTGTGATCCCGGGTTCGACCTTAGCAGCCCACTCTACCCGCTAACCAA	3499
Db	2491	GATAGATAAAAAACATGGTGACCCACTCTTTCTGTGTGATACCTGAGTGTCTGCTCCCT	2550	Db	3568	TTGTAGACTCTGATTCAGGCTTTTCGACCCCTTAGCAGCACCCCTATATCCCTTGACTAG	3627
Qy	2420	CTTAGGTAGACTTATTGACCAAGATGGGACACAAATTTCTTTTGAACAGGGAAACC	2479	Qy	3500	AGAAAAAGGGGAATTCCTCGGCTCCTGAGCACCAAGAGGCAATTTGATGCTATCAAAA	3559
Db	2551	TCGGGACGTGATCTCTTTAAACAAACTAAAGGCTCAAGTTTCAATTTACTTCAAGAGGTCC	2610	Db	3628	GGAGGAATTCCTTTGGAATGGAAAGAAAGAACACCAAGAGCTTTTGGGCTATCAAAATC	3687
Qy	2480	AGAAGTGTCTGCAATAACAAACCTATCACTGTGTTGACCCCTCCAATTAGATGACCAATA	2539	Qy	3560	GGCCCTGTGAGCGCACCTGCTCTGGCCCTCCCTGAGCTAAACACCTTTTACCCCTTTA	3619
Db	2611	ACAGTAAGCTGGGGAAGAGCCCTTGTCTGCTTGTCTCCTCAGCAGCGAAGAGATA	2670	Db	3688	GTCTCTAATGACTGCGCCCTGCGCTAGCATTTACAGACTTGCATTAAGTCTCTCGCTATA	3747
Qy	2540	TCGACTATACTCTCCCTAGTAAAGCCTGATCAAAATATACAAATCTGTTGTTGAAACAGTT	2599	Qy	3620	TGTGATGAGCTAAGGAGTAGCCGGGAGTTTAAACCAAAACCTTAGGACCATAGGAG	3679
Db	2671	CGGTTTGATGAAGACAAACCAAGGTGCAGCCCTTTAGA---CTGGGTAACTCGCTT	2727	Db	3748	TGTGGACGAGAGAGGGGCATAGCCAGAGGGGTGCTGACACAGCACTAGGACCTTGGAA	3807
Qy	2600	TCCCCAAGCCTGGGCAAGAACCGCAGGATGGGTTTGGCANAGCAAGTTCCCCACAAGT	2659	Qy	3680	AAGACCTGTGCGCTACTCTCAAAAGAGCTCGATCTCTAGCCAGTGGTTGGCCCATATG	3739
Db	2728	CCCCAATGTCTGGCGGGAACAAGCAGGAGTGGGGTTGGCTAAACAAGTGCCTCCAGTCGT	2787	Db	3808	GAGACCGGTAGCTATCTCTCAAAAAAATCTGGATCCCGTGTAGTGGATGGCCACATG	3867
Qy	2660	TATTTAACTGAAGCCAGTGCACACACAGTGTCACTCAGACAGTACCCCTTGAGTAAAGA	2719	Qy	3740	CCTGAAGGCTATCGCAGCTGTGGCCATACTGTGCAAGGACGCTGACAAATTTGATTTGGG	3799
Db	2788	GGTAGAACTTAAAGCTAGTGTACTACCCCATCTCAGTAAAGCAATACCCCATGAGCAAGA	2847	Db	3868	TCTGAAAGCTATTTCAGCAGTAGCCCTGTGATCAAGATGCTGATATAAATGCAATGGG	3927
Qy	2720	AGCTCAAGAGGAATTCGGCCGATGTCCAAAGATTAAATCCAAAGGGCATCTAGTTCC	2779	Qy	3800	ACAGATATAAATGTATAATAGCCCCCATGCAATTTGGAGAACATCGTTCCGCGAGCCCCAGA	3859
Db	2848	AGCTAAGGAGGGCATCCGACCTCATATTCGGAGGCTGTAGACCAAGGAATTTTAGTGGC	2907	Db	3928	ACAGCAGGTGACTGTCTGGCCCCCTCATGCCCTGGAGAGTATTGTGGCGAGCCACCTGA	3987
Qy	2780	TGTCGAATCTCCCTGGAATCTCCCTGTCTACCGGTTAGAAAGCCTGGGACTTAATCACTA	2839	Qy	3860	CCGATGGATGACCAACCGCCGATGACCCACTATCAAAAGCCTCTCTCTCACAGAGGGGT	3919
Db	2908	CTGTAGTCCCCCTGGAAACACTCACTTTTGGCAGTACGAAAGCCAGGGACCAATGATTA	2967	Db	3988	TAGATGGATGACTAATATGCCCGGATGACACTATCAGAGTCTGCTGCTAAATGACCGGT	4047
Qy	2840	TCGACCACTACAGGACTTGAGAGAGTCAATAAACGGGTGCAGATATACACCAACAGT	2899	Qy	3920	CACGTTTCGCTCCACAGCCGCTCTCAACCCCTGCCACTCTTTCGCTGGAAGAGACTGATGA	3979
Db	2968	TCGCCGGTACAAGACCTCCGGAGTTAATAAAGGTCCTGGAATTTCACTTCCCTTACAGT	3027	Db	4048	AACCTTTGCCCCCTCTGCAATCTCAACCCAGCACCCCTCCTCCCTTAACGAATGATTC	4107
Qy	2900	CCCGAAACCCCTTATTAACCTTTGTGTCTCTCCACCCCAACCGGAGCTGGTATACATATT	2959	Qy	3980	ACCAGTGAATCATGATTTGCCATCAACTATTGATTGAGGAGACTGGGTCGCAAGGACCT	4039
Db	3028	CCCGAAACCCGTACAACCTTACTAAGCTCTCTCCACCCGAGAGAACCTTGTGTATACGGTCT	3087	Db	4108	CGTCCAGTACATCGATGTGAGACATCTCTGGCTGAAGAAATTTGGGACCCAGAAAGACCT	4167
Qy	2960	GGACTTAAAGGATGCCCTTTCTGCTGTAGATTACACCCCACTAGCCCAACCACTTTTTCG	3019	Qy	4040	TACAGACATAACCGCTCACTGGGAAAGTGTCTTAACTGCTTCACTGACGGAAGAGCTATGT	4099
Db	3088	GGATTTAAAGATGSCCTTTCTTTTGTGCTGTCTGCAACCCCAAGAGTCAACTTCTGTTTC	3147	Db	4168	GACTGACCAACCTCTGGCTGG---AGCTCTAGCTGTACACGATGGCAGCAGTTTCT	4224
Qy	3020	CTTTCGAATGGAGATTCAGGTACGGGAAGAACCGGCGAGCTCACCTGGACCCGACTGCC	3079	Qy	4100	GGTGAAGGTAAAGAGATGGCTGGGGCGCGGTGGTGGACGGGACCCGACGATCTGGGC	4159
Db	3148	CTTTGATGGAGAGACCCAGAGGGGCGGACAGACTGTGTCATTAACCTTGGNCTAGACTACC	3207	Db	4225	GATTTAGGGAAACGGAAGGGCTGGAGCTGCGGTGGTGGATGGAAAAAAGTAATTTGGGC	4284
Qy	3080	CCAAGGGTTCAAGAACTCCCCGACCAATCTTTTGAAGAGCCCTTACACAGAGACTGGCCAA	3139	Qy	4160	CAGCACCTCGCGGAAGGAACTTCAGACAAAGGCTGAGCTCATGSCCTCTACGCAAGC	4219
				Db	4285	AGTGTCTTGCCTGAAGGAACCTTCGCGCACAAAGGGCTGAACTCATAGCGCTTACACAGGC	4344

Qy	4220	TTTGGCGCTGGCCGAGGAAATCCATAAATTTTATACGACAGCAGGTATGCTTTGTC	4279	5300	CCCTATGAATTAATCTCTACGGGGGACCCCCCAATTTGGTAGAAATTG-----CTTCTGT	5353
Db	4345	CCTCGAGAGCGCGAGTAAATCAITTAATATTTACACTGACAGCGCTATGCTTTGTC	4404	5398	TCCTTTTGAAGTTCTGTATGGGGGACCTCCCTTTTAATAAAGATGGTGGAAATTTGGT	5457
Qy	4280	GACTGCACAGTATCATGGGCGCATCTATATAAACAAGGGGGTGTCTTACCTCAGCAGGGAG	4339	5354	ACATAGTGTGAGCTGTCTTTCCAGCGCTTTTGTCTTAGGCTCAAGGCACCTTGAGTG	5413
Db	4405	TACTGCACATATCCATGGGCGCATCTACAGGCGAGGGGTATTGACTTTTCAGCCGGTAA	4464	5458	TCCCGATTGAGGTCTGTCTTACCTCTCTTTGCTTATTTCAATTAAGGCCCTGAAAGT	5517
Qy	4340	GGAATTAAGAACAAAGAGGAAATCTTAAGCCTATTAGAACCGTCAATTTACCAAAAG	4399	5414	GGTGAGACAAACAGCGTGGAGGCAACTCCGGGAGGCTCTCAGAGGAGGAGACTTGCA	5473
Db	4465	AGACATCAAAACAAAGAGAAATCTTGGCCCTGTTAGAACCAATCATGCGCCCAAGAA	4524	5518	AATTAGACCAAAATTTGGGACCAAGCTAAAGAGCGGCTACACCCAGGAGCACCGCAG-	5576
Qy	4400	GCTAGCTATTATACACTGTCTGACATCAGAAAGCTTAAAGATCTCATATCCAGAGAAA	4459	5474	GATCCACATCGTTTCCAGTGGAGATTTCAGTCTAGCTTTAGAGCCACCGTGCAGGAA	5533
Db	4525	GGTAGCCATCATCCACTGTCCCGGTACACAGAAAGGAGAGACTTAGTGCCCAAGGCAA	4584	5577	--TACCCACGAGTTCCAGGTCCGGGACCAAGTCTTTGGTCAGACGACATCGAACCGGTAG	5634
Qy	4460	CCAGATGGCTGACGGGTGTCAGAGCAGGAGGCCAGGGTGTAACTTCTGCTGCTATAAT	4519	5534	CCTCGAGACTCGGTGGAAGGGCCCTTATCTGCTACTTTTGCACACACCAACCGGTGTGAA	5593
Db	4585	CCGATGGCAGACTCAGTAGCAAAACAGGTTGTCTCAGGGGCCATGATCTTAACCTGAAA	4644	5635	CCTTGAACCAAGGTGGAGGACCTTATTTAGTGTACTTAACTCTACGGCAGTGAA	5694
Qy	4520	AGAAATCCCAAGCCCAAGAACCCAGACGACAGTACACCTAGAACACTGGCAAGAGAT	4579	5594	AGTCGAAGGAATCTCCACCTGGATCCATGATCCAGCTTAAACCGGGCC-----	5644
Db	4645	AGGAAATCC---GTCCAAAAGCCCTGA-----GGATGAAA	4677	5695	AGTTGACGGGATTTGCTCTCTGGATCCACGCTTCAAGAGGCGCCCGCAGTCAAGA	5754
Qy	4580	AAAAAGATAGACCACTCTCTGAGACTCCGGAAGGAGCCTGTCTATACCTCAGATGGGA	4639	5645	-----ACCTCCGATTCGGGTGGAAAGCCGAAAGACTGMAAATCCCTTAAAGCTTCG	5698
Db	4678	CTATGATATAAAGAACTATTTTGGACTAGTGATCCCTCCCATCTTTTCGAAGGAA	4737	5755	TGAAGAAACCAACGAAGACAACCTGGGCTGTGGAAGCCACTGATAACCTCTTAAAGCTTCG	5814
Qy	4640	GGAATCCTGCCCAAGAGAGGGTTAGAAATATGTCCAAAGATATCATGTCTAACCCA	4699	5699	CCTCCATCGGCTGCTTCTTACTCTGTCAATTAACC-----	5733
Db	4738	AATAGACTTGACACCCGAGGAGAAATAAATTTGTGAAGGACTACACCACTTTTACCCA	4797	5815	CTTGCTCGCAGAGACCCCTCCATCACCTGGACCTAGGGAACCAACCCCTCATGCC	5874
Qy	4700	CCTAGGAACTAAACCTCGACAGTGTGTGTCAGAACATCCCTTATCATGTTCTGAGGCT	4759	5734	---TCTCAGACTAATGGTATCGCATAGGAGACAGCCTGA-----ACTC	5774
Db	4798	CCTGGAGTTTGAATAAATGATGAGACTGATTAATAAAGTCCCGGTATCAAGTCCCTAACTT	4857	5875	CAGTTCAACAGTCTTGGGAAGTCTTAATGAAGAAGGAGAGCGTTGTATGGGTAGCCTG	5934
Qy	4760	ACCAGGAGTGTCTGCTCGGTGTCAAAATTTGTGTGCTGCTGCGAGTGGTTAATGTAA	4819	5775	CCATAAACCTCTATCTCATCTGTTTAAATTAATGACTCCGGCAGAGTATTATATCA	5834
Db	4858	GAACTAGTGTCTCAAAAGATTAATAACTCTGCAAGAGGTGTGCTACTAATGCAAC	4917	5935	CAGTCCATCCCTTGGACTTGTGGCTGTATCTCACACCTGACATCTGTAATTTAGCAG	5994
Qy	4820	TCCTTCCAGATGCTCCTCAGGGAAGAGACTAAGGGAGGCCACCCAGGCGCTCACTGGGA	4879	5835	CAACACTCAAGGGGAGGCTCTTTTAGGAACTGGTGGCTGTATCTATACGTTTGCCTCAG	5894
Db	4918	TAAACCTTACAAAGAACTTGGAAAGAGACACCGGGAGACCGTCTCGAGTGTATTGGGA	4977	5995	CAGGATCTCCCAATTTGGGACCTTCCCGATCATACTGACTTGAATAACCCACCTCTGAAC	6054
Qy	4880	AGTGGACTTCACTAGGTAAAGCGGTAAATATACGGAACAAATACCTATTTGTTTGT	4939	5895	ATCAGTTATTCTTAGTC-----TGACCTCACCCCCCAG	5926
Db	4978	GGTGGATTTACTGAAGTTAAACCCGGAATGTATGTAATAAGTATCTGTTAGTATTGT	5037	6055	AAAAGTGTCTCCAAACGGGTAGGAGCACTACTGGATGTTTCGGGGCAGTTCTATCGAG	6114
Qy	4940	AGACACCTTTTCAGGATGGGTAGAGGCTTATCTCTACTAAGAAAGAGACTTCAACCGTGGT	4999	5927	ATATCTCCATGCTCAGGATTTTATGTTGCCAGGACCAACCAATAATGGA-----	5980
Db	5038	AGACACCTTTTCAGGATGGGTAGAGGCTTCCCACTAAACTGAGACTGCCAGATTTGT	5097	6115	CTAATCTTAGGGCTGCACAGTTTTATGTTGCTGCTGAGGTGTCAGAAAGGAAAGCTGC	6174
Qy	5000	GGCTAAAAAATACTGGAAGAAATTTTCCAAAGATTTGGAATACCTAAGGTAATAGGGTC	5059	5981	---AACATTTGGGAAATCCCAAGATTTCTTTTGTAAACATGNACTGTGTAACTCTA	6037
Db	5098	GCCCAAGAGATTTTGGAGAAATCCCTGCCAAGATATGGAGTACTTAAGGTAAATCGGTC	5157	6175	AACAAGATGTAGAGGGGCATCAGACTACTTTTTCGGTAAATGGACATGTGAACAACAG	6234
Qy	5060	AGACATGGTCCAGCTTTGTGCCCAGGTAAAGTAAAGTAAAGTAAATTTGGGAT	5119	6038	ATGATGGATATTGGA-----ATGGCCAAACCTCTCAGCAG	6072
Db	5158	CGACAAATGGACCGACCTTTGTGCCCAGGTAAAGTAAAGTAAAGTAAATTTGGGAT	5217	6235	GGGAAGCCTACTGGAAGCCTTCCCTGATTTGGGACCTGATCACGGTAAACCTGGTAGTG	6294
Qy	5120	TGATTGGAACATGCAATTTGTGATACAGACCCCAAGCTCAGGACAGGTAGAGAGATCAA	5179	6073	GATAGGGTAAAGTTTTTCTTATGTCAACACCTATACAGCTCTGGCAATTTAACTTACCTG	6132
Db	5218	TGATTGGAATTTACATTTGTGCTTCCCGCCCTCAAAAGCTTCAGGACAGGTAGAGAGATGAA	5277	6295	GTTATGATAAGCCAAACCAAGGAGAAAGAAACCCATACAAATACCTAGATTTCTGGGTGTG	6354
Qy	5180	TAGAACATTAAGAGACCTTACTTAAATTTGACCGGAGACTGGCGTTTAAATGATTGGAT	5239	6133	ACCTGGATTTAGAACTGGAAGCCCAA--GTGCTCTCTTTCAGACCTAGATTACCTTAAAA	6190
Db	5278	TAGAACATTAAGAGAGACCTTGAATTTGCTTAAATTTGGCCATGGAGACCGGCGGAAAGACTGGGT	5337	6355	CTCTTAAAAATTACAGCCCCCAGGACCATGCAAAAGGTAAATACTGCAACCCCTTACTCA	6414
Qy	5240	AGCTCTCTGCTTGTGCTTTTGTAGGGTTAGGAACAACCCCTGGACAGTTTGGGCTGAC	5299	6191	TAAGTTTCACTGAGAAAGGAAACAAGAAATATCTTAAATGGTAAATGTTGTCTT	6250
Db	5338	GGCTCTCTCCCTTGGCTCTTCCGAGCCCGGAACACCCCGGACGCTTTTGGGCTCAC	5397	6415	TAAAAATTCACGTGAGAAAGGAAACAAG---CTCGCTGAGTTGGCTTAAAGAAATAGT	6471
Qy				6251	GGGGAATGGTATATTATGGAGGCTCGGGTAAACCAACAGGCTCCATTTCTAATTTTCGCC	6310

Db 6472 GGGGTTGGCGAGTATAT---ATTCCAATAAGAGACCCCTGGGTTTATCTTTTACGATTAGAC 6528
Qy 6311 TCATAATAAACACGCTGGAGCCTCCAAATGGCTATAGGACCAATAGCGTCTTTGACGGGTC 6370
Db 6529 TGACAGTAGAGACCTGG---CAGTAAATCATATAGGACCCCAACAGGTCCTTTACGGAC 6585
Qy 6371 AAAGACCCCCA-----ACCCAAGGACACGAGCCATCCTCTTAACATAACTT 6415
Db 6586 AGGCCCCCAGTTGACCGGCTCCCGGAGAGTCCAGCGGTCCAGCTCCACCAACTT 6645
Qy 6416 CTGGATCAGACCCCACTAGTCTAACAGCAGCATTAATATGGGGGAAAA----- 6465
Db 6646 CAGGCGCTACACAGTAGGACCCCTAATTAGAGACAACTTAGCCTCCCAACCACTCCTAG 6705
Qy 6466 -----CTTTTATAGCTCATCCAGGAGCTTTTCAAGCTCTTAACTCCACGA 6511
Db 6706 ATACAGAAAACCGTCTGGTCAGTCTAGTTACGGAGGCCCTTTTATAGTTTAAATAGGACTA 6765
Qy 6512 CTCACAGGCTACTCTTCTTGTGGCTATGCTTAGCTTCGGGCCCACTTACTATGAAG 6571
Db 6766 ATCCATATGACTCAATCATGTTGTTATGCTATGCTCTTAACCCCTTATTATGAAG 6825
Qy 6572 GAATGCTAGAGAGGAAATTCATGTGACAAAAGAAATAGAGACCAATGACATGGG 6631
Db 6826 GAATTGCTCAGACTAGAACTTACAAATATTACTTTCAGATCATTC---TCAATGCTTTGGG 6882
Qy 6632 GATCCCAATATAGCTTACCTTACCTAGGTTTCTCGAAGAGCCACCTCATAGGAAGG 6691
Db 6883 GAGAGAAACGGAAGTTGACTCTGACAGCAGTTTCAGGAATGGGCTTTGTTTAGGTCAGG 6942
Qy 6692 TTCCCCCATCCCAACCAACCTTTGTAACCACTCAAGCCTTTAATCAAACTCTGAGA 6751
Db 6943 TGCCCCAGGATAAATGGCACCTCTGTAAACAGACTCAAAATATCCGACCTAACAAAGTG 7002
Qy 6752 GTCAATATCTGGTACTGCTGTATGACAGGTGGGCGATGTAATATCGGATTAACCCCTT 6811
Db 7003 GTCAGTATCTAGTGCCTCCATAGACACAGTATGGGCTTGCATACAGGCTCTCACTCCTT 7062
Qy 6812 GTGTTTCCACCTTGGTTTAAACCAACTAAGATTTTTCATTTATGCTTATGCTCCAAATGTTTC 6871
Db 7063 GTATATCTATGCTGTGTTTCAATAGCTCCAAAGATTTCTGATTTTATGTTTCAGCTTATTC 7122
Qy 6872 CCGAGTGTATTACTATCCGAAAAGCAATCCTGATGAATATGACTACAGAAATCATC 6931
Db 7123 CTAGACTCTGTATCATGATGATAGTCTATTTCTAGACAAATTTGAACATCG---GGTCC 7179
Qy 6932 GACAAAAGAGAGAACCCATATCTCTGACACTTGTCTGTGATGCTCGGACTTGGAGTG---G 6988
Db 7180 GCTGGAAGAGAGAACCCATTACTTTAAACGTTAGCAGTGTCTTTTAGGATTTGGGAGTGGCG 7239
Qy 6989 CAGCAGGTAGAGAACAGGACAGCTGCCCTGTCTACGGGACCAACAGCAGCTAGAACAG 7048
Db 7240 CAGCTGGGTAGGATCTGGAACCGCTGCTTAATCCAGACCCCGGATCTTTGA----- 7294
Qy 7049 GACTTAGTAACTTACATCGAATTTGAACAGAACTCTCAAGCGCTTAGAAAAATCTGTCA 7108
Db 7295 -----GGNAATTACGTACAGCTATGGATAGTCTCAGAGCTATAGAACACTCTATAA 7347
Qy 7109 GTAACTGGAGGAATCCCTAACCTCTTATCTGAAGTAGTCTTACAGAAATAGAAAGGGT 7168
Db 7348 CCAAACTAGAAGAACTTTAACTTCTCTGCTGAGGTAGTACTGCAAAATAGGAGAGGAT 7407
Qy 7169 TAGATTATATTCTTAAAGAGAGGAGGATATGTTAGCTTGAAGGAGGATGCTGTT 7228
Db 7408 TAGATTGTTATTTCTTAAAGAGAGGAGGACTTTTGTCTGCTCTCTCAAGAGGAATGTTGT 7467
Qy 7229 TTTATGTGATCATTTAGGGGCCATCAGAGCTCCATGAACAGCTTAGAGAAAGGTTGG 7288
Db 7468 TCTATGTGACCACTCTGGGAGTGATCAAGATTCTATGGCCAACTTAGAGAACGCTAG 7527
Qy 7289 AGAAGCGTCAAGGGGAAAAGGAACTACTCAAGGGTGGTTTGAAGGATGGTTCAACAGGT 7348

Db 7528 ATATACGTCAAGAGAGAGAGAGACAAACAAGGATGGTTTGAAGCTGGTTTAATAAGT 7587
Qy 7349 CTCCTTTGGTTGGCTACCCCTACTTTCTGCTTTTAAACAGGACCCCTTAATAGTCTCCTCTGT 7408
Db 7588 CCCCCTGGCTACCACTCTCCCTTTCCACTATATAGCGGACCCCTTGATTATACTTCTGCTTT 7647
Qy 7409 TACTCACAGTTGGGCGATGTATTATTAACAAGTTAATTGCCTTCATTAGAGACGAATAA 7468
Db 7648 TGCCTACTTTTGGCCCTTGCAATTTCTTAATAAGTTAGTACCCCTTATTAGAGAAAGATAA 7707
Qy 7469 GTGAGTCCAGATCATGTGTACTTAGACACAGTACC 7505
Db 7708 ATGCAGTACAGGTATGTGTTATTAACAACAATATCA 7744

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; APPLICANT: Hook, Derek
; APPLICANT: Klimczak, Leszek
; APPLICANT: Laeng, Pascal
; APPLICANT: Palfireman, Michael
; APPLICANT: Rajan, Prithi
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Query Match 27.5%; Score 2237; DB 10; Length 8655;
Best Local Similarity 60.5%; Pred. No. 0;
Matches 4377; Conservative 0; Mismatches 2575; Indels 285; Gaps 31;
Qy 461 CCCTCCGCGACCGTCCGACTCTTTTGCCTGCTTGTGGAAGACGTGGACGGTCACCGTGTG 520
Db 601 CCGACCCCATCATCTGAATCTTTAAGTTGTCTGTGTGTCGACGCGAAGTCGCGCGCGGTT 660
Qy 521 TCTGGATC-TGTTGGTTTCTGTTTGTGTCTTTGTCTTTGTGTGTCCTTGTGTCTACAGTT 579
Db 661 TTGTTTCTTTTGTCTCAGTCTCGTGTCCGCTCTTGTGTGTCTGTCTATT-----ATTT 716
Qy 580 TTAATATGGACAGCGGTGACGCCCTTTAGTTTGTACTCTCGACCATTGGACTGAAG 639
Db 717 TAGAAATGGACAATCTGTCTCCACTCCCTTTTCTTAACCCCTGGAGCATTTGAAGAGG 776
Qy 640 TTAATATCCAGGGCTCATAATTTGTCAAGTTTAAAGAGGACCTTGGCAGACTTTTCT 699
Db 777 TAAATATCAGACCAACATCAGTCACTGGAGTTAGGAAAGGCCCATGCAACCTTTT 836

Qy	700	GTGTC	TCTGAA	TGGCCG	CACATTCGAT	TGTTGGAT	TGGCCAT	CAGAGGG	CACCTTAAT	CTG	759	
Db	837	GC	CCCTCCGAG	TGGCCAA	CGTTTGGAG	TGGGCTGGCCAC	CGGAGGG	TGCTTTTGACT	TGT	896		
Qy	760	AGATTAT	CTCTGG	CTGTTAAAG	CAGTTATATTTT	CAGACT	CGAC	CCGGCTCT	CAATCCCGATC	819		
Db	897	CAC	TGATGCGCGCG	CTCAGCG	AAATGTTTTTCAG	---	GAAGNA	GGGGTCA	CCCTTGATC	953		
Qy	820	AGGAG	CCCTATAT	CTCTTAG	TGTGCAAGAT	TTGSC	CAGAGAT	CCTCCG	CCATGGT	TAAC	879	
Db	954	AGAT	CCCTACAT	TTGTGAC	CTGCGCAGAG	CTCGTCCAG	TTCCAC	CTTCGTGGGT	CAAGC	1013		
Qy	880	CATGG	---	CTGA	ATAAGCAAG	AAGCAG	CTCCCG	AATCTGG	CTCTGGAG	AGAAA	936	
Db	1014	CCTG	GAACCCAAAT	CTCTCGAA	ACTGAC	GGTTG	CCAGTTGCC	CAGTCG	AGCTG	GAG	1073	
Qy	937	ACAA	CAC	CTCGG	CTGAA	AAAGTCA	AGCCCTCT	CCTCAT	ATCTAC	CCCGAGAT	996	
Db	1074	AAT	CTGGT	CGT	CAGCA	CCCCCA	AGATTTAT	CCAGAGAT	TTGAC	AGCTCTCTG	ATGG	1133
Qy	997	CAC	CGGCTTGG	CGGAA	CCCCAATCT	TGTTCCCC	CACCCCTT	ATCTGG	CACAGG	TGCCG	1056	
Db	1134	ACT	CCCAAC	CTCC	---	CCCTTAC	CCCCCTCC	CAGCAG	CCACCTG	CAGCAG	1190	
Qy	1057	CGAG	GGAG	ACCTTT	TG	CCCTCTCT	GTGAG	CTCCGG	GGTGTG	AGGAC	CTC	1116
Db	1191	TGG	CAG	CCCTC	AGC	CGGAA	CCAAAC	AGC	GGGCTCAG	GGAC	CTC	1250
Qy	1117	GGAG	CGGAG	GGGCG	CCAC	CCCGGAG	CGGAC	AGAGAT	TCGG	CACAT	TAC	1176
Db	1251	GGAG	CCCGGG	GTG	GAG	CCC	---	TG	CAG	AGGA	AGGGGG	1308
Qy	1177	CGT	AC	GGCCCTCC	CAC	ACCGGG	GGCCAA	TTG	CAG	CCCCCTC	---	1219
Db	1309	GC	CCCTTAG	AGCTACT	GTGG	GGGGCC	CAAC	CGC	CAG	GACCTTAAT	GTATCTCAT	1368
Qy	1220	GTA	TTGG	CCCTTTT	TCTCT	CGAGAT	CTCTATA	TAAAT	TTG	GA	AAACTAA	1279
Db	1369	GTA	CTGG	CCCTTTT	TCTTCT	GATTTAT	ATAAT	TTG	GA	AAACTAA	CAAC	1428
Qy	1280	GGAG	GATCC	CA	CGCTCT	CAG	GGT	TGGT	GGAT	CTCCT	TAT	1339
Db	1429	AGAA	AC	CCCTCTG	GGCTTACT	GGCTTACT	GGAT	CTAT	GTCTCT	CAT	CAG	1488
Qy	1340	TTGG	ATGAT	TGTC	CAAC	AGCTGCT	GC	CAGAC	ACTCTT	CA	CAAC	1399
Db	1489	TTGG	ATGAT	TGTC	CAG	CAGCTTTT	TG	CAG	GTCTCTT	TAC	CAG	1548
Qy	1400	TCT	ATTAG	AGCTAG	AAAAA	TGTTCT	GGGGCG	CAGCGG	CGAC	CCCA	CGGGT	1459
Db	1549	CCT	GATGG	AGCA	AAAAA	CGTTCT	AGG	AGAG	AGAC	GGCAC	CCCACTCT	1608
Qy	1460	TGAG	ATTG	CAT	TGG	ATTTCC	CTTAA	CTCG	CCCCGGT	TGG	ACTTAC	1519
Db	1609	CCT	CGTGG	AC	GAG	CGTTTCC	CTTGA	AC	CGCCCC	CACTGG	GA	1668
Qy	1520	TAGG	AGAG	CTTGA	AAATCT	TAT	CC	CAG	GGCTCTGG	TGG	CGGGCT	1579
Db	1669	TAG	GGG	AG	CGCTCT	TG	TCTAC	CGT	CGA	CTCTG	TGG	1728
Qy	1580	ACG	CCCCCA	CTA	ATTTGG	CTA	AGGTA	AGT	GAT	GC	AGG	1639
Db	1729	ACG	CCCCA	CCAA	TTTGG	CTA	AGGTA	AGT	GAT	GC	AGG	1788
Qy	1640	TG	TTTTT	CTG	AG	AGG	CTCTT	G	AG	CGGTAC	AC	1699
Db	1789	AGT	CTTT	CTG	AG	GGTCTT	AT	TG	AG	GGGTAC	AC	1848
Qy	1700	AGAG	CCCCAA	AAAG	CGCTCAG	T	GG	CTTTAT	AG	GAC	AGCT	1759
Db	1849	AGAG	GA	CAG	AAAG	CGCGT	G	TAG	CA	ATGG	CCCTT	1908
Qy	1760	AA	GA	AG	CGCTT	C	AG	AG	CTT	G	AG	1819

Db 2968 TCGCCCGGTACAAGACCTCCGGGAAGTTAATAAAGGGTCTTGGACATTCACCCCTACAGT 3027
 QY 2900 CCCGAACCTTATAACCTCTTGTGTCTCTCCACCCCAACGGAGCTGGTATACAGTATT 2959
 Db 3028 CCCGAACCGTACAACTTACTAAGCTCTCTCCCAACCGGAGAACTTGGTATACGGTCT 3087
 QY 2960 GGACTTAAAGATGCTCTTCTGCTGAGATTACACCCACTAGCCAAACCACTTTTGGC 3019
 Db 3088 GGATTTAAAGATGCTCTTCTTGTGCTGCTGTGACCCCAAGAGTCAACTTCTGTTTGC 3147
 QY 3020 CTTGCAATGAGAGTCCAGGTACCGGAAGAACCGGGAGCTCACCTGGACCCGCTGCC 3079
 Db 3148 CTTTGAATGGAGAGCCCAAGGGGGGACAGACTGGTCAATTAACCTGGACTAGACTACC 3207
 QY 3080 CCAAGGGTTCAAGAACTCCCGACCACTTTTGAAGAGCCCTTACACAGAGACTGGCCAA 3139
 Db 3208 ACAGGGGTTCAAAAACCTCCCTACCTCTGTTGAGAGAGCCCTCCATCGGATTTAGCACC 3267
 QY 3140 CTTTCAAGATCCAAACCTCAGGTGACCTCTCTCCAGTACGTGGATGACCTGCTTGTGC 3199
 Db 3268 CTTTGGCGTCAAAAACCCCGAGCTTACCCTACTGCACTAGTACGTAGATGATCTTTTAATCG 3327
 QY 3200 GGGAGCCAAACAGGACTGTTAGAGGACGAGGACACTACTGCTGGAATTGCTCA 3259
 Db 3328 AGCCGCTTCAAAAGAGCTATGTCAACAGGGGACTGAGAGACTCCTCACAGAACTGGGAA 3387
 QY 3260 CTAGGCTACAGAGCTCTGCTAAGAGGCCAGATTTTCAGAGAGAGGTAACTACTT 3319
 Db 3388 TTTTGGGATTCGAGTTTCGGCTTAAAGAGCAAAATTTGTCAAACTGAGGTAACTACTT 3447
 QY 3320 GGGGTACAGTTTTCGGGACGGGAGCGATGGCTGACGGAGGACCGGAAGAACTGTACT 3379
 Db 3448 GGGGTATACTTTGGAGGAGTAAAGATGGCTCACTGAAGCCCGGAAAGACTGTCTAT 3507
 QY 3380 CCAGATACCGGCCCAACACAGGCCAAACAAATGAGAGAGTTTTCGGGACAGCTGGATT 3439
 Db 3508 GATGATTCCACCGCCCAACACACAGCGAGGTACGTGAGTTTCTGGGAGCTGCTGGCTT 3567
 QY 3440 TTGCACTGTGGATCCGGGGTTTCGGACCTTTAGCAGCCCACTCTACCCGCTAACCAA 3499
 Db 3568 TTGTAGACTGTGATTCCAGGCTTTTCGGACCTTTAGCAGCACCCCTATATCCCTTGTACTAG 3627
 QY 3500 AGAAAAAGGGAAATTCCTCTGGGCTCTGAGCACCAAGAGGCAATTTGATGCTATCAAAA 3559
 Db 3628 GGAAGGAATTCCTTTGAATGGAAAGAAAGAACACCAAGAGCTTTTGGAGCTATCAATC 3687
 QY 3560 GGCCTCTGTAGCGCACTGCTCTGGCCCTCTCTGACGTAACTAAACCTTTTACCCTTTA 3619
 Db 3688 GTCTCTAATGACTGCCCCCTGCGCTAGCATTTACCAGACTTGAAGTCTCTGCTCTCTATA 3747
 QY 3620 TGTGGATGAGCGTAAGGAGTAGCCCGGGAGTTTAAACCAACCTTAGGACCATGGAG 3679
 Db 3748 TGTGGACGAGAGCGGGGCATAGCCAGAGGGGTGCTGACAAAGCACTAGGACCCCTGGAA 3807
 QY 3680 AAGACCTGTGCGCTACTGTCAAGAGCTCGATCCTGTAGCCAGTGGTTGGCCCATATG 3739
 Db 3808 GAGACCGGTAGCTATCTGTCAAAAACCTGGATCCCGTTGCTAGTGGATGGCCCATG 3867
 QY 3740 CTTGAAGGCTATCCGAGCTGTGGCCATATGTTGTAAGGACGCTGA CAATTTGACTTTGGG 3799
 Db 3868 TCTGAAGCTATTTCGACGAGTAGCCCTGTGTATCAAGATGCTGATAAACTGACAATGGG 3927
 QY 3800 ACGAATATACGTGTAATAGCCCCCATGTCATTGGAGAACATCGTTTCGGCAGCCCCAGA 3859
 Db 3928 ACAGCAGGTGACTGTGCTGGCCCCCTCATGCCCCGGAGATTGTGCGGACGCCACTGA 3987
 QY 3860 CCGATGGATGACCAACCGCCGATGACCCACTATCAAGGCTGCTCTCACAGAGAGGT 3919
 Db 3988 TAGATGATGACTAATGCCCCGGATGACACTATCAGATCTGCTGCTAAATGACCGGGT 4047
 QY 3920 CAGTTTCGTTCCACAGCGGCTCTCAACCCCTGCCACTTCTTCGCTCGGAAGAGACTGATGA 3979
 Db 4048 AACCTTTGCCCCCTGCCATTCTCAACCCGACGACCCCTCTCCCTCTAACGAATGATTC 4107

QY 3980 ACCAGTACTCATGATTTGCCATCAACTATTGATTTGAGGAGACTGGGTCGCAAGACCT 4039
 Db 4108 CGTCCAGTACATCGATGTGCAGACATCCTGCTGAAGAAATTTGGACACAGAAAAAGCT 4167
 QY 4040 TACAGACATACCGCTGACTGGAGAAGTGTAAACCTTGGTTTCACTGACGGAAGCAGCTATGT 4099
 Db 4168 GACTCACCACCTCGCCTGG---AGCTCTTAGCTTGGTACACGATGGCAGCAGTTTCT 4224
 QY 4100 GGTGAAAGGTAAAGAGATGGCTGGGGCGCGGTGGACGGGACCCGACGATCTGGGC 4159
 Db 4225 GATTGAGGAAAGCGAAGGGCTGGAGCTCGGTGGTGGATGGAAAAAGGTAATTTGGGC 4284
 QY 4160 CAGAGCTGCGCGGAAGAACTTTCAGCAAAAAGGCTGAGCTCATGCGCCCTCACGCAAGC 4219
 Db 4285 AAGTGCTTGCCTGAAGGAACTTCGGCAACAGAGGCTGAACCTCATAGCGCTTACACAGGC 4344
 QY 4220 TTTGGGCTGGCGGAAGGGAATCCATAAACATTTATACGGACAGCAGGTATGCCCTTTCG 4279
 Db 4345 CCTCCGAGAGGCGGAAAGTAAAGATCATTAATATTTACACTGACAGCCGCTATGCTTTTGC 4404
 QY 4280 GACTGCACAGTACATGGGGCCATCTATAAAACAAAGGGGTTGCTTACCTCAGCAGGGAG 4339
 Db 4405 TACTGCACATATCCATGGGCCCATCTACAGGCAGCGGGTTATTGACTTCAGCCGATA 4464
 QY 4340 GGAATAAAGAAACAAAGAGGAAATTTCTAAGCCTATTAGAAAGCGGTACATTTACAAAAAG 4399
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 QY 4400 GCTAGCTATTATACACTGCTCTGGACATCAGAAAGCTAAAGATCTCATATCCAGAGAA 4459
 Db 4525 GGTAGCCATCATCTGCTGCTGGTCAACAGAGGAGGAGGACTTAGTGGCCCAAGGCAG 4584
 QY 4460 CCAGATGCTGACCGGTTGCCAAGCAGGACGCCAGGGGTGTTAACTTCTGCTCTATAAT 4519
 Db 4585 CCGGATGGCAGACTCAGTAGCAAAACAGGTTGCTCAGGGGGCCATGATCTTAACGAAAA 4644
 QY 4520 AGAAATGCCAAAGCCCAAGAACCCAGACAGACAGTACACCCCTAGAAAGCTGGCAAGAT 4579
 Db 4645 AGGAAATCC---GTCCAAAAGCCCTGA-----GGATGAAAA 4677
 QY 4580 AAAAAGATAGACAGTCTCTGAGACTCCGGAAGGGAAGCTGCTATACCTCAGATGGGA 4639
 Db 4678 CTATGATATAAAGAACTATTTTTGGACTAGTATCCCTCCCATCTTTTTCGAAGGAAA 4737
 QY 4640 GGAATTCCTGCCCCCAAAAGAGGTTAGAAATATGTCACACAGATACATCGTCTAACCCCA 4699
 Db 4738 AATGAGACTTGAACCCGAGGAAGGAATAAATTTGTGAAAGGACTACACGAGTTTACCCA 4797
 QY 4700 CTTAGGAATCAAAACACTGACAGTGGTTCAGAACATCCCTTTATCATGTTCTGAGGCT 4759
 Db 4798 CTTGGGAGTTGAAAAAATGATGAGACTGATTAATAAGTCCCGGTATCAAGTCCCTAACTT 4857
 QY 4760 ACCAGAGTGGCTGACTCGGTGGTCAACATTTGTGTGCTTGCACCTGCTTAATCTTAA 4819
 Db 4858 GAAGTCAGTGGCTCAAAAGATTATAAATCCTGCAAGAGGCTGTGCAATCACTAATGCAAC 4917
 QY 4820 TCTTCCAGATGCCCTCCAGGGGAAGAGACTTAAGGGGAAGCCACCCAGGGGCTCACTGGGA 4879
 Db 4918 TAAACCTTCAAGAACCTGGAAAGAGACAAACGGGAGAGCCGCTCCTGGAGTATTTGGGA 4977
 QY 4880 AGTGAAGTCACTGAGGTAAAGCCGGCTAAATACGGAACAAATACCTATGTTGTTTTGT 4939
 Db 4978 GGTGGATTTTACTGAGTTTAAACCCGGAATGATGTAATAAGTATCTGTTAGTATTTGT 5037
 QY 4940 AGACACTTTTTCAGGATGGGTAGAGCTTATCTCTAATAAGAAAGACTTTCACACCGTGT 4999
 Db 5038 AGACACTTTTTCAGGATGGGTGGAAGCGTTTCCCACTAAAACTGAGACTGCCAGATTTGT 5097
 QY 5000 GGTAAAAAATACTCGGAAGAAATTTTCCAGATTTTGAATTTGGAATTAAGGTATATAGGTC 5059
 Db 5098 GGCCAAAGAGATTTTGTGAAGAAATCTGCCAAGATATGGAGTACCTAAGGTATCGGTC 5157

QY	1595	GGCTAAGGTAAGAGAGTGTATGATCAGGGACCGAATGAACCCCTCTGTGTTTCTTGAGAG	1654	QY	2675	CHGTGCCACACAGTGTCTAGTCAGACAGTACCCCTTGAGTAAAGAGCTCAAGAGGAAT	2734
Db	114389	GGCTAAGGTAAGAGAGGCTTGTGAGGGGAGAGCTGAACCAACCTCTAGTCTTCTTGAGCG	114488	Db	115445	TGATGCCACCCCATCTCGGTAAACAATACCCCATGAGCAAGAGCTAGGAGGGCAT	115504
QY	1655	GCTCTTTGGAGCCTTCAGGGGTAACACCCCTTTTGATGCCACCTCAGAGGCCCAAAAGC	1714	QY	2735	TGGCGCGCATGTCCAAAGATTAATCCAACAGGCGATCCTAGTTCCTGTCCAATCTCCCTG	2794
Db	114449	TCTAATGGAGGCATATAGAGGTACACCCCTTTTGACCCCTTGTCTAGAGGGGAGAGAGC	114508	Db	115505	CGGGCTCATATCCAGAGGTTGCTAGACCAAGAGTTTGTAGTGCCTGTCTAGTCCCTG	115564
QY	1715	CTCAGTGGCTTTGGCCTTTATAGGACAGTCAGCCTTGGATTTAGAAAGAGCTTCAGAG	1774	QY	2795	GAATACTCCCTCTGCTACCGGTTAGAAAGCTGGGACTAATGACTATCGACCATGACGGA	2854
Db	114509	CGCTGTAGCCATGGCCTTCATTGGTCAGTCCGTTCCGCAATTAAGAAAGCTGCAAG	114568	Db	115565	GAATACACCACTTCTCGGTTTCAAAAACAGGGGACCAATGACTATCGCCAGTCAAGA	115624
QY	1775	ACTGGAAGGCTTACAGAGGCTGAGTTACGTGTACGTGTATAGTCAAGGAGCAGAGAAATATA	1834	QY	2855	CTTGAGAGAGGCTCAATAAAGCGGTGAGGATATACACCAACAGTCCCGCAACCTTATAA	2914
Db	114569	GCTGGAAGGCTTCAAGATCATACGCTCAAGATTTAGTAAAGAGCAGAGAAAGTCTA	114628	Db	115625	CTTCCGGGAAGTTAAACAAAAGGCTCTGGACATTCACCCACAGTCCCGAACCCATACA	115684
QY	1835	TTACAAAGGGGAGACAGAAAGAAAGGGAACAAAGAAAGAGAGAGAAAGAGAGAAAG	1894	QY	2915	CTCTTGTGTGCTCTCCACCCCAACGGAGCTGGTATACAGTATTGGACTTTAAAGGATGC	2974
Db	114629	TCATAAGAGGAAACAGAAAGAGAGGAGGAGAGAGAGAAAGAAAGATGAGAGAG	114688	Db	115685	TTTATTAAAGCTCTCTCCACCTGAGAGAACATGGTATACAGTCTTGGACTTTAAAGATGC	115744
QY	1895	GAAGGAAGACGTAATAAACGGCAGAGAGAGAAATTTGACTAAGATCTTGGCTGCAGTGT	1954	QY	2975	CTTCTTCTGCTGAGATTACACCCCACTAGCCCAACCACTTTTGTGCTTCCGATGGAGAGA	3034
Db	114689	GGAAATATAGACG---GGGATTTTCAAGAGAGAAATTTAGTAAATTTTGGCCGCGAGTTGT	114745	Db	115745	CTTCTTGTGCTGCTTGACCTTAAGAGTCAGCTCTCTGTGTGCTTCTGATGGAGGGA	115804
QY	1955	TGAAGGGAAGCAATACGGAAGAGAGAGAGATTTTAGGAAATATTAGGTCAAGCCCTAG	2014	QY	3035	TCAGGTACGGGAAGAACCGGGCAGCTCAGCTGGACCCGACTGCCCAAGGTTTCAAGAA	3094
Db	114746	AAATGATAGACAGTCAGGAAGAGTAANAATAGGCTCTGGGCAACAGGCGAG-----	114798	Db	115805	CCAGAGGGCGGACAGACTGGTCAACTTAACCTGGACTAGCTACCAAGGGGTTCAAAA	115864
QY	2015	ACAGTCAGGGAACCTGGGCAATAGGACCCCACTGACAGAGGACCAATGTGCATATTGTAA	2074	QY	3095	CTCCCGACCATCTTTGACGAAGCCCTACACAGAGACTCGGCCAATCTCAGGATCCAACA	3154
Db	114799	--TGAAACCCCGAGGTGGCAGAAAGATACCACTGGAAAGAGCAATATGCACCTATTGCAA	114856	Db	115865	TTCCCGACCATCTTTGACGAGGCGCTCCATCGGATCTCGGCTTTTCTGCTGCTGAAA	115924
QY	2075	AGAAAGGACACTGGGCAAGGAACTGCCCAAGAGGGAACAAAGGACCAAGGATCCT	2134	QY	3155	CCCTCAGGTGACCTCTCCAGTACGTGGATGACCTGCTTCTGCGGGAAGCCACCAACA	3214
Db	114857	AGAAAGGACACTGGGCTAGAGATTGCCCTTAAAAA---ACGGAGCGATCCTCAAGGTCT	114913	Db	115925	CCCTCAGTCTACCTACTACAGTATGGATGATCTCTGCTGCGCGGCTCTCGAAGGA	115984
QY	2135	AGCTCTAGAGAGATTAAGATTAGGGAGACGGGTTCCGACCCCTCCCGAGCCAG	2194	QY	3215	GSACTGCTTAGAAGGCAAGAGGACATCTGCTGGAAATTTGCTGCACTTAGCTACAGAGC	3274
Db	114914	GACCTTAGAG-----ATGATTAGGGAAGTCGGGGCTCAGACCCCTCTCTGAGCCTAG	114967	Db	115985	GCTGTGTACACGAGAACTGAGAGGCTCTTGCAGAACTGAGTGACTTGGGGTATCGAGT	116044
QY	2195	GTTAACTTTGAAGGTGAGGGGCAACAGATTGAGTCTCTGTTGATACCGAGCGAAACA	2254	QY	3275	CTCTGTAAAGAGCCAGATTTTCAGAGAGAGGTAACACTTTGGGGTACAGTTTTCG	3334
Db	114968	GTTAACTTTGCTGAGGGGACTCCGCTCACTCTCTGATAGACACCGGAGCAGAGCA	115027	Db	116045	TTGGGCTTAAGAGGCAAAAATTTGTCAACTGAGGTAACTTCTGCTGGGTTATACCTCCG	116104
QY	2255	TTCACTGCTACTACAGCCATTAGGAAACCTAAAGATTAATAATCTTGGGTGATGGTGC	2314	QY	3335	GGAGGCGACGATGGCTGACGGAGGCAAGGAAACCTGTAGTCAGAGTACCGGCCCC	3394
Db	115028	TTCACTGCTACTACAGCCCTTAGGCAAGCTAGGCTCTAAAGAGACCATGTTGATTGGAGC	115087	Db	116105	AGGGGCAAGAGATGGCTCAGAGGCGCCGGAAGAGACTGTTATGATGATCCCATGCC	116164
QY	2315	CACAGGCAACACAGTATCCATGGACTACCCGAAGACAGTTGACTTTGGAGTGGGACG	2374	QY	3395	AACACAGCCAAACAAATGAGAGAGTTTTGGGACAGCTGGATTTTGCAGACTGTGAT	3454
Db	115088	CACCTGGTAGTAAATTTTACCCCTGGAGACCGAAGAGCCCTACAGATAAACAAGACAT	115147	Db	116165	AACTACCCACGGCAGGTAGCTGAGTTTCTGGGACTGCTGGCTTTTGTAGACTCTGGAT	116224
QY	2375	GGTAACCCACTCTGTTCTGCTGATACCTGAGTGGCCAGACCCCTCTTAGGTAGAGACTT	2434	QY	3455	CCGGGTTTGGACCTTAGGACCCCACTCTACCCGCTAACCAAGAAAGGGAAT	3514
Db	115148	AGTACTCATCTCTCTGCTGATACCTGAGTCTCTGCTCCCTCTTGGGCGGATCT	115207	Db	116225	TCCAGGCTTTGCAACCCCTAGCAGCACCTCTATATCTTGTAGTAAGAGGGTTTCTCTT	116284
QY	2435	ATTGACCAAGATGGAGCACAATTTCTTTTGAACAAGGGAACACAGAGTGTCTGCAAA	2494	QY	3515	CTCCTGGCTCTCTGAGCAGCAAGGAGGCAATTTGATGCTATCAAAAAGGCGCTGCTGAGCGC	3574
Db	115208	GCTAACCAAACTAAAGGCTCAAGTCCAAATTTACTTCAAGAGGCGCCACAAAGTGGGG	115267	Db	116285	TGAGTGAAGAGAGAGCACCNAAGAGCTTTTGGGCTATCAAGTCTCTCTAATGACTGC	116344
QY	2495	TAAACAACCTATCACTGTTGACCTTCAATAGATGACCAATATCGACTATCTCTCC	2554	QY	3575	ACCTGCTCTGGCCCTCCCTGACGTAACTAAACCTTTTACCTTTATGTGGATGAGCGTAA	3634
Db	115268	AAAAGCCCCCTTGCCTCTGCTTGTCTTCAACACAGAGAGAAATATCGTTGCAATGAAGA	115327	Db	116345	CCCCGCTAGCAATTAACAGACTTGAATAAGCCCTTTCCTCTATATGTGGAGAGAGC	116404
QY	2555	CCTAGTAAAGCTGATCAAAATATACAATTTCTGTTGGAACAGATTTCCCAAGCCTGGC	2614	QY	3635	GGGAGTAGCCCGGGAGTTTAAACCAACCTAGGACCATGAGAGAGAGCTGCTGCGCTA	3694
Db	115328	GCAACCCAA---AAATGAGTCTCTTCAAGCTTGGCTTAAGTCTGCTTCCCAATGTGGGC	115384	Db	116405	GGGTGTAGCCAGGGGAGTGTGACACAAGCACTGGGACCTTGGAGAGAGACCTGTAGCCCTA	116464
QY	2615	AGAAACCGGAGGTGGTGTGGCAAGCAAGTTCCTCCCAACAGTTATTCAACAGTGAAGC	2674	QY	3695	CCTGTCAAAGAGCTCGATCCTGTAGCCAGTGGTTGGCCCATATGCTCTGAAGGCTTATCGC	3754
Db	115385	AGAACAGAGGAATGGGTTGGCTTAACAAGTGCCTCCGGTTGTGGTAGAAGCTTAAAGC	115444	Db	116465	TTTGTCAAAGAAATTTAGATCCGTTGTAGTGGATGGCCCACTGCTGAAAGCTATTGCG	116524
				QY	3755	AGCTGTGGCCATACCTGGTCAAGGAGCGCTGACAAATTTGATTTTGGGACAGAAATATACTGT	3814

5891 TCAGATCAGTTATTCCTAGTCTGACCTCAACCCAGATATCCTCCATGCTCAGGATTTT 5950
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118772 ATGTTTCCCGTTCAGGTCAGAGCAAAAGGCTTCAACGAGAATGTCGAGGGGCATCAG 118831
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119243 CAAAGGTCCAGCGCTACCGACTCCCACTCAACGACCCCAATAGTGTACCTTCCC 119302
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119303 TAGGACTAATCTCCCTCATAAAGCTACTTGGCTTCCCGCCCTAGTACAG 119362
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119540 ACAGAAAGTTGACTCTGCAGCAGTTTCAGGAAGGCGCTTGTGTTGGCCAGGTACCTC 119599
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119947 --CTAGTGCAGCTATGGATGTTGATCTTAGAACTATAGAACAGTCTTATAACCAAAATAG 120004
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7178 TATTCTTAAAGAGGAGGATTTATGTTAGCTTGAAGAGGAAATGCTGTTTATGTTG 7237
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7238 ATCATTACAGGGCCATCAGAGACTCCATGAACCAAGCTTAGAGAAAGGTTGGAGAGGCTC 7297
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7358 TGGCTACCTTCTTCTGCTTTTAAACAGGACCTTTAATAGTCTCTCTCTCTCTTACTCAG 7417
120245 TCACACTCTCTCTCCACCATAGCAGGACCTTTGATTACTCTTATGCTTTTGTCTACTT 120304
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; APPLICANT: Laeng, Pascal
; APPLICANT: Palfreyman, Michael
; APPLICANT: Rajan, Prithi
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Best Local Similarity 60.1%; Pred. No. 0;
Matches 4346; Conservative 0; Mismatches 2582; Indels 299; Gaps 33;
QY 471 CCGTCCGACCTCTTTTGCCTGCTTGTGGAAGACGTGACGGGTCACTGTGCTCGATC-T 529
DB 113271 CCACTGATCTCTGAGTTGCTTGTGTCGACGCGAAGTCGCGCGCTTTTGGTTCTT 113330
QY 530 GTTGGTTTCGTTTGTGTGCTTTGCTGTGTGTCCTTGTGTCTACAGTTTAAATATGGG 589
DB 113331 TTTTGTCTTAGTCTCGTGTGCTCTTGTGTGCTACTATTGT----TCTGAAATGGG 113386
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DB 113387 ACAATCTGTGCCACTCCCTTTCTCTAACTCTGGAGCATTTGAAGAGGTGCGGTCTAG 113446
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DB 113447 AGCTCAACACGAGTCGTGTGAGGTGAGAAAGGTCCGTGGCAGACCTTTTGCACCTCCA 113506
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DB 113567 CGCGCTCAGCGCAATTTGTTTTCAGGAGGAA---GGGGGTTCACCTTCAGATCCCTCA 113623
QY 830 TATCCTTACGTGCAAGATTTTGCAGAGGATCTCCCGCATGGTTTAAACCATGGCTGAA 889
DB 113624 CATTTGACCTGGCAGAAATCTGTCCAATTCACCTCCGTGGGTCAAGCCTTG----- 113677
QY 890 TAAAGCAAGAACCCAGGTCCCGCAATTTCTGGCTCTTGGAGAGAAACAAACATCCGC 949
DB 113678 ---GACCCCAAATTTCTGAAACTGACGGTCCGGTTTGCCAGTCTGATCGACCGGAAA 113734
QY 950 TGAAGAGTCAAGCCTCTCTCTCATATCTACCCGAGATTTAGGAGCCACCGCTTGGCC 1009
DB 113735 GTCAGCCCGTCAAGTCCCGCCCAAGATTTATCCAGAGATTTGACGACCTCTC---TGGAT 113791
QY 1010 GGAACCCCAATCTGTTCCCGCCACCCCTTATCTGGCACAGGTGCGCGAGGGGACCTTT 1069
DB 113792 GGAATCCCAACCTCCCGCTTATCCCTGCCCCAGAGCACCTGAGCCGCCCCACACAC 113851
QY 1070 TGCCCTCTCTGAGCTCCCGCGTGGAGGACCTGCTCGAGGACTCGAGCCGAGGGG 1129
DB 113852 GGGACCAAT---AGCGAGGGGCTCAGGACCGCGGGGGGACTCGGAGCCGACGAGG 113908
QY 1130 CGCCAACCGGAGCGACAGACGAGATTCGGCAATTA-----CCGCTGCGCAGC 1178
DB 113909 CCGAAGCCCGGGAGAGGGGGCGGATTTCAACAGTTGCTTACCACCTTAGAGCAC 113968
QY 1179 TAGGCCCCCACCACCGGGGGCCCAAT---TGCAGCCCTCCAGTATTTGGCCCTTTTC 1234
DB 113969 TGTGGAGGGCCACGCGCAGGACCCCAATGATCTCATTTCTTTACGACTGTGCTTTTTC 114028
QY 1235 TTTCTGAGATCTCTATAATTGGAATACTAACCATCCCTTTTCTCGAGGATCCCCAAGC 1294
DB 114029 CTCTTCTGATTTATATAATTGGAATACTAACCATCCCTTTTCTAGAGAACCCCTCTGG 114088
QY 1295 CTTCAAGGGTGTGGAGTCCCTTATGTTTCTCTCAACGACCTTCTTGGATGATTTGTC 1354
DB 114089 GCTTACTGGGCTCTTTGAGTCACTTATGTTTCTCCCATCAACCCACTTTGGGATGATTTGTC 114148

QY 1355 ACAGCTGTGTCAGACACACTTCTCAAAACGAGAGCGAGAGAGAAATTTCTATTAGAGCTAG 1414
DB 114149 GCAGCTTTTGCAGGTTCTTTTACACAGAGGAAAGAGAAATCTCTGATGAGCGGAG 114208
QY 1415 AAAAAATGTTCTTGGGGCGACGGGCGACCCACGGGTGCAAAATGAGATTGACATGGG 1474
DB 114209 AAAAAATGTTCTGGGAGAGGACGCGACACCCCACTGCCCTCCCTAACCTCGTGAGAGGC 114268
QY 1475 ATTTCCCTTAACCTCGCCCGGTTGGGACTACAAACGCGTGAAGGTAGGAGAGCTTGAA 1534
DB 114269 TTTCCCTTGAACCCGCCCACTGGGACTACAAACCGCAGAGGTAGGGAGCGCTCTCT 114328
QY 1535 AATCTATCGCCAGGCTCTGTGGCGGGTCTCCGGGCGCTCAAGACGGCCCACTAAATTT 1594
DB 114329 TGTCTATCGCAGACTCTAGTGGCAGGTCTCAGAGGAGCGCTAGACGGCCCACTAAATTT 114388
QY 1595 GGCTAAGGTAAGAGAGTATCGAGGACCGAATGAACCCCTCTGTTTCTTTGAGAG 1654
DB 114389 GGCTAAGGTAAGAGAGTCTTCAGGGGCGAGACTGAACCACTCAGTCTTCTCTTGAGCG 114448
QY 1655 GCTCTTGGAGGCTTTCAGGCGGTACACCCCTTTTGTATCCCACTCAGAGGCCCAAAAGC 1714
DB 114449 TCTAATGGAGGATATAGAGGTACACCCCTTTTGACCCCTTGTGAGAGGGCAGAGAGC 114508
QY 1715 CTGAGTGGCTTTGGCTTTTATAGGACAGTCAGCTTGGATTTAGAAAGAGCTTCAGAG 1774
DB 114509 CGCTGTAGCCATGGCCTTCATTGGTCAGTCCGTTCOCGACATTAAGAAAAAGCTGCAAG 114568
QY 1775 ACTGGAAGGTTTACAGGAGGCTGAGTTAGCTGATCTAGTGAAGGAGGAGAGAAAGTATA 1834
DB 114569 GCTGGAGGGGCTCCCAAGATCATACGCTCCAAGATTTAGTAAAGAGACGAGAGAACTCTA 114628
QY 1835 TTTACAAAGGGAGACAGAGAGAAAGGAAACAAAGAAAGAGAGAGAAAGAGAGAAAG 1894
DB 114629 TCTAAGAGGAGAAACAGAAAGAGAGAGGCGGAGAGAGAGAGAAAGAAATGAGAGAG 114688
QY 1895 GGAGGAAAGACGCTAATAAACGCGAAGAGAAATTTGACTAAGATCTTGGCTGCAGTGGT 1954
DB 114689 GGAATAATAGCG---GGGATTTTCAGGAGAGAAATTTGAGTAAAAATTTTGGCCGCACTGT 114745
QY 1955 TGAAGGAAAGCAATATACGGAAGAGAGAGAGATTTTAGGAAAAATTAGTTCAGGCCCTAG 2014
DB 114746 AAATGATAGACAGTCAGGAAAAAGTAAATAGGGCTCTCTGGGCAACAGGCGAG--- 114798
QY 2015 ACAGTCAGGGAACCTTGGGCAATAGGACCCACTCGACAAAGGACCAATGTGCAATTTGTA 2074
DB 114799 ---TGAACCGCAGGTGGCAGAAAGATACCACTGGNAAGAACCAATGACCATTTGCAA 114856
QY 2075 AGAAAGAGACACTGGGCAAGAACTGCCCCAAGAGAGGAAACAAAGGACCAAGGATCCT 2134
DB 114857 AGAGAAAGGACACTGGGCTAGAGATTGCCCTTAAAAA---ACGGGAGCGATCCAAGTCTCT 114913
QY 2135 AGCTTAGAAGAGATAAAGATTTAGGGAGACGGGTTTCGGACCCCTCCCGAGGCCAG 2194
DB 114914 GACCCCTAGAAG-----ATGATTAGGGAAGTGGGGCTCAGACCCCTCCCTGAGCCTAG 114967
QY 2195 GGTAACTTTGAAGGTGGAGGGCAACCACTGAGTTCTCTGTTTGTATACCGGAGCGGAAACA 2254
DB 114968 GGTAACTTTGTCGAGGGGAGACTCCCGTCAACTCTCTGATAGACACCGGAGCAGAGCA 115027
QY 2255 TTTGAGTGTACTACAGCCATTAGGAAAACTAAAAAGATAAAAAATCTCTGGGTGATGGGTGC 2314
DB 115028 TTTGAGTGTACTACAGCCCTTAGGCAAGCTAGGCTCTAAAAAGACCATGTTGATTTGGAGC 115087
QY 2315 CACAGGGCAACCAAGATATCCATGGAATACCCGAGAAACAGTTGACTTGGGAGTGGGAGC 2374
DB 115088 CACTGTGTAAATTTTACCCCTTGGACGACCGAAACGAGCCCTACAGATAAACAGAAACAT 115147
QY 2375 GGTAAACCACTGTTTCTGTCATACCTGAGTGCACGACCCCTCTTATAGGTAGAGACTT 2434
DB 115148 AGTGACTCAATCTCTCTGATACCTGAGTGTCTCTGCTCCCTCTTGGGGCGCATCT 115207

QY	2435	ATTGACCAAGATGGAGCACAAATTTCTTTGACAAAGGGAAACCGAAGTGTCTGCAAA	2494	Db	116285	TGAGTGGAAAGAGAGACCAAAAGAGCTTTTGAGGCTATCAGTCTCTTAATGACTGC	116344
Db	115208	GCTAACCAAACTAAAGGCTCAAGTCCAAATTTACTTTCAGAAGGCCCAACAAGTGGGG	115267	QY	3575	ACCTGTCTCTGGCCCTCCCTGACCTAACTAAACCTTTTACCTTTATGTGTGATGAGCGTAA	3634
QY	2495	TAACAAACCTATCAGTCTGTGTGACCTCCAAATTTAGATGACGAATATCGATATCTCTCC	2554	Db	116345	CCCCGGCTAGCATTAACAGACTTGACTAAGCCCTTCCTCTATATGTGACGAGAGAGC	116404
Db	115268	AAAAGCCCCGTTGCTCTGCTTGTCTCAACACAGAGGAAGATATCGTGTGATGAAGA	115327	QY	3635	GGAGTAGCCCGGGAGTTTTTAAACCAACCCCTAGGACCAATGGAGAAGACTGTGCGCTA	3694
QY	2555	CCTAGTAAAGCCTGATCAAAATATACAAATTTCTGTTGGAACAGTTTTCCCAAGCCTGGGC	2614	Db	116405	GGGTGTAGCCAGGGAGTGTGACACAAGCACTGGGACCCCTGGAAGAGACTGTAGCCTA	116464
Db	115328	GCAACCCAA--AAATGAGTCTCTTCAGGCTGGCTAACTGCGTTCCCAATGTCTGGGC	115384	QY	3695	CCTGTCAAGAAAGCTCGATCCCTCTAGCCAGTGTGSCCCATATGCCCTGAAGGCTATCGC	3754
QY	2615	AGAAACCGCAGGATGGGTTTGGCAAGCAAGTTTCCCCCAACAAATTTCAACTGAAGGC	2674	Db	116465	TTTTGTCAAGAAATTAGATCCCTGTGCTAGTGAATGGCCCACTGCTGAAAGCTATGCT	116524
Db	115385	AGAACAGCAGGAATGGGTTGGCTAAACAAGTGCCTCCGTTGTGTGAACCTTAAAGC	115444	QY	3755	AGCTGTGGCCCATACTGTCAAGGACGCTGACAAATTTGACTTTTGGGACAGAAATATACTGT	3814
QY	2675	CAGTGCCACACAGCTGTCACTGACAGAGTACCCCTTGAGTAAAGAACTCAAGNAGAAAT	2734	Db	116525	GGCAATGGCCCTCTGTATCAAGATGCTGACAAATTTGACAATGGACAACACAGGTGACTGT	116584
Db	115445	TGATGCCACCCCACTCTCGTAAAGCAATACCCCATGAGCAAGAACTAGGGAGGCGAT	115504	QY	3815	AATAGCCCCCATGCAATTTGGAGAACATCGTTTGGGAGCCCCCAGACCGATGGATGACAA	3874
QY	2735	TGSCCGCATGTCACAAAGATTAAATCCCAACAGGGCATCTTGTCTTCCAAATCTCCCTG	2794	Db	116585	TGTGGCCCTCATGCTTGGAAAGTATCGTGGGACGCCACCTGACAGATGGATGACAA	116644
Db	115505	CGGCGCTCATATCCAGAGTTGTAGACCAAGGATTTTGTAGTCCCTGTGATCCCTG	115564	QY	3875	CGCCCGCATGACCACTATCAAGCCCTCTTCTCACAGAGAGGTCACGTTTGGCTCCACC	3934
QY	2795	GAATACTCCCTGCTACCGGTTAGAAAGCCCTGGGACTAATGACTATCGACAGTACAGGA	2854	Db	116645	TGCCCGAATGACACTATCAGAGCTTGTCTGCTAAATGAGCGGTAACTTTTGGCCCTCC	116704
Db	115565	GAATACACCACTTCTGCGGTTTCGAAACACAGGACCAATGACTATCGCCAGTGAAGA	115624	QY	3935	AGCGCTCTCAACCCCTGSCCACTCTTCTGCTGCTGAAGAGACTGATGAACACGATGACTATGA	3994
QY	2855	CTTGAGAGAGGTCAATAAAGGGTGCAGGATATACCCCAACAGCTCCCGAACCCCTTATA	2914	Db	116705	TGCCATCTCAACCCCTGSCCACTCTTCTGCTGCTGAAGAGACTGATGAACACGATGACTATGA	116764
Db	115625	CTCCGGGAGTTTAAACAAAGGGTCTTGGACATTTACGCCACAGCTCCGCAACCCATCAA	115684	QY	3995	TTGCGATCAACTATTTGATTGAGGAGACTGGGGTCCGCAAGGACTTACAGACATACCGCT	4054
QY	2915	CTCTTGTGTGCTCTCCACCCCAACGGAGCTGTATACAGTATTTGACTTTAAAGGATGC	2974	Db	116765	ATGTACAGACATCTCTGCTGAAGAGACTGGGACCCAGAAGAGACTGACTGACCAACCCCTG	116824
Db	115685	TTTATTAAGCTCTCTCCACCTGAGAGAACATGTGTATACAGTCTTGGACTTTAAAGATGC	115744	QY	4055	GACTGGAGAAAGTGTCTAATCTGTTCTGACTGAGGAGCAGCTATGTGTGTGAGAGTAAAG	4114
QY	2975	CTTCTCTGCTGAGATTACACCCCACTAGCAACCACTTTTGGCTTTCGAATGGAGAGA	3034	Db	116825	GCCTGG---AGCTCCCAAGTTGGTATACGATGGCAGCAGTTTCTGTATAGAGGGGAGCG	116881
Db	115745	CTTCTTTTGGCTTGGCTTGACCTTACAGTACAGTCTGCTGTTTGGCTTTGATGAGGGA	115804	QY	4115	GATGGCTGGGGCGGCGGTGGAGCGGACCCGACCATCTGGGCCACGAGCCTGCGCGA	4174
QY	3035	TCCAGGTACGGGAAGAACCGGGCAGCTCACCTGGACCCGACTGCCCCCAAGGTTCAAGAA	3094	Db	116882	AAAGCTGGAGCTGCGGTGGACGGGAAAAGGTAATTTTGGCAAGCGCTTGGCTGTA	116941
Db	115805	CCCAAGGGCGGACAGACTGCTCAACTAACTGAGTACAGTACCAAGGGGTTCAAAA	115864	QY	4175	AGGAATCTTACGACAAAGGCTGAGCTCATGGCCCTCACGCAAGCTTTTGGGCTGGCGGA	4234
QY	3095	CTCCCCGACATCTTTTGAAGAGCCCTACACAGAGACTGCGCAACTTCAGGATCCAAACA	3154	Db	116942	AGNAAGCTCGCACAAAGGCTGAATTTATAGCACTTATACAGCCCTCCGAGAGGCTAA	117001
Db	115865	TTCCCCCACCCTGTTTGAAGAGGCTCCATCGGGATCTCGGCTTTTCTGTCTCGAAA	115924	QY	4235	AGGAAATCCATAAACAATTTATACGACAGCAGGATGCTTTCGGACTGACACAGTACA	4294
QY	3155	CCCTCAGGTGACCTCTCCAGTACGTGATGACTGCTTCTGCGGGAGCCACCAACA	3214	Db	117002	AGGTAAGATCGTTAACTACTACACTGACAGCCGCTATGCTTTTGTACTCCGACACATCCA	117061
Db	115925	CCCTCAGCTTACCTTACTACAGTATGTGATGATCTCTTGTGCGGGGCTCGAAGGA	115984	QY	4295	TGGGGCCATCTATAAACAAGGGGTTGCTTACCTCAGCAGGGAGGAAATAAAGAACAA	4354
QY	3215	GGACTGCTTAGAAGCAGCAAGGCACTACTCTGGAATTTGCTGACCTTAGGCTACAGAGC	3274	Db	117062	TGGGGCCATCTTACAGGCGAGGAGGCTTATGACTTCGGCTGGTAAAGACATTAATAACA	117121
Db	115985	GCTGTGTACCAAGGAACTGAGAGGCTCTTTCGACAGCTGAGTACTTGGGGTATCGAGT	116044	QY	4355	AGAGAAATTTCTAAGCCCTATTAGAACGCGTACATTTTACCAAAAAGGCTAGCTATTATACA	4414
QY	3275	CTCTGCTAAGAGGCCCAAGATTTCAGGAGAGAGTAAATCATCTTGGGGTACAGTTTGGC	3334	Db	117122	AGAAGAAATTTCTGGCCCTGTTTGGAGCCATACATGCACTTAAAGAGGTAGCCATCATCCA	117181
Db	116045	TTCCGCTAAGAAGGCACAAATTTGTCAAACTGAGGTAACTTACCTGGGGTATACCCCTCG	116104	QY	4415	CTGTCTGGACATCAGAAAGCTAAAGATCTCATATCCAGAGGAAACCGAGTGGCTGACCG	4474
QY	3335	GGAAGGCGAGTGGCTGACGAGGACCGAAGAACTGTAGTCCAGATACCGGCC	3394	Db	117182	CTGCCCCGCCACCAAGAGAGAGAACTTGGTGGCCCAAGGGCAACCGAATGGCAGACTC	117241
Db	116105	AGGGGGCAAAAGATGGCTCAAGAGGCCCGGAAGAAAGTGTATGATGATCCCATGCC	116164	QY	4475	GTTTGGCCAGGACGCCCGGCTGTTTAACTTCTGCTCTATATAGAAATGGCCCAAGC	4534
QY	3395	AACCAAGCCAAACAAATGAGAGAGTTTTTGGGACAGCTGGAATTTTGCAGACTGTGGAT	3454	Db	117242	AGTGGCAAAACAAGTTGCTCAAGGGG-----CCATGATCTTAACTGAAAGGTGATCCAC	117297
Db	116165	AACACCCCAAGGAGTACGTGAGTTTCTGGGACTGCTGCTTTTGTAGACTGTGAT	116224	QY	4535	CCCAAGAACCCAGACGACAGTACACCTTAGAAGACTGGCAAGAGATATAAAGAGATAGACCA	4594
QY	3455	CCCGGGTTTGGACCTTTAGCAGGCCCACTCTTACCCGCTAACCAAGAAAGAGGGAAT	3514	Db	117298	CCAAAAGCCCTGA-----GGATGAGAGGTATTAACNTAAAGA	117334
Db	116225	TCCAGGCTTTGCAACCCCTAGCAGCACCCTTATATCTTTGACTTAAGGAAGGTTTCCCTT	116284	QY	4595	GTTCTCTGAGACTCCGGAAGGGACCTGCTATACCTCAGATGGGAAGGAAATCTCTGCCCA	4654
QY	3515	CTCTGGGCTCTGTAGACCCAGAGGCAATTTGATGCTATCAAAAGGCCCTGCTGAGCGC	3574				

Db	117335	GCTATTGTGGACGAGTGATCCCTCCCATACATCTTTTGAAGGGAATAAGATTGACTCC	117394	QY	5712	-----GTTCTTACTCTGTCTATTAACCTCTCAGACTAATGTT	5748
QY	4655	CAAGAAGGTTTAGAATATGTCACACAGATACATCGTCTAAACCCTAGGAACCTAAACA	4714	Db	118472	CCACCTGAGCCTAGGGAACCAATACCCTCATCTCCATTCACAGCTTGGGAAGTGC	118531
Db	117395	CGAAGAAGGAATAAATTTGTGAAGGACTACACCAATTCACCCACCTGGAGTTGAAAA	117454	QY	5749	ATGCGCATAGGAGACGCTGAACTCCCATAAACCTTATCTCTCACCTGGTTAAATTACT	5808
QY	4715	CTGCGAGCAGTTGGTCAGAACATCCCTTATCATGTTCTGAGGCTACACGAGTGCTGCA	4774	Db	118532	TTAATGAGGAGGGAACATTTGTGGGCAACCACTGCGAGTCAATCCCTCTCGACTTGGT	118591
Db	117455	AATGATGAGACTAAATTAAGAAATTCGCGATACCAAGTCCCAACTGAAGTCAGTGGCTCA	117514	QY	5809	GACTCCGGCACA-----GGTATTAAATCAACAACACTCAAGGGGAGGCTCC	5855
QY	4775	CTCGGTGGTCAACATTTGTGCGCTGCCAGCTGGTGTAACTTAATCCTTCCAGATGCC	4834	Db	118592	GGCCTGATCTCACACTGACATCTGTAACTAGTGTAGTGGAGGATCCACCAATGGGACTCC	118651
Db	117515	AAAGATTATAGACTCTCTGCAAAACCATGTGCATTCACTAATGGGACTAAAAGCCTACAAAG	117574	QY	5856	TTTAGGAACCTG-----GTGGCTGATCTATACGTTTGGC	5890
QY	4835	TCCAGGGAAGAGACTAAGGGGAAGCCACCAGGCGCTCACTGGGAAGTGGACTTCACCTGA	4894	Db	118652	CTGATCATACCGATCTTAGTAACCAACCCCTGAAGAGCGGTGTGCCCAACCGGATAG	118711
Db	117575	ACCTGGAAGAGACAACGGGAGACCGTCTTGAGTGTATTGGAGGTAGATTTTACTGA	117634	QY	5891	TCAGATCAGTTATTCTTAGTCTGACCTCACCCCCAGATATCTCCATGCTCAGCGATTTT	5950
QY	4895	GTTAAAGCCGGCTAAATAACGGAACAAATACCTATTGGTTTTGTAGACACCTTTTCAGG	4954	Db	118712	GGAGCACATATTGGTGTTCGGGGCAGTTTACCGAGCTAATCTTAGAGCTGCACAATTTT	118771
Db	117635	AGTTAAACCTGGAATGTATGTTAAACAAGTATCTGTAGTATTGTAGACACTTTTTCAGG	117694	QY	5951	ATGTTTGGCCAGGAC-----CACCAATAATGGMAAACATTGCGGAAATCCACAG	6001
QY	4955	ATGGGTAGAGGCTTATCTCTAAGAAAGAGACTTCAACCGTGGTGGCTAAAABAATACT	5014	Db	118772	ATGTTTGGCCTGGTCAGGTCAGAGCAAAAGGCTTCAACGAGAAATGTGAGGGGATCAG	118831
Db	117695	ATGGGTGAGGGCTTTCCCACTAAAACCTGAGACTGCCAGATTGTGGCCCAAGAAGATCCT	117754	QY	6002	ATTCTCTTTGTAAACAATGGAACTGTGTAAACCTCTAATGATGATATTTGGA--	6053
QY	5015	GGAGAAGATTTTCCCAAGATTGGAATACCTAAGGTAATAGGTCAGACAATGGTCCAGC	5074	Db	118832	ATTACTTTTGTGTTAAATGGACATGTGAAACGACAGGGGAAGCTTACTGGAAGCCCTCCT	118891
Db	117755	TGNAAGAAATCCTGCCAAGATTTGAATCCTTAAGGTAAATCGGTCGATTAATGGACCAG	117814	QY	6054	-----ATGGCCAACCTCTCAGCAGGATAGGTAAGTTTTCATTATGTCACACCC	6102
QY	5075	TTTTGTGCCCCAGGTAAAGTCAGGACTGGCCAAAGATATTGGGGAATTGATTGGAACCTGA	5134	Db	118892	CTGACTGGGACCTAATACCGGTAAACCGAGGAAGTGGCTATGATAGGTCAAAACGAGGAG	118951
Db	117815	CTTTGTGCCCCAGTAAAGTCAGGGCTTGGCCACTCAGTTGGGCATCGATTGGAAATTACA	117874	QY	6103	TATACCAAGCTCTGGACAATTTAATTACCTGACTCGATTAGAACTGGAAAGCCCAAG---	6159
QY	5135	TTGTGCATACAGACCCCAAGCTCAGACAGGTAGAGAGGATGAATAGAACCTTAAGA	5194	Db	118952	AAAGAAACCCCTATAAATATCCAGAGATGGTGGCTTTTAAACACAGCCCCCAGGAC	119011
Db	117875	CTGTGCTTACCGCCCTCNAAGCTCAGACAGGTAGAGAGGATGAATAGGACCTTAAAGA	117934	QY	6160	--TGCTCTCTTTCAGACCTTAGATTACCTAAATAAATAGTTTCTACTGAGAAAGGAAACAAG	6217
QY	5195	GACCTTACTATAATTGACCGCGAGACTGGCGTTAATGATTGGATAGCTCTCTCGCCCTT	5254	Db	119012	CATGCAAGGTAATATCTGCAACCCCTACTTTATAAAGTTCAACCGAGAAAGGGAACAAC	119071
Db	117935	GACCTTGACTAATATTAGCCATTGAGACCGCGGGAAGACTGGTGGCTCTCTCTCTCT	117994	QY	6218	AAAAATCTAAATGGGTAAATGTTATGCTTTGGGAATGGTATATATTATGGAGGCTCGG	6277
QY	5255	TGTGCTTTTATAGGTTTATGGAACACCCCTGAGACAGTTTGGCTGACCCCTATGAATTACT	5314	Db	119072	ACCGT---CTAAGTTGGCTTAAAGGAAATAGTGGGGTTGGCGAGTATA---CTTTCAC	119125
Db	117995	TGGCTCTTCCGAGCCGGAACACACCTCGACGTTTTCGGGCTCACTCCTTTTGAAGTTCT	118054	QY	6278	GTAAACAACACGAGCTCCATTCTAACTATTTCGCTCAAAAATAAACACAGCTGGAGCCTCCAA	6337
QY	5315	CTACGGGGACCCCCCATTTGTTAGAAATTG-----CTTCTGTACATAGTCTGACGT	5368	Db	119126	TAAAGATCCTGGGTTCAATTTTCAAGATCAGGCTGACAGTGAAGACCTGGCGGTGACA-	119184
Db	118055	GTATGGAGGACCTCCCCCTTTAATGGAAGCTGGTGGAAATTTGGGTTTCCGGCTCTGACCC	118114	QY	6338	TGGCTATAGGACCAATACGCTTTGACGGGTCAAGAGACCCCAACCCAAAGGACCAAGGAC	6397
QY	5369	GTGCTTTCCAGCCTTTGTTCTTAGGCTCAAGGCACATTGAGTGGGTGAGACAACGAGC	5428	Db	119185	--CCTGTTGGGCCCAACAGGTCTTATAGAACAGGGCCCCCAGTCGTACCGGCTCCCC	119242
Db	118115	TGTCCTTACCTCTCTTTGCTTATTCATTTAAAGGCCCTTAGAAGTGATTAGACCAGAT	118174	QY	6398	CA-----TCCTCTAACATAACTTCTGGATCAGACCC	6428
QY	5429	GTGAGGCAACTCCGGGAGCCTTACTCAGGAGGAGGAGACTTGCAGATCCCAATCGTTT	5488	Db	119243	CAAAGTCCAGCCGTACAGCTCCACCACTCCACAGCCCAACATAGTGGTACCTCCTCC	119302
Db	118175	TTGGGACCACTGAAGGAGCCTATACCCAGGAGCCACCGCAG---TACCCCAACGGTT	118231	QY	6429	CACTGAGCTTAACAGCACACTAAA-----ATGG	6457
QY	5489	CCAAAGTGGAGATTACGTTTACGCTTAGACGCAACCGTCAGGAAACCTCGAGACTCGGTG	5548	Db	119303	TAGGACTAATACTCCCTCATAAAGCTACCTTGGCTTCCCCACCGCCCTTAGGTACAG	119362
Db	118232	CCGAGTTGGAGATAAAGTCTTGTGTCAGACGCGCATCGAACCGGCAGCTCGAGCACAGTG	118291	QY	6458	GGGCAAAACCTTTTATAGCCTCATCCAGGGAGCTTTTCAAGCTCTTAACTCCACGACTCCAG	6517
QY	5549	GAAGGCCCTTATCTCGTACTTTTGAACCAACCAACCGCTGTGAAAGTGTGAAGGAATCTC	5608	Db	119363	AGGACCGTCTGCTCAGTCTACTCCAGGAGCTTTTATAGCTTTAAATAGAACTAAACCTTA	119422
Db	118292	GAAGGACCCATTTTGGTGTACTGACAAACCCCTACTCGGTAAAGTGAACGGGATTCG	118351	QY	6518	AGGCTACCTCTCTTGTGGCTATGCTTAGCTTCGGGCCCACTTACTACTAGAGGATGG	6577
QY	5609	CACCTGGATCCATGCACTCCACGTTTAAACCGGCGCCACCTCCCGATTTCGG-----	5658	Db	119423	ATATGACTCAATCATGCTGGTTATGCTATACCTCTAGCCCCCTTATTATGAGGAATAG	119482
Db	118352	CTCCTGGATCCACGCTCCACGCTCAAGAGGGCCGCAAGTCAAGATGAAGAAACCATGA	118411	QY	6578	CTAGAGAGGGGAAATTCATATGTGACAAAAGAAACATAGAGACCAATGCACATGGGGATCCC	6637
QY	5659	-----GGTGAAGCCGAAAGACTGAATAATCCCTTAAGCTTCGGCTCCATCGCGTG--	5711	Db	119483	CTCAGATCAGGACTTATAATATATTCTTCAGATCATTTCT---CAATGCTCTTTGGGAGAAA	119539
Db	118412	AGACAAATTGGACAGTGGCGCCACTGACAAATCCTCTTAAGCTTCGTTTGTGCGCGAGGCG	118471				

Qy 6638 AAAATAAGCTTACCTTTACTGAGGTTTCTGAAAAGGCACTGATAGGAAAGGTTCCCC 6697
Db 119540 ACAGAAAGTTGACTCTGCGACGCTTTTCAGAGAGGCGCTTTGTTGGCGCAGGTACCTC 119599
Qy 6698 CATCCACACACCTTTGTTAAACACACTGAAGCTTTAATCAAACTCTGAGAGTCAAT 6757
Db 119600 AGGATAAAGGCGCCTCTGTAATCAGACCCAGAACATCCAGTCTAGCAAAAGTGTGTCAGT 119659
Qy 6758 ATCTGGTACCTGGTTATGACAGGTTGGGCTATGATCTGGAATTAACCCCTTGTGTTT 6817
Db 119660 ATCTAGTGCCTCCCTTAGACACAGTATGGGCTGCAATACCGGTCTCCTCTTGTGTGT 119719
Qy 6818 CCACCTTTGGTTTAAACAACTAAAGATTTTTCATTTATGCTCCAAATTTGTTCCCGAG 6877
Db 119720 CTATGCTGTTTAAATAGTTTCCAAAGATTTCTCAITTTGTTGCTCAGTATTCTCTAGAC 119779
Qy 6878 TGTATTACTATCCCGAAAGCAATCTTGTATGATATGACTACAGAAATCATCGACAAA 6937
Db 119780 TCCTGTATCATGATGATAGTCTCTTTTATAGACAAATTTG---AGCGTTGGGTCCGCTGGA 119836
Qy 6938 AGAGAGAACCATATCTCTGACACTTGTGTGATGCTCGGACTTGGAGTGGCAGCAGGTG 6997
Db 119837 GAAGAGAGCCGTTTACCTTAATCTTGGCAGTTCTATTAGGATTTAGGAGTAGCGCTGAG 119896
Qy 6998 TAGGAACAGGAACAGCTGCCCTGCTGCTGATGCTCGGACCAACAGCAGCTAGAACAGGACTTAGTA 7057
Db 119897 TAGGTACAGNAACGCTGCCTTAATTAAGACCCCACTATCTATGAAGAA----- 119946
Qy 7058 ACCTACATCGAATTTGTAACAGAGATCTTCAAGCCCTAGAAAATCTGTCTAGTAACCTGG 7117
Db 119947 --CTAGTGCAGTATGATGATGCTTATAGAACTATAGAACAGCTCTATAACCAAAATTAG 120004
Qy 7118 AGGAATCCCTAACTCTTATCTCAAGTAGTCTTACAGATAGAGAGGTTAGATTAT 7177
Db 120005 AAGAATCTTTAACTTTCCCTGTCGAGGTTGCTACAGAAAGGAGGATTTAGACTTAT 120064
Qy 7178 TATTTCTAAAGAGGAGGATTTATGTGTAGCTTTGAAGGAGGATGCTGTTTTTATGTGG 7237
Db 120065 TATTTCTTAAGAGGAGGATCTGTGCTGCTTAAAGAGAGATGTTGTTTTATGTG 120124
Qy 7238 ATCATTCAGGGGCCATCAGACATCCATGAACAAGCTTTAGAAAGGTTGGAGAAGGCTC 7297
Db 120125 ACCATTCAGGAGTAAATCAAGATTTCTATGGCAAACTTTAGAGAACGCTAGATATAGTA 120184
Qy 7298 GAAGGAAAAGAACTACTCAAGGCTGTTTGGAGGATGTTCAACAGGTCTCTTTGGT 7357
Db 120185 AAAGAGAAAGAAAGGCAACAGGATGTTTCGAAAGCTGTTTAAATAGTCCCTTTGGC 120244
Qy 7358 TGGCTACCTACTTCTCTTTTAAAGGACCTTAAATAGTCTCTCTCTGTTACTCAG 7417
Db 120245 TCACACTCTCTCTCCACCATAGCAGGACCTTTGATTTACTTTTGTCTTACTT 120304
Qy 7418 TTGGGCCATGATTTATTAACAGTTAATTTGCTTCTTATAGAGAACGATAAGTCAGTCC 7477
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Qy 7478 AGATCAGGTTACTTAGACAAACAGTACC 7504
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; Publication No. US20030124704A1
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; APPLICANT: STRITTMATTER, STEPHEN M.
; APPLICANT: CAHE, RICHARD L.
; APPLICANT: SAH, DINAH W.Y.
; TITLE OF INVENTION: NOGO RECEPTOR HOMOLOGS
; FILE REFERENCE: A116US
; CURRENT APPLICATION NUMBER: US/09/972,546
; CURRENT FILING DATE: 2001-10-06

; PRIOR APPLICATION NUMBER: 60/238,361
; PRIOR FILING DATE: 2000-10-06
; NUMBER OF SEQ ID NOS: 19
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QY	3825	CATGCAATTGAGAACATCTGTTCCGGCAGCCCAAGACCGAT-GGATGACCAACCCCGCAT	3883	Dd	172357	CTGAAATGTATGGTAAACAAGTATCTGTTAGTATTTGTAGACACCTTTTCAGGATGGTTG	172416
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QY	3884	GACCCATATCAAGGCTGTTCTCACAGAGAGGTCACGTTGCTTCACAGCCGCTCT	3943	Dd	172417	AGGCATTTCCCACTAAAACAGAGACTGCCCAATTTGGGCCAAGAGATCCTTTGAAGAAA	172476
Dd	171366	GACACATATCAGAGCCTGTGCTAAATGAGCGGTAAACCTTTGCGCCCCCTGCCATCCT	171425	QY	5023	TTTTTCCAGATTTGGAATACCTAAGGTAAATAGGCTCAGACAAATGGTCCAGCTTTGTTG	5082
QY	3944	CAACCTGCCACTCTTCTGCTGAGAGACTGATGAACAGTGAATCATGATTGCCATCA	4003	Dd	172477	TCCTGCCAAGATTTGAAATCCCTAAGGTAAATCGGTTCCGACAAATGGACCGCTTTGTTG	172536
Dd	171426	CAACCCAGCTACCTCTCTCCCTCTAAACAATGATCCGTCCTCCAGTACATCAATGTATGGA	171485	QY	5083	CCAGGTAAGTCAGGACTGGCCCAAGATATTGGGATTTGATTTGGAACTGCATTTGTCAT	5142
QY	4004	ACTAATTGATTGAGAGACTGGGTCCGCAAGGACCTTTACAGACATACCCGCTGACTGGAGA	4063	Dd	172537	CCAGGTAAGTCAGGCTTTGGCCACTCTCAGTTGGGATCCGATTTGGAATTAACATGTGCTT	172596
Dd	171486	CATCCTCGCTGAAGAACTGGGACCAAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG	171545	QY	5143	ACAGACCCCAAGCTCAGGACAGGTAGAGAGATGAATAGAACCATTAAAGAGACCCCTTA	5202
QY	4064	AGTGCTAACTGTTCTACCTGACGGAAGCAGCTATGTGGTGAAGGTAAGAGGATGCTGG	4123	Dd	172597	ACCGCCCTCAAAAGCTCAGGACAGGTAGAGAGATGAATATAGGACCTTAAAGAGACCTTGA	172656
Dd	171546	T---CCAGTTGGTACACGACGCGCAGCTTTCTCTGATAGAGGGGAAGCAAAAGGCTGG	171602				

Qy	5203	CTAAATTGACCGCGAGACTGGGTTTAATGATGATAGTCTCTCGCGCCCTTTGTCCTTT	5262
Db	172657	CTAAATTAGCCATTGAGACCGCGCAGAAAAGACTGGGTGGCTCTCTCTCTCTCTGCGCT--	172714
Qy	5263	TTAGGGTTAGGAACACCCCTGGACAGCTTTGGGCTGACCCCTTATGAAATTACTCTACGGGG	5322
Db	172715	-----CAAAACCCCTGGTCTGGTCTCGGGCTCACTCTCTTTGGAAGTTCTGTATGGAG	172765
Qy	5323	GACCCCTCCCATTTGGTAGAAATTG-----CTTCTGTACATAGTCTGACGTGCTGCTTT	5376
Db	172766	GACCTCCCTCTTAATGGGAAGCTGGTGGAAACAATTAGTTTCCGACTCTGACCTGTCTTAC	172825
Qy	5377	CCAGCCTTTGTTCTCTAGCTCAAGGCACTTGAGTGGGTGAGACAAAGAGGTGGAGGC	5436
Db	172826	CCTCCTCTTTGCTTATTCTATTAAAGGCCCTAAAGTGTATAGGACCCAGATTTTGGGACC	172885
Qy	5437	AACCTCCGGGAGGCTACTCAGGAGGAGGAGCTTGCCAGATCCCATCGTTTCCAAAGTGG	5496
Db	172886	AACGTAAAGCAGCCTATACCCAGGAGCACCGCAG-----TACCCCAACGGGTTCCGAGTTG	172942
Qy	5497	GAGATTCACTCTACGTTAGACGCAACCGCTGCAGGAAACCTCGAGACTCGGTGGGAAGGCC	5556
Db	172943	GAGACAAAGTCTTTGGTCAGAGGCACTCGAACCGGTAGCTTGAAGCCAGGTGGGAAGGAC	173002
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Db	173003	CCTATTGGTGTACTGACAAACCCCTACTCGCGGTAAAGTTGACGGGAATCGCCTCCTGGA	173062
Qy	5617	TCCATGCATCCACAGTTAAACGGCGCCACCTCCCGATTTCGG-----GGT	5661
Db	173063	TCCACGCTCCCAAGCTCAAGAGGCGCGCAGTCAAGATGAAAGAAACCAACGACGAATTT	173122
Qy	5662	GGAAAGCCGAAAAGACTGAAAATFCCCTTTAAGCTTCGCCTCCATCG-----	5707
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Qy	5708	-----CGTGGTTCCTACTCTGTCTCAATAACCTCTCAGACTAATGTTATCGCGAT	5756
Db	173183	GACCTAGGGAAACCTTAACCTCATGTCTCAATTTCAACAGTCTCTGGGAGGTGCTTAATGAA	173242
Qy	5757	AGGAGCAGCTCAACTCCCATAAACCTTATCTCTCAGCTGTTAAATTACTGACTCCGG	5816
Db	173243	AAGAAACAACTGTATGGGCAACCACTGCAGTCCATCCCTCTGGAATTTGGTGGCTGAT	173302
Qy	5817	CACAGGTATTAATATCAACAACTCAAGGGGAGGCTCCTTTAGGAACCT-----	5866
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Db	173423	TATGGGTGTTCGGGCGAGTTCTACCGAGCTAATCTTAGAGCTGCAATTTTTATGTTTGC	173482
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Qy	6010	TGTAACAATGGAACTGTGTAAACCTCTAATGATGGATATTGAA-----ATGGCCCACTCT	6066
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Qy	6771	TTATGACAGGTGGTGGGCACTGTAATACTGGATTAAACCCCTTGTTGTTCCACCTTGTTTT	6830
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Job time : 4181 secs

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Copyright (c) 1993 - 2006 Bioceleration Ltd.
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Run on: February 5, 2006, 06:44:23 ; Search time 1194 Seconds
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
Searched: 6068529 seqs, 41903697 residues
Total number of hits satisfying chosen parameters: 12137058
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1400	17.2	2036	7	US-10-996-217A-8
2	1278.4	15.7	1657	7	US-10-996-217A-7
3	1278.4	15.7	1657	7	US-10-996-217A-9
4	1028	12.6	1557	7	US-10-996-217A-6
5	835.6	10.3	9603	8	US-11-128-061-1069
6	835.6	10.3	9603	8	US-11-128-049-1069
7	287	3.5	177175	8	US-11-121-086-79
8	287	3.5	189993	8	US-11-121-086-78
9	266.2	3.3	55763	7	US-10-972-766-1
10	253.6	3.1	5234	7	US-10-821-234-357
11	218.4	2.7	110711	7	US-10-995-561-13264
12	202	2.5	13187	8	US-11-136-527-3585
13	200.4	2.5	317876	7	US-10-995-561-13227
14	182.2	2.2	203	7	US-10-996-217A-20
15	162.6	2.0	180	7	US-10-996-217A-24
16	153.4	1.9	5569	7	US-10-821-234-231
17	136.4	1.7	581	8	US-11-128-061-1847
18	136.4	1.7	581	8	US-11-128-061-5489
19	136.4	1.7	581	8	US-11-128-049-1847
20	136.4	1.7	581	8	US-11-128-049-5489
21	135.4	1.7	266	7	US-10-996-217A-10
22	121.8	1.5	179666	8	US-11-121-086-67

23	110	1.4	215308	8	US-11-121-086-77	Sequence 77, Appl
24	103.6	1.3	241805	7	US-10-995-561-13215	Sequence 13215, A
25	102.8	1.3	45268	7	US-10-995-561-13203	Sequence 13203, A
26	101.6	1.2	576	8	US-11-128-061-1747	Sequence 1747, Ap
27	101.6	1.2	576	8	US-11-128-061-5389	Sequence 5389, Ap
28	101.6	1.2	576	8	US-11-128-049-1747	Sequence 1747, Ap
29	101.6	1.2	576	8	US-11-128-049-5389	Sequence 5389, Ap
30	99.2	1.2	33042	7	US-10-995-561-13340	Sequence 13340, A
31	97.2	1.2	29616	7	US-10-995-561-13265	Sequence 13265, A
32	97	1.2	196200	8	US-11-121-086-9	Sequence 9, Appl
33	94.2	1.2	199321	8	US-11-121-086-10	Sequence 10, Appl
34	93.8	1.2	189539	8	US-11-121-086-16	Sequence 16, Appl
35	92.6	1.1	235033	8	US-11-157-389-1	Sequence 1, Appl
36	92.6	1.1	237326	8	US-11-157-389-2	Sequence 2, Appl
37	89.8	1.1	142605	8	US-11-121-086-64	Sequence 64, Appl
38	89.8	1.1	169725	8	US-11-121-086-63	Sequence 63, Appl
39	89	1.1	169047	8	US-11-121-086-15	Sequence 15, Appl
40	89	1.1	178877	8	US-11-121-086-17	Sequence 17, Appl
41	86.6	1.1	207835	8	US-11-121-086-39	Sequence 39, Appl
42	86.6	1.1	207835	8	US-11-121-086-40	Sequence 40, Appl
43	85.8	1.1	163	7	US-10-996-217A-31	Sequence 31, Appl
44	85.8	1.1	203467	8	US-11-121-086-50	Sequence 50, Appl
45	81.6	1.0	159781	8	US-11-121-086-92	Sequence 92, Appl

ALIGNMENTS

RESULT 1
US-10-996-217A-8
; Sequence 8, Application US/10996217A
; Publication No. US20050266561A1
; GENERAL INFORMATION:
; APPLICANT: Revivicor, Inc.
; APPLICANT: Wells, Kevin
; TITLE OF INVENTION: Use of Interfering RNA in the Production of Transgenic Animals
; FILE REFERENCE: 10785.105070 REV 1015 US
; CURRENT APPLICATION NUMBER: US/10/996,217A
; CURRENT FILING DATE: 2004-11-22
; PRIOR APPLICATION NUMBER: 60/523,938
; PRIOR FILING DATE: 2003-11-21
; NUMBER OF SEQ ID NOS: 272
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 8
; LENGTH: 2036
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-10-996-217A-8

Query Match	17.2%	Score	1400;	DB	7;	Length	2036;
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Gaps	5;						
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Qy	5683	ATCCCTTAAAGCTTCGCTCCATCGGTGTTCTTACTCTGTCAATAAACCCTCTCAGACT	5742				
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Qy	5743	AATGGTATGGCATAGGACAGCTGAACTCCCATACCCCTTATCTCTCAGCTGGTTA	5802				
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Db 1921 CATGTATTATTAAAGTTAATTTGGCTTCATTAGAGAAACGAATAAGTG 1968

RESULT 2

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; Sequence 7, Application US/10996217A
; Publication No. US20050266561A1
; GENERAL INFORMATION:
; APPLICANT: Revivicor, Inc.
; APPLICANT: Wells, Kevin
; TITLE OF INVENTION: Use of Interfering RNA in the Production of Transgenic Animals
; FILE REFERENCE: 10785.105070 REV 1015 US
; CURRENT APPLICATION NUMBER: US/10/996,217A
; CURRENT FILING DATE: 2004-11-22
; PRIOR APPLICATION NUMBER: 60/523,938
; PRIOR FILING DATE: 2003-11-21
; NUMBER OF SEQ ID NOS: 272
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 7
; LENGTH: 1657
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-10-996-217A-7

Query Match 15.7%; Score 1278.4; DB 7; Length 1657;
Best Local Similarity 88.2%; Pred. No. 0;
Matches 1471; Conservative 0; Mismatches 186; Indels 11; Gaps 7;
QY 2320 GGCACCAACAGATATCCATGACTACCCGAAAGAAAGTTCACCTTGGAGTGGGACGGGTAA 2379
Db 1 GGCACCGCAGTATCCATGACTACCCGAAAGAAACCGTTCAGCTTGGCAGTGGGACGGGTAA 60


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QY 2380 CCACCTCGTTCTGCTCATACCTGAGTGGCCAGCACCCCTCTTAGGTAGAGACTTATGA 2439
Db 61 CCACCTCGTTCTGCTCATACCTGAGTGGCCAGTACCCCTCTTAGGTAGAGACTTACTGA 120
QY 2440 CCAAGATGGAGGACAAAATTTCTTTTGAACAAGGGAACAGAGTGTCTGCAATTAACA 2499
Db 121 CCAAGATGGAGGCTCAAATTTCTTTTGAACAAGGGAACAGAGTGTCTGCAATTAACA 180
QY 2500 AACCTATCACTGTGTGACCCCTCCAATTAGATCAGCAATATCAGCTATATCTCCCTCTAG 2559
Db 181 AACCCATCACTGTGTGACCCCTCCAATTAGATGATGAATATCAGCTATATCTCCCAAG 240
QY 2560 TAAAGCCTGATCAAAATATATAAATTTCTGTGTGGAACAGTTTCCCAAGCCTGGGAGAAA 2619
Db 241 TAAAGCCTGATCAAGATATACAGTCTCTGTGTGGAGCAGTTTCCCAAGCCTGGGAGAAA 300
QY 2620 CCGCAGGATGGGTGTGGCAAGCAAGTTCCCCCAAGAGTTTATTAAGTGAAGGCCAGTG 2679
Db 301 CCGCAGGATGGGTGTGGCAAGCAAGTTCCCCCAAGAGTTTATTAAGTGAAGGCCAGTG 360
QY 2680 CCACACAGTGTCACTCAGACAGTACCCCTTGAGTAAAGAGCTCAAGAGGAATTCGGC 2739
Db 361 CTACACAGTATCAGTCAGACAGTACCCCTTGAGTAGAGAGCTCGAGAAAGGAATTTGGC 420
QY 2740 CGCATGTCCAAAGATTAATCAACAGGGCATCTAGTTCTCTGTCCTCAATCTCCCTGGAATA 2799
Db 421 CGCATGTTCAAGATTAATCCACAGGGCATCTAGTTCTCTGTCCTCAATCTCCCTGGAATA 480
QY 2800 CTCCTCTGCTACCGGTTAGAAAGCCTGGGACTAATGACTATCGACAGTACAGACTTGA 2859
Db 481 CTCCTCTGCTACCGGTTAGGTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTGA 540
QY 2860 GAGAGTCAATAAAGGGTGAGAGATATACCCCAAGTCCCGAACCTTTATAACCTCT 2919
Db 541 GAGAGTCAATAAAGGGTGAGAGATATACCCCAAGTCCCGAACCTTTATAACCTCT 600
QY 2920 TGTGTGCTCTCCACCCCAAGGAGCTGTTATACAGTATTGGACTTAAAGATGCTCTTCT 2979
Db 601 TGAGCGCCCTCCCGCCTGACCGGAACCTGTGTACACAGTATTGGACTTAAAGATGCTCTTCT 660
QY 2980 TCTGCTCTGAGATTACACCCCACTAGCCCAACACCTTTTGTCTTCCGAATGAGAGATCCAG 3039
Db 661 TCTGCTCTGAGATTACACCCCACTAGCCCAACACCTTTTGTCTTCCGAATGAGAGATCCAG 720
QY 3040 GTACGGGAAGAACGGGAGCTACCTGAGCCCACTGCCCCAAGGTTCAAGAACTCCC 3099
Db 721 GTACGGGAAGAACGGGAGCTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 780
QY 3100 CGACCATCTTTGACGAAGCCCTACACAGAGACCTGGCCAACTTCAGATCCAAACACCTC 3159
Db 781 TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT 840
QY 3160 AGGTGACCTCTCTCCAGTACGTGGATGACCTGCTTTCTGGGGAGGCCAACCAAGGACT 3219
Db 841 AG--TGACCTCTCCAGTACGTGGATGACCTGCTTTCTAGTGG--AGCCACCAACAGGACT 896
QY 3220 GCTTAGAAGGACGAGAGCACTACTGTGGAATTTGTCTGACCTAGGCTACAGAGCCTCTG 3279
Db 897 GC-TAGAAGGTACGAAGGCACTACTACT-GAATTTGTCTGACCTAGGCTAC-GAGCCCTCAG 953
QY 3280 CTAAGAGGCCAGATTTGACGAGAGAGGTAAACATCTTCGGGTACAGTTTTCGGGAGC 3339
Db 954 CTAAGAGGCC--AGATTGACGAGAGAGGTAAACATCTT-GGGTACAGTCTGGGAGC 1009
QY 3340 GCGAGCAGTGTGCTACGAGGAGGACGGAAGAAACTGTAGTCCAGATACCGCCCCCAACA 3399
Db 1010 GCGAGTGTGCTGACGAGGAGGACGGAAGAGAACTGTAGTCCAGATACCTTTTTTTTTT 1069
QY 3400 CAGCCAAA CAAATGAGAGAGTTTTTGGGACAGCTGGGATTTTGCAGACTGTGGATCCCG 3459
Db 1070 TTTTTTTTCAAGTGAGAGAGTTTTTGGGACAGCTGGGATTTTGCAGACTGTGGATCCCG 1129
QY 3460 GGTTCGACCTTAGCAGCCCACTCTACCCGCTTAACCAAGAAAAGGGGAATTTCTCT 3519
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Db 1130 GGTTCGACCTTAGCAGCCCACTCTACCGGTAAACCAAGAAAAGGGAGTTCTCCT 1189
QY 3520 GGGCTCTCAGCACACGAAGGCAATTTGATGCTATCAAAAAGGCCCTGCTGAGCGCACTG 3579
Db 1190 GGGCTCTCAGCACACGAAGGCAATTTGATGCTATCAAAAAGGCCCTGCTGAGCACACTG 1249
QY 3580 CTCTGGCCCTCCTCAGCTAGTAACACCTTTTACCTTTTACCTTTTATGTGGATGAGCGTAAGGAG 3639
Db 1250 CTCTGGCCCTCCTCAGCTAGTAACACCTTTTACCTTTTACCTTTTATGTGGATGAAATGTAAGGGGG 1309
QY 3640 TAGCCCGGGAGTTTAAACCCAAACCTAGGACCATAGGAGAACCTGTGCGCTACCTGT 3699
Db 1310 TAGCCCGGGAGTTTAAACCCAAACCTAGGACCATAGGAGAACCTGTGCGCTACCTGT 1369
QY 3700 CAAAGAAGCTCGATCTCTAGCCAGTGGTGGCCCATATGCTTGAAGGCTATCGCAGCTG 3759
Db 1370 CAAAGAAGCTCGATCTCTAGCCAGTGGTGGCCCATATGCTTGAAGGCTATCGCAGCCG 1429
QY 3760 TGCCCATATCGTCAAGGAGCTGACAAATTTGACTTTTGGACAGAAATATACTGTAATAG 3819
Db 1430 TGCCCATATCGTCAAGGAGCTGACAAATTTGACTTTTGGACAGAAATATACTGTAATAG 1489
QY 3820 CCCCCATGCAATGGAGAACATCGTTCGGCAGCCCCCAGACCGATGGATGACCAACGCC 3879
Db 1490 CCCCCATGCTTTGGAGAACATCGTTCGGCAGCCCCCAGACCGATGGATGACCAACGCC 1549
QY 3880 GCATGACCCACTATCAAGCCTCTCTTCTCAAGAGAGGCTCACGTTTCCTCCACCGCCG 3939
Db 1550 GCATGACCCACTATCAAGCCTCTCTTCTCAAGAGAGGATCACGTTTCCTCTACCGCTG 1609
QY 3940 CTCTCAACCTCGCCTCTCTTCTGCTGGAAGAGACTGATGAACCACTGA 3987
Db 1610 CTCTCAACCTCGCCTCTCTTCTGCTGGAAGAGACTGATGAACCACTGA 1657
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RESULT 3

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US-10-996-217A-9
; Sequence 9, Application US/10996217A
; Publication No. US20050266561A1
; GENERAL INFORMATION:
; APPLICANT: Revivacor, Inc.
; APPLICANT: Wells, Kevin
; TITLE OF INVENTION: Use of Interfering RNA in the Production of Transgenic Animals
; FILE REFERENCE: 10785.105070 REV 1015 US
; CURRENT APPLICATION NUMBER: US/10/996,217A
; CURRENT FILING DATE: 2004-11-22
; PRIOR APPLICATION NUMBER: 60/523,938
; PRIOR FILING DATE: 2003-11-21
; NUMBER OF SEQ ID NOS: 272
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 9
; LENGTH: 1657
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-10-996-217A-9
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Query Match 15.7%; Score 1278.4; DB 7; Length 1657;
Best Local Similarity 88.2%; Pred. No. 0;
Matches 1471; Conservative 0; Mismatches 186; Indels 11; Gaps 7;

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QY 2320 GGCAACAACAGTATCCATGGACTACCCGAAGAACAGTGTGACTTGGAGTGGGACGGGTAA 2379
Db 1 GGCAACGGCAGTATCCATGGACTACCCGAAGAACAGTGTGACTTGGCAGTGGGACGGGTAA 60
QY 2380 CCCACTCGTTTCTGCTCATACCTCAGTGGCCAGCACCCCTCTTAGGTAGAGACTTATGA 2439
Db 61 CCCACTCGTTTCTGCTCATCCCTGAGTGGCCAGTACCCCTCTTAGGTAGAGACTTACTGA 120
QY 2440 CCAAGATGGGAGCAAAATTTCTTTTGAACAAGGGAACCAAGAGTGTCTGCAATTAACA 2499
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[illegible]

/	OTHER INFORMATION: n is a, c, g, or t	Db	3202	AGAGCTCAAAATACACTTTGAGAGGTCAGAAGTCAAAGTCAAGGTCACAGGGCCAGAGGAAATTCCC	3261
/	FEATURE:				
/	NAME/KEY: misc feature	Qy	2505	ATCACTGTGTTGACCCCTCAATTTAGATGACGAATATCGACTATACTCTCCCTAGTAAAG	2564
/	LOCATION: (5618)..(5648)				
/	OTHER INFORMATION: n is a, c, g, or t	Db	3262	CTTACCACTTTGACAAATGTCATAGAAGATGAATACAGANNNNNNNNNNNNNNNNNNN	3321
/	FEATURE:				
/	NAME/KEY: misc feature	Qy	2565	CCTGATCAAAATATACAATTCCTGGTTGGAAC-----AGTTTCCCAAGCCCTGGGCAGAA	2618
/	LOCATION: (5699)..(6078)	Db	3322	NN	3381
/	OTHER INFORMATION: n is a, c, g, or t				
/	FEATURE:				
/	NAME/KEY: misc feature	Qy	2619	ACCGCAGGATGGGTTTGGCAAGCAAGTTCCTCCCAAGTTATTCACATGAGGCCAGT	2678
/	LOCATION: (6145)..(6295)				
/	OTHER INFORMATION: n is a, c, g, or t	Db	3382	ACAGGAGGAATGGCCTT-GCCATCAACCAAGGCCCAATATATAGTAACCTTAAAGAGTGCC	3440
/	FEATURE:				
/	NAME/KEY: misc feature	Qy	2679	GCCACACAGTGTCAGTGACAGCAGTACCCCTTGAGTAAAGAGCTCAAGAAAGGAAATTCGG	2738
/	LOCATION: (7036)..(7101)				
/	OTHER INFORMATION: n is a, c, g, or t	Db	3441	ATCCTCTCTGCATCCGTGACAGATATCAATGCTTAAAGAGCCGAGAGGAATTCGG	3500
/	FEATURE:				
/	NAME/KEY: misc feature	Qy	2739	CCGATGTCCAAAGATTAAATCAACAGGGCATCTTAGTTCCTGTCCAATCTCCCTGGAAAT	2798
/	LOCATION: (7322)..(7444)				
/	OTHER INFORMATION: n is a, c, g, or t	Db	3501	CCACATATTTAAAG-TTACTTGAAACAAGGGATTCTGGTCCCTGTAAATCTCCTTGGAAAT	3559
/	FEATURE:				
/	NAME/KEY: misc feature	Qy	2799	ACTCCCTCTACCGTTAGAAAGCTGGGACTATGACTATCGACCTACAGACTACAGACTTG	2858
/	LOCATION: (7935)..(8343)				
/	OTHER INFORMATION: n is a, c, g, or t	Db	3560	ACACCTTTGTGGCCGTGAGGAAGCCAGGAACCAATGACTATAGGCAGTACAGGATCTG	3619
/	FEATURE:				
/	NAME/KEY: misc feature	Qy	2859	AGAGAGGTCAATAAAGCGGTGAGGATATACACCAACAGTCCCGAAACCTTTATACCTC	2918
/	LOCATION: (8803)..(8825)				
/	OTHER INFORMATION: n is a, c, g, or t	Db	3620	AGGAGGTCAATAAAGGATAGAGACATACACCTACTGTCCCAACCTTTATATTTG	3679
/	FEATURE:				
/	NAME/KEY: misc feature	Qy	2919	TTGTGTGCTCTCCACCCCAACGGAGCTGGTATACAGTATTGGACTTAAAGATGCTCTC	2978
/	LOCATION: (8919)..(8944)				
/	OTHER INFORMATION: n is a, c, g, or t	Db	3680	CTGAGCGGATTGCCACCCCAACTATACCTGTGTATACAGTCTTAGATCTTTAAGATGCTCTC	3739
/	FEATURE:				
/	NAME/KEY: misc feature	Qy	2979	TTCTGCCTCAGATTACACCCACTAGCCAAACCACTTTTTCCTTCGAAATGGAGAGATCCA	3038
/	LOCATION: (9236)..(9277)				
/	OTHER INFORMATION: n is a, c, g, or t	Db	3740	TTCTGCCTCCGCTGCATCCCAACAGCCAACTATATTTGCTTTGAAATGGNNNNNNNN	3799
/	US-11-128-061-1069				
/	Query Match			10.3%; Score 835.6; DB 8; Length 9603;	
/	Best Local Similarity			44.2%; Pred. No. 6.2e-234;	
/	Matches 1632; Conservative			0; Mismatches 2024; Indels 37; Gaps 13;	
Qy	2038	GGACCCCACTCGACAGGACCAATGTGCATATTGTAAAGAAAGAGACACTGGGCAAGGA	2097		
Db	2782	GGCCCACTGGACAGGATCAATGCGCTTACTGCAAGAAAGAGACATTGGGCAAG	2841		
Qy	2098	ACTGCCCCAAGAGGAAACAA-----AGGACCAAGGATCCTAGCTCTAGAAGAG	2148		
Db	2842	AATGCCCTAAGAACCCCGGCCAAGCCTCCACGGCCAAAGACCTCTGACCTTCTAAACC	2901		
Qy	2149	ATAAAGATTAGGGAGACGGGTTCCGACCCCTCCCGAGCCAGGGTAACCTTTGAAG	2208		
Db	2902	TAGAAGATTAGAAAGTCAAGGCGCAGGACCCCTTCCGCTTCCGCTTCTGAATC	2961		
Qy	2209	TGGAGGGCAACAGTTGAGTTCTCTGTTGATACCGGACGGAAACATTCAGTGCTACTAC	2268		
Db	2962	TCGGGGGCATCCGGTCACTTCTTAGTAGATACAGGGCAACATTCGGTCTGAAATC	3021		
Qy	2269	AGCCATTAGGAAAACTAAAGATATAAAATCTCGGTGATGGGTGACAGGGCAACAC	2328		
Db	3022	GGTCAACCCGACCCCTGAGTCAACCGACTCGCATGGGTACAGGGAGCTACAGGCGGAAAGC	3081		
Qy	2329	AGTATCCATGGACTACCCGAAGAACAGTTGACTTTGGGAGTGGGACGGGTAAACCTCGT	2388		
Db	3082	AGTACCATTTGGACTACAAATTCGGAGCTCCAGCTCCGACTGTGAAGGTTATGCAATCTT	3141		
Qy	2389	TTCTGTGTCATACCTAGTGTCCAGCACCCCT-CTTAGGTAGAGACTTATTGACCAAGATG	2447		
Db	3142	TCCTCCATGTGCAGATTGCCCTTACCTTACCTAGGACGGGACCTATTGACCAATTA	3201		
Qy	2448	GGAGCAAAATTTCTTTTGAACAGGGAAACCAAGAGTGTCTG---CAAATACAAACCT	2504		


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RESULT 6
US-11-128-049-1069
; Sequence 1069, Application US/11128049
; Publication No. US20060010513A1
; GENERAL INFORMATION:
; APPLICANT: Melville, Mark W.
; APPLICANT: Charlebois, Timothy S.
; APPLICANT: Mounts, William M.
; APPLICANT: Hann, Louane E.
; APPLICANT: Sinacore, Martin S.
; APPLICANT: Leonard, Mark W.
; APPLICANT: Brown, Eugene L.
; APPLICANT: Miller, Christopher P.
; TITLE OF INVENTION: OLIGONUCLEOTIDE ARRAYS TO MONITOR GENE EXPRESSION AND METHODS FOR
; TITLE OF INVENTION: MAKING AND USING SAME
; FILE REFERENCE: 01997.027700
; CURRENT APPLICATION NUMBER: US/11/128,049
; CURRENT FILING DATE: 2005-05-11
; PRIOR APPLICATION NUMBER: US 60/570,425
; PRIOR FILING DATE: 2004-05-11
; NUMBER OF SEQ ID NOS: 7285
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1069
; LENGTH: 9603
; TYPE: DNA
; ORGANISM: Cricetus griseus
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (598)..(2723)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (3301)..(3353)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (3791)..(3889)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (4504)..(4612)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (4665)..(4698)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (5185)..(5217)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (5246)..(5293)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (5314)..(5351)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (5618)..(5648)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (5699)..(6078)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (6145)..(6295)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (7036)..(7101)
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; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (7322)..(7444)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (7935)..(8343)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (8803)..(8825)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (8919)..(8944)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (9236)..(9277)
; OTHER INFORMATION: n is a, c, g, or t
US-11-128-049-1069

Query Match      10.3%; Score 835.6; DB 8; Length 9603;
Best Local Similarity 44.2%; Pred. No. 6.2e-234;
Matches 1632; Conservative 0; Mismatches 2024; Indels 37; Gaps 13;

QY 2038 GGACCCCTCGACAAAGGACCAATGTGCATATTGTAAGAAAGAGGACACTGGGCAAGGA 2097
    |||||
Db 2782 GGCCCCACCTGGACAGGGATCAATGCGCTTACTGAAAGAAAGACATTTGGGCAAG 2841
    |||||
QY 2098 ACTGCCCCCAAGGAGGAAACAA-----AGGACCAAGGATCCTAGCTCTAGAAGAAG 2148
    |||||
Db 2842 NATGCCCTAAGAACCCCGGGCCAAAGCCTCCACGGCCAAAGACCTCTGACCTTCTAAACC 2901
    |||||
QY 2149 ATAAAGATTAGGGGAGACGGGTTTCGGACCCCTCCCGAGCCCGAGGTAACCTTTGAAGG 2208
    |||||
Db 2902 TAGAAGATTAGAGAAAGTCAGGGCCAGGAGCCCCCTGAGCCAGGATAACACTGCAAG 2961
    |||||
QY 2209 TGGAGGGCAACACAGTTGAGTTCTCTGGTTGATACGGAGCGAAACATTCAGTGCTACTAC 2268
    |||||
Db 2962 TCGGGGGCATCCGGTCACCTTCCTAGTAGATACAGGGGCAACACATTCGGTCTGAATC 3021
    |||||
QY 2269 AGCCATTAGGAAACCTAAAGATAAAAAATCCTGGGTGATGGGTGCACAGGCGCAACAAC 2328
    |||||
Db 3022 GGTCAACCGGACCCCTGAGTCACCGACTGATGGGTGATGAGGAGCTACAGGCGGAAAGC 3081
    |||||
QY 2329 AGTATCCATGGACTACCCCGAAGACAGTTGACTTTGGGAGTGGGCGGTAAACCACTCGT 2388
    |||||
Db 3082 AGTACCATTTGGACTACAAATCGGCAGCTCCAGCTCGCGACTGGTAAAGGTTATGCAATCTT 3141
    |||||
QY 2389 TTCTGTGCATACCTGAGTCCCGCAGACACCCCT--CTTAGGTAGAGACTTATTGACCAAGATG 2447
    |||||
Db 3142 TCCTCATGTGCCAGATTGCCCTTACCCTTACTTAGGACGGGACCTATTGACCAATTA 3201
    |||||
QY 2448 GGAGCACAAATTTCTTTTGAACAAGGGAACACAGAGTGTCTG---CAAAATAACAACCT 2504
    |||||
Db 3202 AGAGCTCAAATACACTTTTGAGAGGTCAGAAAGTCAGAAAGTCACAGGCGCAGAGGAATCCG 3261
    |||||
QY 2505 ATCACTGTGTGACCCCTCAATTAGATGACGAATATCGACTATCTCTCCCTAGTAAAG 2564
    |||||
Db 3262 CTTACCATCTTGACCAATGTCCATAGAAGATGAATACAGANNNNNNNNNNNNNNNNNN 3321
    |||||
QY 2565 CCGTATCAAATATACAATTCCTGGTTGGAAC-----AGTTTCCCCAACGCTGGGCGAGAA 2618
    |||||
Db 3322 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 3381
    |||||
QY 2619 ACCGAGGAGTGGGTTTGGCAAAAGCAAGTTCGCCCAACAAGTTATTCAACTGAAGGCCAGT 2678
    |||||
Db 3382 ACAGAGGAATGSCCTT--GCCATCAACAGGCCCCCAATTATAGTAACCTTAAAGCTGCC 3440
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QY 2679 GCCACACCAAGTGTGAGTCAGACAGTACCCCTTGAGTAAAGAGCTCAAGAGGAATTCGG 2738
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QY 3545 TGATGCTATCAAAAAGCCCTGCTGAGCGACCTGCTCTGGCCCTCCCTGACGTAACTAA 3604
Db 142891 CCAGGCCCTTAAGAGGCCCTTAACCCAAAGCCCGAGTGTAAAGCTTGCCAAAGG---GCA 142946
QY 3605 ACCCTTTACCTTTATGTGATGAGCTAAGGAGTAGCCCGGGAGTGTAAACCCAAAC 3664
Db 142947 AGACTTTCTTTATATGTCAGAGAAAACAGGAATAGCTCTAGGAGCCATCACACAAGT 143006
QY 3665 CCTAGGACCATGGAGAGACTGCTGCTTACCTGTCTCAAGAAGCTCGATCCTGTAGCCAG 3724
Db 143007 CTGAGGAGCTAGCTTGGCAACCGGTGGCATACCTGATTAAGAAATGATGTAGTACCAA 143066
QY 3725 TGGTTGGCCCATATGCTGAAAGGCTATCGCAGCTGTGGCCATCTGCTCAAGACGCTGA 3784
Db 143067 GGATTGGCTTCATTTTACAGGTAGTGTGGCAGTAGCAGTCTTAGTGTCTGAAGTGT 143126
QY 3785 CAAATTGACTTTGGGACAGAAATATACTGTAAATAGCCCCCGATGTCATTTGAGAACATCGT 3844
Db 143127 TAAATGATACAGGGAAGAGATCTTACTGTGTGGACATCTCATGATGTGAATGCCATACT 143186
QY 3845 TCGCGACCCCGCAGACCGATGGATGACCAAGCCCGCATGACCCACATATCAAAAGCCCTGCT 3904
Db 143187 CACTGTAAAGGAGACTTGTGGCTGTGAGAACACCGTTTACTTAAATATCAGGCTCTATT 143246
QY 3905 TCTCACAGAGAGGCTCACGTTGCTGCCACAGCGCTCTCAACCCCTGCCACTCTTCTGCC 3964
Db 143247 ACTTGAAGGCCAGTGTGCACTGCGCATCTGTGTAACTCTTAAACCCAGTCACTTTCT 143306
QY 3965 TGAAGAGACTGATGAACAGTGACTCATGATGTGCATCACTATTTGATTTAGGAGACTGG 4024
Db 143307 TCCAGACATGAAGAAAAGATAGAACATTAACGCAACAAAGTAAATTTGCTCAAACTATGC 143366
QY 4025 GGTCCGCAAGGACTTACAGACATACCGCTGACTGGAGAGTGTCACTGTTCACTGA 4084
Db 143367 CGCTCGAGGGGACTTTTATAGAGTGTCCCTTACTGATCCCCACCTCAACTTGTATCTGA 143426
QY 4085 CGGAAGCAGCTATGCTGTGAAGGTAAAGAGATGGCTGGGGCGGCTGTGTGACGGGAC 4144
Db 143427 TGGAAAGTTCCTTTGTAGAAAAGGACTTCAAAAAGTGGGTATGCACTGGTCACTGATAA 143486
QY 4145 CCGCAGCATCTGGCCAGCAGCTCTCGGAAAGGAACTTTCAGCAAAAAGGCTGAGCTCAT 4204
Db 143487 TGGAAATCTTGAAGTAAATCCCTCACTCCAGGAATAGTGTCTCAGCTGGCAGAACTAAT 143546
QY 4205 GGCCTCAGCGAGCTTTGGCGCTGGCGGAAGGGAATCCATAAATTTATACGGACAG 4264
Db 143547 AGCCCTCACTCGGCTACTAGAAATCAGGAGAAAGGGAATTAATATATACAGACTC 143606
QY 4265 CAGGTATGCTTTGCGACTGACAGCTACATGGGGCCATCTATAAACAAGGGGTTGCT 4324
Db 143607 TAAGTGTCTTACCTAGTCTCCATGCCCCATGCGCAATATGGAGAGAAAGGAAATTCCT 143666
QY 4325 TACCTCAGCAGGAGGGAATATAAGAAACAAGAGGAAATCTTAAGCCTATTAGAAGCGGT 4384
Db 143667 AACTTCGAGGGAACACCTATCAAAACATCAGGAAGCCATTAGGAAATTAATTTGGCTGT 143726
QY 4385 ACATTTACAAAAGGCTAGCTATTAATACATGCTCTGGACATCAGAAAGCTAAAGTCT 4444
Db 143727 ACAGAAACCTTAAGAGGTGGCAGTTTATACCTGCGGGGTCTATCAGAAAGGAAG 143786
QY 4445 CATATCCAGAGGAACCATGAGTGGCTGACCGGTTGCCAA 4483
Db 143787 GGAATAACAGGAGCCCAAGTTGATTTGAAGTCAA 143825

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RESULT 8

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US-11-121-086-78
; Sequence 78, Application US/11121086
; Publication No. US2005026459A1
; GENERAL INFORMATION:
; APPLICANT: POULSEN, TIM S.
; APPLICANT: NIELSEN, KIRSTEN V.
; TITLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES

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; FILE REFERENCE: 09138.6000-00000
; CURRENT APPLICATION NUMBER: US/11/121,086
; CURRENT FILING DATE: 2005-05-04
; PRIOR APPLICATION NUMBER: 60/567,570
; PRIOR FILING DATE: 2004-05-04
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: Patent in version 3.3
; SEQ ID NO 78
; LENGTH: 189993
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-11-121-086-78

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Query Match 3.5%; Score 287; DB 8; Length 189993;
Best Local Similarity 49.1%; Pred. No. 1.2e-71;
Matches 932; Conservative 0; Mismatches 930; Indels 37; Gaps 5;

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QY 2600 TCCCAAGCTGGCGAGAAACCCGAGGATGGGTTTGGCAAAACAGTTTCCCCCAACAAGT 2659
Db 11322 TCCTGAAGTCTAAGCAACAGAGGACAAATATAGCAGGCAAAAGATGCCCATCTCTGTTC 11381
QY 2660 TATTCAACTGAAGCCAGTGCACACAGTGTCTCAGTCAGACAGTACCCCTTTGAGTAAAGA 2719
Db 11382 AGTTAACTAAAGATTCGCGCTCTTCCCTACCAAGGAGTACCCCTTAGACCCAA 11441
QY 2720 AGCTCAAGAAAGAAATTTGGCCGATGTCCAAAGATTAATCCAAAGGGCATTCCTAGTTCC 2779
Db 11442 GGCCCAACAGGACTCCAAAAAACTGTTAAGGACCTAAAAAGCCCAAGGCTTAGTAAACC 11501
QY 2780 TGTCCAAATCTCCCTGNAATCTCCCTGCTACCGTTAGAAAGCCTGGGACTAATGACTA 2839
Db 11502 ATCAGTAGCCCTGCAATCTCCAACTGTAGAGTACAGAAACCC---AACGGACAGTG 11558
QY 2840 TCGACAGTACAGACTTTGAGAGAGGTCAATAAACGGGTGTCAGGATATACACCCAAACAGT 2899
Db 11559 GAGTTAGTGCAAAATCTCAGGATTAATCATGAGACTGTTGTTCTCTATACCCAGCTGA 11618
QY 2900 CCGCAACCTTTAAACCTCTTGTGTCTTCCCAACCCCAACGGAGCTGGTATACAGTATT 2959
Db 11619 ACCTAACCTTTACTCTGCTTTCCCAAAATACCAAGAGGAGAGTGGTATATAGTCTCT 11678
QY 2960 GGCATTAAGAGATGCTCTTCTGCTGAGATATACCCCACTAGCCCAACCACTTTTTCG 3019
Db 11679 GGCATTTAAGAGATGCTCTTCTGCTATCCCTGATCTCTGATTTCCCAATTTCTGTTGC 11738
QY 3020 CTTTCAATGAGAGATCCAGGTACGGGAAGAACCGGCGAGTCACTACCTGGACCCGACTGCC 3079
Db 11739 CTTTGA-----GATCCTTCAAACTCAAGCTCTCACTCACTGGACTGTTTACG 11789
QY 3080 CCAAGGCTTCAAGAACTCCCGACCATCTTTTGACGAAGCCCTACACAGAGACCTGGCCAA 3139
Db 11790 CCAAGGCTTCAAGGATAGCCCCCATCTATTGTCAGGATAGTCCCAAGATTTGAGCCA 11849
QY 3140 CTTGAGGATCCAAACCTCAGGTGACCTCTCCTCAGTACGTGATGACCTGCTTCTGCG 3199
Db 11850 ATTCTCATACCTGACACTCTTG-----TCCTTTGGTATGAGTATTTACTTTTACG 11903
QY 3200 GGGAGCCCAACAAACAGGACTGCTTTAGAAGGCAAGGACACTACTGCTGGAATTTGCTGA 3259
Db 11904 CACTGTTTCAAGAACTTTGTCCTATCAAGCCCAAGCTGCTCTTAATTTTCTTCCACAC 11963
QY 3260 CCTAGGCTTACAGAGCTCTGCTTAAGAAAGGCCCAAGATTTGCAAGGAGAGTAAACATCTT 3319
Db 11964 CTGTGGCTTACAGGTTTCCAAACCAAGGCTCAGCTCTGCTCAGCAGAGGTTAAATACTT 12023
QY 3320 GGGGTAAGTTTGGGAGCGGAGCGATGCTGACGAGGACGGAAGAAACCTGAT 3379
Db 12024 AGGGTAAATTTATCCAAAGGCTTTGAGGGCCCTCAGTGAGGAACACATCCAGCCTATCT 12083
QY 3380 CCAGATACCGGCCCCCAACCCAGCCAAACAAATCAGAGAGTTTTGGGAGCAGCTGGATT 3439
Db 12084 GGCTTATCTCTTCCCAAAACCCCTAAAGCAACTAAGAGGGTTCCTTGGCATACAGGTTT 12143

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QY	3440	TTGCAGACTGTGATATCCCGGGGTTTCGGACCTTTAGCAGCCCCACATCTTACCCGCTAACCA	3499	RESULT 9	US-10-972-766-1/c
Db	12144	CTACCCAATGTGGATTCACAGTACAGCAAAATAGGCAGATCATTTATATACACTAATTA	12203	; Sequence 1, Application US/10972766	; Publication No. US20050250118A1
QY	3500	AGAAAAAGGGA-----ATTCTCTGGGCTCTGAGCAGCCAGTATTA	3544	; GENERAL INFORMATION:	; APPLICANT: Aerssens, Jeroen
Db	12204	AGAAATCAGAAGCCAATACCAATTTAGTAGTGACACCTGAAGCAGACGACTTT	12263	; APPLICANT: Athanaslou, Maria	; APPLICANT: Brain, Carlos
QY	3545	TGATGTATCAAAAAGGCGCTGTGAGCGCACCCTGTCTGGGCCCTCCCTGAGTAACATA	3604	; APPLICANT: Cohen, Nadine	; APPLICANT: Dain, Bradley
Db	12264	CAAGGCCCTAAGAGGCGCCTTAACCAAGCCCGAGTTTAAAGTTGCCAAGG-----GCA	12319	; APPLICANT: Denton, R. Rex	; APPLICANT: Judson, Richard
QY	3605	ACCTTTTACCTTTATGTGTGATGAGCGTAAAGGAGTAGCCCGGGGAGTTTAAACCCAAAC	3664	; APPLICANT: Ozdemir, Vural	; APPLICANT: Reed, Carol R
Db	12320	AGACTTTTCTTTATATGTACAGAAAAACAGGAATAGCTCTAGGAGCCATCACAAAGT	12379	; TITLE OF INVENTION: EPHX2 Genetic Markers Associated with Galantamine Response	; FILE REFERENCE: 2300.0030001
QY	3665	CCTAGACCATGGAGAAGACCTGTGCGCTACCTGTCAAGAGCTCGATCCTGTGACCCAG	3724	; CURRENT APPLICATION NUMBER: US/10/972,766	; CURRENT FILING DATE: 2004-10-26
Db	12380	CTGAGGGACTAGCTTGCAACCCGTGGCATACCTGTAGTAAGAAATTTGATGTAGTACAAA	12439	; PRIOR APPLICATION NUMBER: 60/515,378	; PRIOR FILING DATE: 2003-10-28
QY	3725	TGTTGGCCCATATGCTGAAGGCTATCGCAGCTGTGGCCATACCTGTCGAAGGACGCTGA	3784	; NUMBER OF SEQ ID NOS: 50	; SOFTWARE: PatentIn version 3.3
Db	12440	GGATGGCTTCTTTTACAGGTAGTGTGGCAGTAGCAGTCTTAGTGTCTGAAGTGT	12499	; SEQ ID NO 1	; LENGTH: 55763
QY	3785	CAAAATGACTTTGGGACAGAAATATAACTGTATAGCCCCCATATGCAATTCGAGAAACATGT	3844	; TYPE: DNA	; ORGANISM: Homo sapiens
Db	12500	TAAATGATACAGGAAGAGATCTTACTGTGTGGACATCTCATGATGTGAATGCCATCT	12559	; FEATURE:	; NAME/KEY: misc feature
QY	3845	TGGGACGCCACAGACCGATGATGACCAACGCCCGCATGACCCACTATCAAGCCTGTCT	3904	; LOCATION: (11006)..(11006)	; LOCATION: (11006)..(11006)
Db	12560	CACTGTAAAGGAGACTTTGGCGTGTGACAGCAACCGTTTACTTAAATATCAGGCTTATT	12619	; OTHER INFORMATION: n is the reference allele 'c' which can also be the variant	; OTHER INFORMATION: allele 't'
QY	3905	TCTCACAGAGGGTCACTGTCTCCACAGCGCTCTCAACCCCTGCCACTCTTCTGCC	3964	; FEATURE:	; NAME/KEY: misc feature
Db	12620	ACTTGAGGCCNGTCTGCACTGGCACTTGTGTAACTCTTAACCCAGTCACATTTCT	12679	; LOCATION: (21845)..(21845)	; LOCATION: (21845)..(21845)
QY	3965	TGAAGAGACTGATGAACCACTGACTCATGATGCCATCAACTATTGATTTGAGGAGACTGG	4024	; OTHER INFORMATION: n is the reference allele 'a' which can also be the variant	; OTHER INFORMATION: allele 'g'
Db	12680	TCAGACAATGAAGAAAAGATAGAAACATAACTGCCAAAGTAATTTGCTCAAAACCTATGC	12739	; FEATURE:	; NAME/KEY: misc feature
QY	4025	GGTCCGCAAGGACCTTACAGACATACCGTGTACTGAGAGTGTCTAACCTGTGTTACTGA	4084	; LOCATION: (26376)..(26376)	; LOCATION: (26376)..(26376)
Db	12740	CGCTCAGGGGACTTTTAGAGGTTCCCTTGACTGATCCCCACCTCAACTTGTATACTGA	12799	; OTHER INFORMATION: n is the reference allele 't' which can also be the variant	; OTHER INFORMATION: allele 'c'
QY	4085	CGGAACGACTGTGTGGAAGTTAAGAGGTAGGCTGGCGGGCGGTGTGACGGGAC	4144	; FEATURE:	; NAME/KEY: misc feature
Db	12800	TGGAAGTTCCTTTGTAGAAAAGGACTTCAAAAAGTGGGGTATGCAGTGTGTCAGTGATAA	12859	; LOCATION: (46768)..(46768)	; LOCATION: (46768)..(46768)
QY	4145	CCGACGATCTGGGCCAGCAGCTGCGGAAGAACTTCAGCACAAAAGGCTGAGTCTAT	4204	; OTHER INFORMATION: n is the reference allele 'c' which can also be the variant	; OTHER INFORMATION: allele 't'
Db	12860	TGGAATACTTGAAGTAATCCCTCACTCCAGGAAGTGTGCTCAGCTGGCAGAACTAAT	12919	; FEATURE:	; NAME/KEY: misc feature
QY	4205	GGCCCTCAGCAAGCTTTGGGGTGGCCGAGGGAATCCATAAACAATTTATACGACAG	4264	; LOCATION: (54475)..(54475)	; LOCATION: (54475)..(54475)
Db	12920	AGCCCTCACTCGGGTACTAGAATTCAGGAAGAAAAGGGTAAATATATATATACAGACTC	12979	; OTHER INFORMATION: n is the reference allele 'a' which can also be the variant	; OTHER INFORMATION: allele 'c'
QY	4265	CAGGTATGCTTTGCGACTGCACACGTACATGGGGCCATCTATAAACAAGGGGTTGCT	4324	US-10-972-766-1	Query Match 3.3%; Score 266.2; DB 7; Length 55763;
Db	12980	TAAAGTGTCTTACCTAGTCTCTCATGCCATGCAGCAATATGGAGAAAGGAATTCCT	13039	Best Local Similarity 49.2%; Pred. No. 6.1e-66;	Mismatches 1218; Indels 102; Gaps 18;
QY	4325	TACCTCAGCAGGGAGGGAATAAAGAACAAAGAGGAAATTTCTAAGCCTTATTAGAAGCCT	4384	Matches 1279; Conservative 0;	2601 CCCCAGGCTGGGCGAGAACCCGAGGATGGGTTTGGCAAGCAAGTTCCCCCACAAGTT 2660
Db	13040	AACTCCGAGGGAACACCTTATCAACATCAGGAAGCCATTAGGAATTTATTATGCTGT	13099	6871 CTGAAGCTGGGCATTGAAGGCAATTCGAGGCAAAATGCTCGCCCA-GTCCA 6813	2661 ATTCAACTGAAGCGCAGTGCCACACGAGTGTGTCAGTGTGACAGTACCCCTTTAGTAGTAA 2720
QY	4385	ACATTTACAAAAGGCTAGCTATTATACACTGTCTTGACATCAGAAAGCTAAAGATCT	4444	6812 AATCAGGTTAAAGACCCCACTTTTCTTATCAAGGCAATATCCCTTTAAGGCTGAA 6753	2721 GCTCAAGAGGAAATTCGGCGGCATGTCCAAAGATTAAATCCACAGGCAATCTAGTTCCT 2780
Db	13100	ACAGAAACCTTAAAGAGGTGGCAGTTTATCACTSCCGGGTCTACAGAAAGGAAGGAAG	13159	6752 GCTCAAGAGGATTACATGATATTTTATAGACATTTTAAAGTTCAAGGCTTAGTAGAAA 6693	
QY	4445	CATATCCAGAGGAACACAGATGCTGACCGGGTTGCCAA	4483		
Db	13160	GGAAATACAGGGAGCCACCAAGTTGATTTGAGTCAA	13198		

Qy	2781	GTCCAATCTCCCTGGAAATACCTCCCTGCTACCGGTTAGAAAGCCTGGGACTAATGACTAT	2840	Qy	3846	CGGACGCCCCCAGACCGGATGGATGACCAACGCGCCGATGACCCACTATCAAGCCCTGCTT	3905
Db	6692	TGACGAGTCCCTTGGACACCCCAATTCACGAGTACAAAACCC---GACGTTTCAGTGG	6636	Db	5636	GGTGCCAAAGGAAATTTATGGCTGTGACAACTGCTCTTAGATACACGAGCGCTTGT-	5578
Qy	2841	CGACCACTACAGACTTGGAGAGGTCATTAACAAAGGTCGAGGATATACACCAACAGTC	2900	Qy	3906	CTCACAGAGAGGTCACGTTGCTCCACGACGCGCTCTCAACCTGCGCACTCTTCTGCGCT	3965
Db	6635	AGACTAGTACAAGATTTAGACTCATCAGTGAGGCAAGTATTCCTCTATATCAGCTATA	6576	Db	5577	-----GTGTGGCCCTGNAACCTGCGCACTTCTCTC-	5547
Qy	2901	CCGAAACCTTTAACTTGTGTGCTCTCCACCCCAACGGAGCTGGTATACAGATTG	2960	Qy	3966	GAAGAGACTGATGAACCACTGACTCATGATGGCCATCAACTATTGATTTAGGAGACTGGG	4025
Db	6575	CCCAACCCCTATACCTCTCTCTCAATACCAAGAGAGCAAGATGTTTCATTGTTCTG	6516	Db	5546	--AGAGGATGGGAAACCAATCGAGCATGAATGCCAACAAATTGTAGCCAGACTTATGCT	5489
Qy	2961	GACTTAAAGGATGCTCTCTCTGCTGAGATTAACCCCACTAGCCCAACCACTTTTGGC	3020	Qy	4026	GTCCGCAAGACCTTACAGACATACGCTGACTGGAGAGTGTACTCTGTTTCACTGAC	4085
Db	6515	GACTCAGAGATGCTCTCTCTGATCTCTGATCTCTGACTCTGACTCCTGCTTCTTGGC	6456	Db	5488	GCCCGAGATGATCTCTTGAAGTCCCTTAGCTTAATCTGACCTTAACCTATATACCAAT	5429
Qy	3021	TTCCGATGGAGAGATCCAGGTACGGGGAAGAACCGGGGAGCTCACTGTGACCCGACTGCC	3080	Qy	4086	GGAAGCAGCTATCTGTGTGAAGGTAAAGAGATGGCTGGGGCGCGGTGGTGGACGGGACC	4145
Db	6455	TTTGAGG-----ATCCCAACAGACCAACAGCTCCCAACTTTCTGTGATGGTCTTGGCT	6405	Db	5428	GGAAATTTGTTGGAGATGGGATATGAAGGCGAGGTTATACCATAGTTAGTGATGTA	5369
Qy	3081	CAAGGTTCAAGAACTCCCGACCATCTTTGACGAGCCCTACACAGAGACTGGCCAC	3140	Qy	4146	CGCACGATCTGGGCCAGCAGCTGCCGGAAGGAACTTCAGCAAAAAGGCTGAGCTCATG	4205
Db	6404	CAAGGTTTAGGATAGCTCTCTCTGTTTGGTCAAGCACTGGCCCAAGATCTAGGCCAC	6345	Db	5368	ACAGTACTTGAAGTAAGCCTCTTTCCCGAGGACCTGCACCCAGTTAGCAGAACTAGTG	5309
Qy	3141	TTCAGGATCAACACCTCTCAGGTGACCTCTCCAGTACGTGGATGACCTGCTTCTGGCG	3200	Qy	4206	GCCCTCAGCAAGCTTTGGGCTGGCGGAAGGAAATCCATAAACATTTATACGACAGC	4265
Db	6344	TTCTCAAGTACAGGCACTCTGG-----TCTTCAAGTATGGATGATTTACTTATGTT	6291	Db	5308	GTGCTTACCTGAGCTTAGAACTGGGA-AAAGAAAAAAATNAATGTGTATACAGATAAC	5250
Qy	3201	GGAGCCACCAACAGGACTGTTAGAGGCAAGGACACTACTGCTGGAAATGTTCTGAC	3260	Qy	4266	AGTATGCTTTTGGGCTGCACACGATACATGCGGCCCATCTATAAAACAAAGGGGTTCCTT	4325
Db	6290	ACGATTTCAAGGCTCATGCCAGCAGCTACTAGCTCTCTTTGAACCTTCTAGCTAAT	6231	Db	5249	AAATATGCTTATCTAATCTTACATGCCCAATG---CTGCAATATGGAAAGGGGTTCCTA	5193
Qy	3261	CTAGGCTACAGAGCTCTGTGAAGAGCCAGATTTGAGAGAGAGGTTAACTACTTG	3320	Qy	4326	ACCTCAGCAGGAGGAAATATAAGAAACAAAGAGGAAATTTCAAGCTTATTAGAACCGTA	4385
Db	6230	CAAGGTTACATGGCATCTAAACTGAAGCCCAAGCTCTGC---CTACAAGTCAATATCTA	6174	Db	5192	ACCTCAGGGAACCCCATTTAATACCAAGGAAATCATGGAGTTATTGACGCGAGT	5133
Qy	3321	GGGTACAGTTTGGGAGGCGCAGCTGCTGACGAGGACGAGGACGGAAGAACTGTAGTC	3380	Qy	4386	CATTTACAAAAAGGCTAGCTATTATACATGCTGTCGACATCAGAAAGCTAAAGATCTC	4445
Db	6173	GGCCTAATCTTAGCCAGAGGAACAGGGCTCTAAGCAAGAAATGATACAGCTTACTG	6114	Db	5132	CAAAAACCAAGAGGTGGCAGCTTACACTGCCAAAGCCATCA-AAAGGTGAAGGAGAA	5074
Qy	3381	CAGATACCGGCCCCCAACACAGCCCAACAAATGAGAGAGTTTTTGGGGACAGCTGGATT	3440	Qy	4446	ATATCAGAGGAACAGATGGCTGACCGGTTGCCAAGCAGGCGAGCCAGGGTGTAAAC	4505
Db	6113	GCTTGTCTTGGCCCTAAGACATTAACAGTTGTGGGGTTCTTGGGATCACCAGCTTT	6054	Db	5074	AAGCAGAGAAACCAATTAGGCGAGACACTGAGGCCAAATTTGCTGCAGGTGGAACCTC	5014
Qy	3441	TGCAGACTGTGGATCCCGGGTTTGGACCTTTAGCAGCCCACTCTACCCGCTAACCAA	3500	Qy	4506	CTTC-----TGCTATAATAGAAATGCCCAAGCCCCCAGAACCCAGACGACGTACAC	4559
Db	6053	TGCCGACTATGGAATCCCAATACAGCAGATGGCCAGGCCACTCTATGCTCTAATCAAG	5994	Db	5013	CCATTAGAAATACCTACGGAAGGACCTTGGTATGGAAACAACCTCTCCAGAGATTAA	4954
Qy	3501	GAAGAGGGGA-----ATTCTCTGGGCTCTGAGCACCAGAGGCAATTT	3545	Qy	4560	CTAGAAGACTGGCAAGAGATAAAAGATAGACAGTTCTCTGAGACT-----CCG	4610
Db	5993	GAGACCCAGAGGGCAACATTAATCTAGTAGAATGGGAACAGAGGCGAAGAACGCTTC	5934	Db	4953	CCCCAGTTTCCCAACCGAAACAGAAATGAGGACTTTTCATGGGGGCTAGTTTCTCCCC	4894
Qy	3546	GATGCTATCAAAAGGCCCTCTGAGCGCACTGCTCTGGGCCCTCCCTGACGTAACTAAA	3605	Qy	4611	GAAGGACCTGCTATACCTCAGATGGGAAGGAAATCTGCCCAACAAAGAGGTTAGAA	4670
Db	5933	AAAACCTTAAAGAGGCCCTTAGTACAGCTCCAGCTTTAAGCCTTCCCAAGGAC---AA	5877	Db	4893	TCCAGGTGGTTAAACAGAGAGGGAAGGATCTCATGCCCCGAGCCAGCCAGCTGGAAA	4834
Qy	3606	CCCTTTTACCTTTATGTGGATGAGCGTAAAGGAGTAGCCCGGGAGTTTAAACCAACC	3665	Qy	4671	TATGTCCAACAGATATACGTCTAAACCACTTAGGAACTAAACACCTGACGAGTTGTC	4730
Db	5876	GACTTCTTTATATACATCACAGAGAGAGCAGGAATAGCTCTCTGAGTCTTACTCAGACT	5817	Db	4833	ATACCTTAAGACCTTCCACCAAACTTTTCATATGGGTATTGAAACACTCATCAATGSCC	4774
Qy	3666	CTAGACCATGGAGAGACCTGTGCTTACCTGTCAAGAGAGCTGATCTCTGTAGCCAGT	3725	Qy	4731	AGAACTCCCTTATCATGTTCTGAGGCTACAGAGTGGGTGATCTCGTGGTCAAAAT	4790
Db	5816	CGTGGCAACCCCAACACAGTGGCATACCTTAAGTAAAGGAACTGATGTAGTGGCAAAA	5757	Db	4773	---AAATCCCTATTTTACAGGSCCAATCTCTCTCAGACCATCCCAAGTAGTCAAGGCC	4717
Qy	3726	GTTGGCCCATATGCTGAAGCTATCGAGCTGGGCCATCTAGTCAAGGACGCTGAC	3785	Qy	4791	TGTGTGCCCTGCGAGCTGTTTAAATGC---TAACTCTCCAGAAATGCTCCAGGGAGAGA	4847
Db	5756	GGCTGGCCCTTACTGTTTATGGGTAGTTGCAGAGTGGCCATCTTAGTATCGAGGCTATC	5697	Db	4716	TGTGAGGTGTGCCAAAGGAATAATCCCTTGCTTCCATATAAGGCCCTCTCGGGGAAACA	4657
Qy	3786	AAATGACTTTTGGGACAGATATTAATCTGTAATAGCCCCCATGCAATGGAGAAATCGTT	3845	Qy	4848	CTAAGGGAAGCCACCCAGGCGCTCACTGGGAAGTGGACTTCACTAGAGGTAAAGCCGCT	4907
Db	5696	AAATATACAAAGAAAGATCTCACTCTCTGGACTACTAATGATGTAATGGGCATACTA	5637	Db	4656	AGAATAGGGCACTACTTAGGAGAAAGACTGGCAGTTAGACTTCGCCCAT---ATGCTAAG	4600
				Qy	4908	AAATACGGAACAAATACCTATTGTTTTTTGTAGACACCTTTTTCAGGATGGGTAGAGCT	4967

Db	4599	TCAAGGGGATTTCAATACCTTTGTTGGTCTGTTGTGATACCTTTGCAAAATGGATGAAGCCT	4540
Qy	4968	TATCCTACTAAGAAAGAGACTTCAACCGTGGTGGCTAAAAAAATACTGGGAAGAAATTTTT	5027
Db	4539	TGTCCTGC-AAGACAGAGAAGGCTCAAGAAGTGGTTAAGCTCTAAATTCATGAAGTAATT	4481
Qy	5028	CCAAGATTTGGATACCTTAGGTAATAGGGTCAGACAATGGTCAGACTTTTGTGGCCAG	5087
Db	4480	CCTAGATTTGGGCTTCCCAAGGTTCAAAAGTGACAATGGTCTGGGCTTTTAAAGCCATG	4421
Qy	5088	GTAAGTCAGGCACTGGCCAAGATATTGGGGATTGATTGGAAACTGCAATTGTGCATACAGA	5147
Db	4420	GTAAGTCAGGCACTGGCCAAGATATTGGGGATTGATTGGAAACTGCAATTGTGCATACAGA	5147
Qy	5148	CCCCAAAGCTCAGGACAGG	5166
Db	4360	CCAAATCCTCAGGAAAAG	4342

RESULT 10

US-10-821-234-357

Sequence 357, Application US/10821234

Publication No. US2005025114A1

GENERAL INFORMATION:

APPLICANT: Labat, Ivan

APPLICANT: Stache-Crain, Birgit

APPLICANT: Andarmani, Susan

APPLICANT: Tang, Y. Tom

TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia

FILE REFERENCE: 821A

CURRENT APPLICATION NUMBER: US/10/821.234

CURRENT FILING DATE: 2004-04-07

PRIOR APPLICATION NUMBER: US 60/462,047

PRIOR FILING DATE: 2003-04-07

NUMBER OF SEQ ID NOS: 1704

SOFTWARE: pc_seq_genes Version 1.0

SEQ ID NO 357

LENGTH: 5234

TYPE: DNA

ORGANISM: Homo sapiens

US-10-821-234-357

Db	2229	TTCACTGGAGCTGACCCCTGACACCCCTCCAGTCAACAACACTCACTAGATGGACTGTCCTCCCT	2288
Qy	3081	CAAGGGTTCAAGAACTCCCGAGCATCTTTTGACGAAGCCCTACACAGAGACCTGGCGAAC	3140
Db	2289	CAGGCTTCAGGA----TAGCCCTCTTTTGGACAAGCTCTAGCCGAAACCTCACATTCC	2344
Qy	3141	TTCAGGATCAACAACCCCTCAGGTGACCCCTCTCCAGTACGTGATGACCTGCTTCTGGCG	3200
Db	2345	TTAAACCTGTCTCCAGTCAT-----CTTCAATATGTGACGACCTTCTCTTTTGC	2395
Qy	3201	GGAGCCACCAACAGGACTCTTTAGAGGCACGAAGCCACTACTGCTGGAAATGT---CT	3257
Db	2396	AGCCCTCTCTAAAGAAGACTCTAAACTCACAGGCCACTGCTCTCTTAAACTTCTCGCT	2455
Qy	3258	GACCTAGGCTACAGAGCTCTGTCTAAGAGGCCACAGATTTGCAGGAGAGAGGTAAACATAC	3317
Db	2456	ATCAAGGGTATAGGGTCTCCCTCCAAGGCCAACTCTCCATCTCCATGATGACTTAC	2515
Qy	3318	TTGGGGTACAGTTTTCGGGACGGGACGAGTGGCTGACGGAGGACGGGAAGAAACGTGTA	3377
Db	2516	TTAGGAATTCAACTTTCCCTTGGGCCAGGCTATGACTCAGCCAGGGCAGCATTAATA	2575
Qy	3378	GTCAGATACGGGCCCCAAACACAGCCAAACAATAGAGAGTTTTTGGGGACAGCTGGA	3437
Db	2576	GAAATCTACCCCCACCCTCTCCAAAGCGAAATCCCTTTCTTCCAGGGCTAGCAGGC	2635
Qy	3438	TTTTGCAGACTGTGATCCCGGGTTTGACACTTAGCAGCCCACTCTACCCGCTAAC	3497
Db	2636	TTCTTTAGAATATGGATTTCAACTTTGCCCTCTAGCTCATCCCTCTATGAAGTGCC	2695
Qy	3498	AAAG-----AAAAAGGGGAATTTCTCTGGGCTCTTGAGCACCAAGAGGCAATTTGATGCT	3551
Db	2696	AAAGCCCTCCCAATGAACCCCTAAACCCCTCAATAAATACTCCCCAGCTCCACAA	2755
Qy	3552	ATCAAAAGGCCCTCTGAGGGACCTGCTCTGGCCCTCCCTGAGCTAACTAAACCTTT	3611
Db	2756	CTCAAACTGCTCTGTCTACCTGGGTACAGTCCGCTTACTGATATCTCCCAACCTTTC	2815
Qy	3612	ACCTTTATGTGATGACGTGAAGGAGTAGCCGGGGAGTTTTAAACCCAAACCTAGGA	3671
Db	2816	ACTCTATACTGCTGAAAGCTGAGGAATAGCCCTCGGTGCTTTAGACAACAGAAAGGA	2875
Qy	3672	-----CCATGGAGAACCTGTGCGCTACTGTCTCAAAGAAGCTCGATCTCTGTAGCCAGT	3725
Db	2876	AACTCTCTCTTTGCCCCCTGTAGCTTACTCTCTAAACAATAGATAACAGTCAA	2935
Qy	3726	GGTTGGCCCATATGCTCTGAAGGTATCGAGAGCTGTGGCCATATCTGTTCAAGGACCTGAC	3785
Db	2936	GGTGGCCAGCTGCTTTTAAAGCACTAGAAAGTGGTAGCCAGCTTAGCTCTAGAAGACGG	2995
Qy	3786	AAATTGACTTTGGACAGAAATAAATGTAATAGCCCCCATGCTATGGAGACATCGTT	3845
Db	2996	AAACTAACTTTCAGCCAGAAATACACCGTCCACAGTTCTCATAACTTCAAGATCTCCTC	3055
Qy	3846	CGGACGCCCCAGACCGATGGATGACCAAGCCCGCATGACCCCACTATCAAAGCTCGTT	3905
Db	3056	TCCTCCCAAGAGTAAGCTCCCTCTCTCTCCAGGATTCNAATTACTCCATGCCCTCTT	3115
Qy	3906	CTCACAGA---GAGGGTCACTTGGCTCCACACGCGCTCTCAACCTCGCCATCTTTCTG	3962
Db	3116	ATAAAAAATCCAAATTCAGTCTTACCAGAAGTGCTTCCCTCAACCCAGCATCTCTATCTC	3175
Qy	3963	CCTGAAGAGCTATGAACCGTAGCTCATGATGGCCATCACTATTGATTGGAGACT	4022
Db	3176	CCCGTATCTCTTCCCTTCC---TACTCATTTCTTCCACTGATATCTCTGGACCGATACAG	3232
Qy	4023	GGGTCCGCAAGGACCTTACAGACATACCGCTGACTGGAGAAGTGCTAAACCTGGTCTCACT	4082
Db	3233	CCACATTTCCCAACACTTCTCTCGAGCTCTCACCAACCCCAATGATCAACTATTATA	3292
Qy	4083	GACGGAAAGCACTATGTGGTGAAGGTGAAGAGATGCTGGGGCGCGGTGGTGGACGGG	4142
Db	3293	GATGGCTCTCTTCCAGGCCCAACAGCTACCCCCAGAT-----TGCTGGATATG	3342

Query Match	3.1%; Score 253.6; DB 7; Length 5234;
Best Local Similarity	47.8%; Pred. No. 5.1e-63;
Matches 1232; Conservative	0; Mismatches 1269; Indels 77; Gaps 14;
Qy	2661 ATTCAACTGAAGGCCAGTGCACACACAGTGTCAGTCAGACAGTACCCCTTGAGTAAAGAA 2720
Db	1872 ATCCAGGTAAAGAGACTCTTCAAAATTTCCCGACGGTCTCCTCAATACCCGCATCTCTCTAACC 1931
Qy	2721 GCTCAAGAGGAATTCGSCGCGCATGTCCTCAAGATTATTCACACAGGCGATCCCTAGTTCCCT 2780
Db	1932 CACCAAAAGGGCCCTACAGCCCATCGTAAACAAGCTCTGTCTCATGCGAGTCTTCTTAGACCA 1991
Qy	2781 GTCCAAATCTCCCTGGAAATATCTCCCTCTGTACCGGTAGAAAGCCTGGAGTAATGACTAT 2840
Db	1992 ACACACTCTCCATATACACCCCTATCTCTCCTGTTAAAAGTCTG---ATGGCTCATAC 2048
Qy	2841 CGACAGTACAGGACTTTGAGAGAGGTCAATAAACGGGTGCAGGATATACACCCAACAGTC 2900
Db	2049 CGACTCGTTCAACAACCTCCAAGCCATCAGTCAAGCTGTCTCCCTATTATCCCATAGTC 2108
Qy	2901 CCGAACCCCTTATAACCTCTTGTGTGCTCTCCACCCCAACGGAGCTGGTATACAGTATTG 2960
Db	2109 CATAAACCCCTATCCACTTCTCTCTCGTGTACCAACACCAACCCCTCTACACTGCAATT 2168
Qy	2961 GACTTAAAGGATGCTTCTTCTGCTCGATTTACACCCCACTAGCCAAACACACTTTTGGCC 3020
Db	2169 GACCTGAAGGATGCTTCTTTTACCATTTCCTCCCTACACCCCTGATTCCTCCAAAACCTTATTGCT 2228
Qy	3021 TTCCGAATGGAGAGATCCAGGTACGGGAGAACCGGGCAGCTTCACCTCGACCCGACTGCC 3080

4143 ACCGACACGATCTGGGCGCAGCAGCTGCGGAAGGAATTTTCAGCACAAAGGCTGAGCTC 4202
4144 |||||
3343 CAGTTGTTTCTTACCAAGTAATTAAGACCCAGGATCTCTCCCAAAAGCAGAACTC 3402
4203 ATGGCCCTACGCAAGCTTTTGGGCTGGCGGAAGGGAATTCATAACATTTATACGGAC 4262
4204 |||||
3403 ATAGCTCTACACAGGCGCCCTAAATCTTTCCAAAGGCAACAGAGTCAACATTTATACAGAC 3462
4263 AGCAGGTATGCTTTGGACGTGCACAGTACATGGGCGCATCTATAAACAAAGGGGGTTG 4322
4264 |||||
3463 TCCAAATATGCTTATCATTCTCTGTTCCCGCTGCTATCTGGCAAAAGAGAGACTC 3522
4323 CTTTACCTCAGCAGGAGGGAATAAAGAACAAAGAGGAATTTCTAAGCCCTATTAGAAGCC 4382
4324 |||||
3523 CTTTACTGCCAAAGAACCCCTATCACTAATGGCCACCTTATTTACTAACTCTCTCAGGCC 3582
4383 GTACATTTTCAAAAAGGCTAGTATTAATACATCTGTCTGGACATCAGAAAGCTAAAGAT 4442
4384 |||||
3583 ACACACCTCCAGCTAAAGCAGGAGTTATACACTGTTGAGGACATCGAACAGGTTTCAGAT 3642
4443 CTATATCCAGGAACAGATGGCTGACCGGGTTGCCAAGCAGGAGCCAGGCGTTT 4502
3643 GAAATCTCAAAAGGAATAGAAAGACCGCAGGAGCAGCAAAACAGGACTCCCTTTCTCT 3702
4503 AACCTTCTGCTTATATAGAAATGCCCAAGCCCCAGAACCCAGACGACAGTACACCCCTA 4562
3703 CTCTGCTGCCCATCTCTCTTGTGTCACCCAGCAGTCCCGCCAGATACCTCCCACTGAA 3762
4563 GAAGACTGGCAAGAGATATAAAGAGATAGACAGTCTCTGAGACTCCGGGAAGGACCTGC 4622
3763 AAGTCTTTCAC-----TACTACAGCAGGAGCTCCCTTCAAGGGGACTGG 3807
4623 TATACCTCAGATGGGAAGGAATCCTGCCCAACAAGAGGTTAGATATGTCCACAG 4682
3808 ATAATCAAAATCAAAAGCCGTGTTCTTCCCAAGAGCAAGCAAGGAATTTCTAAACCT 3867
4683 ATACATCGTCTAACCCACCTTAGGAATCAACACCTCGCAGCATGTGTC-----AGAA 4734
3868 CTTTACCAACCCCTTCATATCAGTGATGCCCATACCTACTCTCTCGCCCTGTTTCT 3927
4735 CATCCCTTATCATGTTCTGAGGCTACAGGAGTGGCTGACTCGGTGGTCAAAACATGTG 4794
3928 CTTCCCTCCCATCTATTCTCATCTAAAGGACATAAAGCTCAAGTGTGATATGCTCTG 3987
4795 TGCCCTGCCAGCTGGTTAATGCTAATCTTCCAGATGCTCTCCAGGGAAGAGACTAAGG 4854
3988 TTAATCTCTCCCAAGGGGCGCTCTGCGCTCTCTCTCATCTTACATACCAG---CTCAG 4044
4855 GAAGCCACCCAGGCGCTCACTGGGAAGTGGACTTCACTGAGGTAAAGCCGGCTAAATACG 4914
4045 GAACACTCCAGGGGAGACTGGCAAGTAACCTTCCACCATGCTCCCGCTCCGTCANAAA-- 4102
4915 GAAACAAATACCTATTGGTTTTGTAGACACCTTTTTCAGGATGGGTAGAGCTTATCCTA 4974
4103 -ATCTAATATCTTCTTACCTCGTAGACACTTTTTCAGGTTGAGTAGAAGCATTTCCCTA 4161
4975 CTAAGAAGAGACTTCAACCGTGTGGTGAATAAATACTGGAAGAAATTTTTCGAAGAT 5034
4162 CCCCCTTCAGAAAAGCTGCGAAGTCTCTCAAAATCTTGTGAACAGAAATCATCTCCTAGAT 4221
5035 TTGGAATACCTTAAGGTATAGGTTACAGCATGTGCTCCAGCTTTTGTGGCCAGGTAGTC 5094
4222 TTGCTCTCCCTGGCTCCATACATCAGACATATCCCATATCCCATGCTGGCCCCAGA 4280
5095 AGGACTGGCCCAAGATATGGGGATGTATTGGAACCTGCAATGTGTCATACAGACCCCAAA 5154
4281 AACAGGTTTCTCAGTCCCTTGGCATCCAGTGGCTCTCCATATCCCATGCTGGCCCCAGA 4340
5155 GCTCAGGACAGGTAGAGAGGATGAATAGAACCATTAAGAGACCTTACTTAAATGTAC 5212
4341 CATCCGGAAGAGTGCAGAAAGGCAATGGGATCTCTTAAGGCTCACTTAAACCAAACTCAC 4398

RESULT 11

US-10-995-561-13264/c
; Sequence 13264, Application US/10995561
; Publication No. US20050272054A1

; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF

; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24

; NUMBER OF SEQ ID NOS: 85702

; SOFTWARE: PastSeq for Windows Version 4.0

; SEQ ID NO 13264

; LENGTH: 110711

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: misc feature

; LOCATION: (1)....(110711)

; OTHER INFORMATION: n = A,T,C or G, or insertion/deletion polymorphism (see Tables 1

US-10-995-561-13264

Query Match 2.7%; Score 218.4; DB 7; Length 110711;
Best Local Similarity 49.3%; Pred. No. 1.2e-51;
Matches 914; Conservative 5; Mismatches 891; Indels 44; Gaps 12;

Qy 2652 CCACAATGTTATTCACCTGAAGGCCAGTGGCCACACCACTGTCAGTCAGACAGTACCCCTTG 2711
Db 55744 CCTATAGCAATTCAGCTCAAGGATCTCTAGTTATCTCTTGCAGAGGGCAGTTTCTCTT 55685

Qy 2712 AGTAAAGAGCTCAAGAGGAATTCGGCCGCATGTCCTCAAGATTTAAATCCCAACAGGGCATC 2771

Db 55684 CAGTTGAGGCCAAAGAGGACCTTCAGCCCTGATTTAAATTTCTTAAACATGG---A 55628

Qy 2772 CTAGTTCTCTGTCACATCTCCCTGGAAATATCTCCCTGCTACCGTTAGAAAGCCCTGGGACT 2831

Db 55627 TTAATATCTCTGTAATCACTACCTATATACACCCCTATCTTAACTGTGTTAAAGAGACT---AAC 55571

Qy 2832 AATGACTATCGACGACGATGACGAGCTTGAAGAGTCAATTAACGGGTGACGATATACAC 2891

Db 55570 GGAGAATACAGGTTAGTCCAGAAATCTGTAGTCAATAAGGAGGAGTGTCCGGAATACAC 55511

Qy 2892 CCACAGTCCCGAACCTTATAACCTCTGTGTGCTCTCCACCCCAACGGAGCTGGTAT 2951

Db 55510 CCAATGTGCTCCCAACCTTTATGTAATCTTAGAAGATTTCCAGATGCTCAG---TGGTTT 55455

Qy 2952 ACAGTATGGACTTTAAAGGATGCTCTTCTGCTGAGATTTACACCCCACTAGCCCAACCA 3011

Db 55454 TCGGCTTAGACTTTCAAAAT---TTCTTCTGTATCCCTTAGACCATCTCTCCCAATTT 55398

Qy 3012 CTTTGTGCTTTCGAATGGAGAGATCCAGGTACGGGAAGAACCCGGGAGCTCAGCTGACCC 3071

Db 55397 ATATTTGTAATGGAGTTGGAGAAATGAA---AAAGGAAGAAATTTAAAGCTCAGCTGACCA 55341

Qy 3072 CGAGTCCCAAGGTTCAAGNACTCCCGACCATCTTTGACGAAGCCCTACACAGAGAC 3131

Db 55340 GTGCTTCCAAAGGTTTCAGAGATGATCCCATTTGTTTGGGCAAGCCTTGGCTAGATAT 55281

Qy 3132 CTGGCCAACTTCAGGATCCAAACACCTTCAGGTGACCCCTCTCTCAGTACGTGGATGACCTG 3191

Db 55280 TTGAGGACCTAAGTCTTTATATGGG---AGGGCATCTCTCTACAGTACATGATGACCTG 55224

Qy 3192 CTTTCTGGGGAGCCCAACCAAGAGTGTCTTAGAAGGCGAAGAGGCACTACTCTGCGAA 3251

Db 55223 TTAATC-----TGCTCCCAACCAAGAGAGTTAGGAATCCCAACTCTAAATTTCTCTGCA- 55170

Qy 3252 TTGCTCAGCTAGCTACAGGCTCTGCTTAAGAGGCCCGCAGATTTGCAGGAGAGAGGTA 3311

Db 55169 -----GACGAAGGTAACAAAGTGTCCAAGGCCCAAGACACAGCTACTTAAGACAAGCAATC 55116

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QY 3312 ACATACCTGGGGTACAGTTTGGGGACGGGCGAGCGGATGCTGACGGAGGCACGGAAGAAA 3371
Db |||||
QY 55115 CAATACCTGGGATATCATGAGCCTCAAGAAACAAGAGCTTTCTGCAGATAGATACAG 55056
Db |||||
QY 3372 ACTGTAGTCAGATCCGCCCCACACAGCCAAACAAATGAGAGAGTTTGGGGACA 3431
Db |||||
QY 55055 GCAATCCTTAGAATACTA-CACCAACCCCAAAAGCAATTTGAGCTTTCTGGGGATC 54997
Db |||||
QY 3432 GCTGGATTTGCAGACTGGGATCCCGGGTTTGGGACCTTAGCAGCCCCACTCTACCG 3491
Db |||||
QY 54996 ACAAGATATCGAGACTTTGGATCTGGATCTGGTGAATTTATAATCCTTATATCAG 54937
Db |||||
QY 3492 CTAACCAAG-----AAAAAGGGGAATTCCTCTGGGCTCCTGAGCACCAAGAGGAT 3543
Db |||||
QY 54936 GCTTTAAAAGAGGGACTAATAGGAGACAAATCTCTGGGAAAAGAAATCAGGAGCAAGCCT 54877
Db |||||
QY 3544 TTGATGCTATCAAAAAGGCCCTGCTGAGCGCAGCTGCTGCGCCCTCCCTGAGCTAACTA 3603
Db |||||
QY 54876 TTAGGTAGTTAAAAAGTGCCCTCTCAAGAGCCCGAGCCCTTGAGCTACCCTACTAACCA 54817
Db |||||
QY 3604 AACCCCTTTACCTTTATGTGGATG-AGCGTAAGGGAGTAGCCCGGGGAGTTTAAACCCAA 3662
Db |||||
QY 54816 AACCATTCAGTTTTCATCACTGAAAGGCAAGGTATAGCACTAGGAGTTCTTAAGTAA 54757
Db |||||
QY 3663 ACCCTAGGACCATGGAGAGACCTGTGCGCTACCTGTCAAAGAGCTCGATCCTGTAGCC 3722
Db |||||
QY 54756 ACCTTTGGGCCAGTCAAAACATGCTGTAGGTTATTTTCAAAGAACCTTAGACCCAGCAGCA 54697
Db |||||
QY 3723 AGTGGTTGGCCCATATGCTGAGAGCTATCGGAGCTGTGGCCATCTAGTCAAGAGCGT 3782
Db |||||
QY 54696 CAATGGTGGCCCATTTGCCCTCAAGGTAGTGGGTACAGAGCCCTTATTTCTCAGAGGAG 54637
Db |||||
QY 3783 GACAAATTCACCTTTGGGACAGAAATAAAGTAAATAGCCCCCAGTCATTTGGAGAACATC 3842
Db |||||
QY 54636 TTCARTATCAATGGGACAAATCAATCTGGCTCCTATGTCCTCCACCAATAGACCTTTA 54577
Db |||||
QY 3843 GTTGGGACGCCCGAGACCGATGGATGACCAACGGCCCGCATGACCCACTATCAAGCCCTG 3902
Db |||||
QY 54576 TTGAAATTTAAAGGACCAATAATGGCTCACTGACCAACACATTTGATAAAGTACCAAGTCTTG 54517
Db |||||
QY 3903 CTTCTCAGAGA--GAGGGTCAGTTCGCTCCACGAGCGCTCTCAACCTGCCACTCTT 3959
Db |||||
QY 54516 TTGTTGGAAACCCACAGGTAAACAGTTGAGCAGTGTTCACCACTTAACCCAGCCCTCTTA 54457
Db |||||
QY 3960 CTGCTTGAAGAGACTGATCAACCCAGTGACTCATGATTGGCATCAACTATTGATTGAGGAG 4019
Db |||||
QY 54456 CTGCCACTACGAGGATGATTAACCAATATTCATGCTGTGAGATTTCTTAACAAATTT 54397
Db |||||
QY 4020 ACTGGGGTCCGCAAGGACCTTACAGACATACCGCTGACTGGAGAAAGTGCTAAACCTGGTTC 4079
Db |||||
QY 54396 TATGCCAGCTGGGAAGACTTAAAGGATCAGCCCATAGATAATCCAGACAAATATGTTT 54337
Db |||||
QY 4080 ACTGACGGAAGCAGCTATGTGTGGAGAGTAAGAGATGGCTGGGGCGCGGTGTGGAC 4139
Db |||||
QY 54336 TCAGATGGGCMGTAGCTTCGTCTAGGGGTGGAACCTAGATATGCAAGGTTATCTACAGAGTCC 54277
Db |||||
QY 4140 GGGACCCGACGATCTGGGCCAGCAGCTCGCGGAAGGAACCTTCAGCACAAAAGGCTGAG 4199
Db |||||
QY 54276 CATCAACCAAGTTGTAGAGACTAAAGCTCTGTCCCAGGAGCCTCAGTGCAACTAGCCGAA 54217
Db |||||
QY 4200 CTCATGGCCCTCAGCAAGCTTTTGGCGCTGGCGGAAGGGAATTCATAAACATTTATACG 4259
Db |||||
QY 54216 TTCATCACACTAACAGAGCCCTTAAAGCTAGGGGAAGAAAGAAATAACCATCTATACA 54157
Db |||||
QY 4260 GACAGCAGTATGCTTTTGGAGCTGACACAGGTATACATGGGGCCCTCTATATAACAAAGGGGG 4319
Db |||||
QY 54156 GATTCAAATATGCTTCTTGGTGTCTCATGCCACATGGCTATCTGGAAGGAAGAAGG 54097
Db |||||
QY 4320 TTGCTTACCTCAGCAGGGGAGGAAATAAAGAACAAAGAGGAATTTCTAAGCCTATTAGAA 4379
Db |||||
QY 54096 TACCTAACAGCTCAGGATGCTCTTAAAGTATGGGTCTCAATCTTAGAGCTACTGGAG 54037
Db |||||
QY 4380 GCGGTACATTTTACCAAAAAGGCTAGCTATTATACACTGCTCGGACATCAGAAAGCTAAA 4439
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Db 54036 GCTGCTCATTTGCCCCCAGGAAGTGCAGTAGAGCAATTTGAAGGACACACAGGGGCTTC 53977
QY 4440 GATCTCATATCCAGAGGAAACAGATGGCTGACCGGTTGCCAAGCAGGACGCC 4493
Db 53976 TATTAACTACATGGGGAAACAGGTAGCTGACAAAAYGCTGAGAGGCGGCC 53923

RESULT 12
US-11-136-527-3585/c
; Sequence 3585, Application US/11136527
; Publication No. US20050287570A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
; FILE REFERENCE: 031896-041000 (AM101086)
; CURRENT APPLICATION NUMBER: US/11/136,527
; CURRENT FILING DATE: 2005-05-25
; PRIOR APPLICATION NUMBER: US 60/574,294
; PRIOR FILING DATE: 2005-05-26
; NUMBER OF SEQ ID NOS: 362830
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3585
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-11-136-527-3585
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Query Match 2.5%; Score 202; DB 8; Length 13187;
Best Local Similarity 61.8%; Pred. No. 1.5e-47;
Matches 376; Conservative 0; Mismatches 220; Indels 12; Gaps 3;

QY 4619 CTGCTATACCTCAGATGGGAAGAAATCCTGCCCCACAAAGAGGGTTAGAATATGTCCA 4678
Db |||||
QY 3807 CTGGTACACCTCAAGGGAAGAGATCTGCTACAAAACAGGAGGAGCCATGATAA 3748
Db |||||
QY 4679 ACAGATACATCGTCTAAACCCACCTAGGAACCTAAACCTGCGAGCAGTTGGTCAGAACATC 4738
Db |||||
QY 3747 ACAAT-----GGACTCACTTAGGGTAAAGCAAACTCATCCAGATGTTTCAAAAAC 3696
Db |||||
QY 4739 CCCTTATCATGTTCTGAGGCTACAGGAGTGCTGACTCGGTGGTCAACATGTGTGCC 4798
Db |||||
QY 3695 TAAATATTATTGTACAGGTCTCAAAATATCTCGTGGAAACAGATAGTACACTGATGTATACT 3636
Db |||||
QY 4799 CTGCCAGCTGGTTAATGCTTAATCCTTCCAGAAATGCTCCAGGGAAGAGACTAAGGGGAAG 4858
Db |||||
QY 3635 ATGCCAAAGGTAA---CTGTTTTCAGGAAGTTGACTGTGTAGGAGGCTCCGTGGGA 3579
Db |||||
QY 4859 CCACCCAGCGCTCACTGGGAAGTGGACTTCACTGAGGTAAAGCCGGCTAAATACGGA 4918
Db |||||
QY 3578 ACAGCCTGGATCCTACTGAGAAGTGGACTTTCACAGAGATAAAAACAGGAATAATATGATTT 3519
Db |||||
QY 4919 GAAATACCTATTGGTTTTTGTAGACACCTTTTCAGG-ATGGGTAGAGGCTTATCCTACTA 4977
Db |||||
QY 3518 CAAATGTCTCCTAGTGTATTATAGATATCTTTTCAGGAATAGGTAAAGTTTTCACCA 3459
Db |||||
QY 4978 AGAAGAGACTTCAACCGTGGTGGCTTAAATAATACTGGAAGAAATTTTTCAGAAATTTG 5037
Db |||||
QY 3458 ACAAGAGAGCGCTCAATAGTATCATCAGAGATACTAGAGAAATCTTCTCCCTGTTG 3399
Db |||||
QY 5038 GAATACCTAAGGTAATAGGGTCAGACAAATGGTCCAGTGTGTGCCCCAGGTAAGTCAGG 5097
Db |||||
QY 3398 GAGTGCCCAAGTTAATTTGGGTGAGACACTGGCCCTCGCTTCGTTGTCAAGAGTAAGCCAGA 3339
Db |||||
QY 5098 GACTGGCCAGATATTGGGGATTGTAAGAACTGCAATGCTGTCATACAGACCCCAAGCT 5157
Db |||||
QY 3338 GTGTGGCCAGGTATTTAGAGGTCAATTAATAATATTATTCATCTACAGACCTTCAAGGT 3279
Db |||||
QY 5158 CAGGACAGGTAGAGAGTGAATAGAACCATTTAAAGAGAGCCCTTACTATAATGACCGCG 5217
Db |||||
QY 3278 CAGGACAGGTAGAGAGATAAATAAATTTTAAAGAGAGCCCTGACTAATGACTGTGG 3219
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QY 5218 AGACTGGC 5225
Db 3218 AGACTGGC 3211

RESULT 13
US-10-995-561-13227
; Sequence 13227, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13227
; LENGTH: 317876
; TYPE: DNA
; ORGANISM: Homo sapiens
; NAME/KEY: misc feature
; LOCATION: (1)...(317876)
; OTHER INFORMATION: n = A,T,C or G, or insertion/deletion polymorphism (see Tables 1-
US-10-995-561-13227

Query Match 2.5%; Score 200.4; DB 7; Length 317876;
Best Local Similarity 48.5%; Pred. No. 5.1e-46;
Matches 918; Conservative 5; Mismatches 876; Indels 95; Gaps 10;

QY 2601 CCCAAGCCTGGGAGAAACCGCAGGAGTGGTTGGCAAGCAAGTCCGCCCAAGATT 2660
Db 120521 CCTGGAGTCTGGACACTGGAAGGCAATTTGGAAGGTTAAATAATGCCACCCAGTCCAA 120580

QY 2661 ATTCACCTGAAGCCAGTGGCCACACCAAGTGTCACTGACAGAGTACCCTTGAGTAAAGAA 2720
Db 120581 ATCAGGCTAAAGAACCCACCACTTTTCCTTATCAAGGCCATATCCCTCAAGCCCTGAA 120640

QY 2721 GCTCAAGAAGAAATTCGGCCGCATGTCCAAAGATTAAATCCAAAGGCGCATCTAGTTTCT 2780
Db 120641 GCTCATTAAGGATTACAGGATATTGTTAAACATTTAAAGCTCAAGCTTAGTAAGGAA 120700

QY 2781 GTCCAAATCTCCCTGGAATATCCCTGCTACCGGTTAGAAAGCTGGGACTAATGACTAT 2840
Db 120701 TGCAGCAGTCCCTGCAACACCCCAATTTCTAGGAGTACAATAATCAAAAGGTCTAT---TGG 120757

QY 2841 CGACAGTACAGGACTTGAGAGAGGTCAATAAAGGTTGCGAGGATATACACCCAAAGTC 2900
Db 120758 AGACTAGTGCAGGATCTTGGACTCATCAATGAGTGGTGTCTCTATGTCCAGTTGTA 120817

QY 2901 CCGAACCTTATAACCTCTGTGTGCTCTCCACCCCAAGCGAGCTGTATACAGTATTG 2960
Db 120818 CTGAACCCCTGTACCTGCTCTCAATATGCAAGGAGGAGGAGATGGTTGCTGTTCTG 120877

QY 2961 GACTTAAAGGATGCTTCTTCTGCTGAGATTACACCCACTAGCCAAACCACTTTTGGCC 3020
Db 120878 GACCTCAAGGATGCTTCTTCTGTATTCTCTGCACTCTGACTCCCACTTCTCTTGGCC 120937

QY 3021 TTCGAATGAGAGATCCAGGTACGGGAAGAACCCGGGAGCTCACTTGGACCCGACTGCC 3080
Db 120938 TTTGAGGATA-----CCACAGACCAACRTCCCAACTTATACAGGATGTTGTGCC 120988

QY 3081 CAAGGTTTCAAGAACTCCCGACCATCTTTCAGCAAGCCCTACACAGAGACTCGGCCAAC 3140
Db 120989 CAAGGTTTAGGATAGCCCTTCATCTGTTGCTCAGGACCTGGCCCAAGATCTAGTTAAC 121048

QY 3141 TTCAGGATCCAAACCTTCAGGTGACCCCTCTCCAGTACGTGGATGACCTCTTCTGGCG 3200
Db 121049 TTCTCAAGTCCAGGACCTCTCG-----TCCTTCAATATGTGGATGATTACTTTTGGCT 121102

QY 3201 GGAGCCACCAACAGAGACTGCTTTAGAGGACGAGGACGAGGACTACTGCTGGAATTTGTCGAC 3260
Db 121103 ACCTGTTTGGAGCCTCATCCAGCAGGCGACTCTAGATCTCTTGAATTTCTAGCTAAT 121162

QY 3261 CTAGGCTACAGAGCCTCTGCTAAGAAAGGCCAGATTTGAGGAGAGAGGTAACAATCTTG 3320
Db 121163 CAAGGGTACAAAGCATCTAGGTGGAAGACCCAGCTTTGCTACAGGAGGCAATATCTA 121222

QY 3321 GGGTACAGATTTTGGGACGAGGCGAGCGATGCTGACGAGGACGAGCAAGAAACTGTAGTC 3380
Db 121223 GGCYTAATCTTACCCAGAGGACGAGGCGCTCAGCAAGGAAAGAAAGAGCCTTACACTG 121282

QY 3381 CAGATCCGCGCCCAACACAGCAGCAACAAATAGAGAGTATTTTGGGACAGCTGGATTT 3440
Db 121283 GATTATGCTCACCTTAAGACATTTAAACAGTTTGTGGGGTTCCTTGGAAATCATCGGTTT 121342

QY 3441 TGCAGACTGTGGATCCGGGGTTTGGACCTTAGCAGCCCCACTCTACCCGCTAACCAAA 3500
Db 121343 TGTGACTGTGGATCCCCAGATACAAGGAGATAGCCAGGCCCTCTATCTATCTSTANTCAG 121402

QY 3501 GAAAAAGGG-----GAATTCCTCTGGGCTCTCTGAGCACCAAGAGGCAATTT 3545
Db 121403 GAGACCCAGAGGCAATATCTCATYTAGTAGAATGGAAACGAGGGCAGAAACAGCCTTC 121462

QY 3546 GATGCTATCAAAAAGGCCCTGTGAGCGCACCTGCTCTGCGCCCTCCCTGAGTAACTAAA 3605
Db 121463 AAAACCTTAAAGCAGACCCCTAGTAAAGCTCCAGCTTTAAAGCTTTCC---CACAGGACAA 121519

QY 3606 CCTTTTACCCTTTATGTGGATGAGCGTAAGGAGTAGCCGGGAGTCCCGGGAGTTTAAACCCAAACC 3665
Db 121520 AACTTTTCTTTATACATCACAGAGAGAGCAGGAATAGCTCTTGGGGT-----CCTTAGACT 121575

QY 3666 CTAGGACCATGGAGAAAGCCTGTGCGCTACTGTCAAAAGAGCTCGATCTCTGTAGCCAGT 3725
Db 121576 CATGGGACAAACCCCAACACAGTGGCATACCTAAGTAAGAAAATGATATAGTAGCAATA 121635

QY 3726 GGTGGGCCCATATGCTTGAAGGCTATCGCAGCTGTGGCCCATACCTGGTCAAGGACGCTGAC 3785
Db 121636 G-----TCAGAGGCTATC 121648

QY 3786 AAATTGACTTTGGACAGAAATATACTGTAAATAGCCCCCATGCAATTTGGAGAAATCGTT 3845
Db 121649 AAAATAATAAAGGAAAGGATCTCACTGTCTGGACTACTCATGATGTAATTTGGCATATA 121708

QY 3846 CGGCAGCCCCCAGACCCGATGATGACCAACGCGCCGATGACCCCACTATCAAAAGCTGCTT 3905
Db 121709 GGTGCCAAAGGAAGTTTATGGCTATCAGACAAACGCGCTACTTAGTATACCAGGTGCTACTC 121768

QY 3906 CT---CACAGAGAGGGTCAAGTTTCGCTCCACAGCCGCTCTCAACCTGCGCACTTTCTG 3962
Db 121769 CTTGAGGGACCAAGTGTCTTCAGMTACGTACATGACGCGCCCTCAACCTGCGCACTTTCTC 121828

QY 3963 CTTGAAGAGACTGATGAACCCAGTACTCATGATTTGCCATCAACTATTGATTGAGAGACT 4022
Db 121829 CC---AGAGGATGGGAAACCAATTTGAGCATGACTGCCAACAAATTTATAGTCCAGATTAT 121885

QY 4023 GGGTCCGCAAGGACTTTACAGACATACCGCTGACTGGAGAAGTGTCTAACCTGGTTCCT 4082
Db 121886 GCAGCCTGAGATGATCTTTTCAAGTCCCTTAGCTAATCTGACCTTAACTATATACT 121945

QY 4083 GACCGAAGCAGCTATGTGGTGAAGTAAGAGTATGGCTGGGGCGGGGCTGGTGGACGGG 4142
Db 121946 GATGAAGTTCAITTTTGGAAAAATGGGATACAAAGGAGGCTGTGGCCATAGT---TAGTG 122003

QY 4143 ACCCGCAGATCTGGGGCAGCAGGCTGCGGGAAGAACTTCAGGACAAAGAGGCTGAGTCT 4202
Db 122004 ATGTAACCATACTCAAGTAAGCCCTCTTCCCGCAGGGAACCAACTAGTTTAGAGAACTA 122063

QY 4203 ATGGCCCTCAGCAGGCTTTGCGGCTGCGGAGGAAATCCATAAACTATTATACGAC 4262
Db 122064 GTGGCACTTACTCGAGCCTTAGAACTGGGAAAGGGAAGAAATATGCTGTATACAGT 122123

QY 4263 AGCAGGTATGCTTTTGGACTGCAACGTCATATGGGGCCATCTATATAAAAGGGGGTTG 4322
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Db 122124 AGCAAGTATGCTTATCTAATCTTACATGCCGCTGCAATATGGAAGAAAGGGAGTTTC 122183
QY 4323 CTTACCTCAGCAGGAGGAAATAAAGAAAGAGAAATTTCTAAGCCTATTAGAGCC 4382
Db 122184 CTAACCTCTGGGGAWCCCTATTAAATACCACAGGAATCATGGAGTTATTGCACTCA 122243
QY 4383 GTACATTTTACAAAAAGGCTAGCTATTATACACTGTCCTGGACATCAGAAAGCTAAAGAT 4442
Db 122244 GTGCCAAAACCCAAAGAGGTGGCAGTCTTACACTGCTGAAGCCATCAAAAAGGGGAAGGA 122303
QY 4443 CTCATATCCAGAGGAACACAGATGCTGACCGGG 4476
Db 122304 GAGAGGAGAACGACGACATAAGTGGCTGGCAGAG 122337
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RESULT 14

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US-10-996-217A-20/c
; Sequence 20, Application US/10996217A
; Publication No. US20050266561A1
; GENERAL INFORMATION:
; APPLICANT: Revivicor, Inc.
; TITLE OF INVENTION: Use of Interfering RNA in the Production of Transgenic Animals
; FILE REFERENCE: 10785.105070 REV 1015 US
; CURRENT APPLICATION NUMBER: US/10/996,217A
; CURRENT FILING DATE: 2004-11-22
; PRIOR APPLICATION NUMBER: 60/523,938
; PRIOR FILING DATE: 2003-11-21
; NUMBER OF SEQ ID NOS: 272
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 20
; LENGTH: 203
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-10-996-217A-20
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Query Match 2.2%; Score 182.2; DB 7; Length 203;
Best Local Similarity 93.6%; Pred. No. 4.3e-43; Indels 0; Gaps 0;
Matches 190; Conservative 0; Mismatches 13;

QY 2858 GAGAGAGGTCAATAAAGGGTGCAGGATATACACCAACAGTCCCGAACCCCTTATAACCT 2917
Db 203 GAGAGAGGTCAATAAAGGGTGCAGGACATACACCAACGGTCCCGAACCCCTTATAACCT 144
QY 2918 CTTGTGTGCTCTCCACCCCAACGGAGCTGGTATACAGTATTGGACTTAAAGGATGCCTT 2977
Db 143 CTTGAGCGCCCTCCCGCCCTGAAACGGAACTGGTACACAGTATTGGACTTAAAGGATGCCTT 84
QY 2978 CTTTGCCTGAGATTACACCCACATAGCCACACCTTTTGGCTTCCGAATGGAGATCC 3037
Db 83 CTTTGCCTGAGATTACACCCACATAGCCACACCTTTTGGCTTCCGAATGGAGATCC 24
QY 3038 AGGTACGGGAAGAACCGGGCAGC 3060
Db 23 AGGTACGGGAAGAACCGGGCAGC 1
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RESULT 15

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US-10-996-217A-24/c
; Sequence 24, Application US/10996217A
; Publication No. US20050266561A1
; GENERAL INFORMATION:
; APPLICANT: Revivicor, Inc.
; TITLE OF INVENTION: Use of Interfering RNA in the Production of Transgenic Animals
; FILE REFERENCE: 10785.105070 REV 1015 US
; CURRENT APPLICATION NUMBER: US/10/996,217A
; CURRENT FILING DATE: 2004-11-22
; PRIOR APPLICATION NUMBER: 60/523,938
; PRIOR FILING DATE: 2003-11-21
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; NUMBER OF SEQ ID NOS: 272
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 24
; LENGTH: 180
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-10-996-217A-24

Query Match 2.0%; Score 162.6; DB 7; Length 180;
Best Local Similarity 94.9%; Pred. No. 2.3e-37; Indels 0; Gaps 0;
Matches 168; Conservative 0; Mismatches 9;

QY 2493 AATAACAAACCTATCACTGTGTGTGACCCCTCCCAATTAGATGACGAATATCGACTACTCT 2552
Db 177 AATAACAAACCTATCACTGTGTGTGACCCCTCCCAATTAGATGATGAATATCGACTATATCT 118
QY 2553 CCCCTAGTAAAGCCTGATCAAAATATACAAATCTCTGGTTGGAAACAGTTTCCCAAGCCTGG 2612
Db 117 CCCCAAGTAAAGCCTGATCAGATATACAGTCTCTGGTTGGAGCAGTTTCCCAAGCCTGG 58
QY 2613 GCAGAAACCGCAGGGATGGTTTGGCAAGCAAGTTCCCCCAAGTTATTCAACTG 2669
Db 57 GCAGAAACCGCAGGGATGGTTTGGCAAGCAAGTTCCCCCAAGTTATTCAACTG 1

Search completed: February 5, 2006, 07:04:51
Job time : 1217 secs
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